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(54) **CO-PACKAGING TO MITIGATE INTERMOLECULAR RECOMBINATION**

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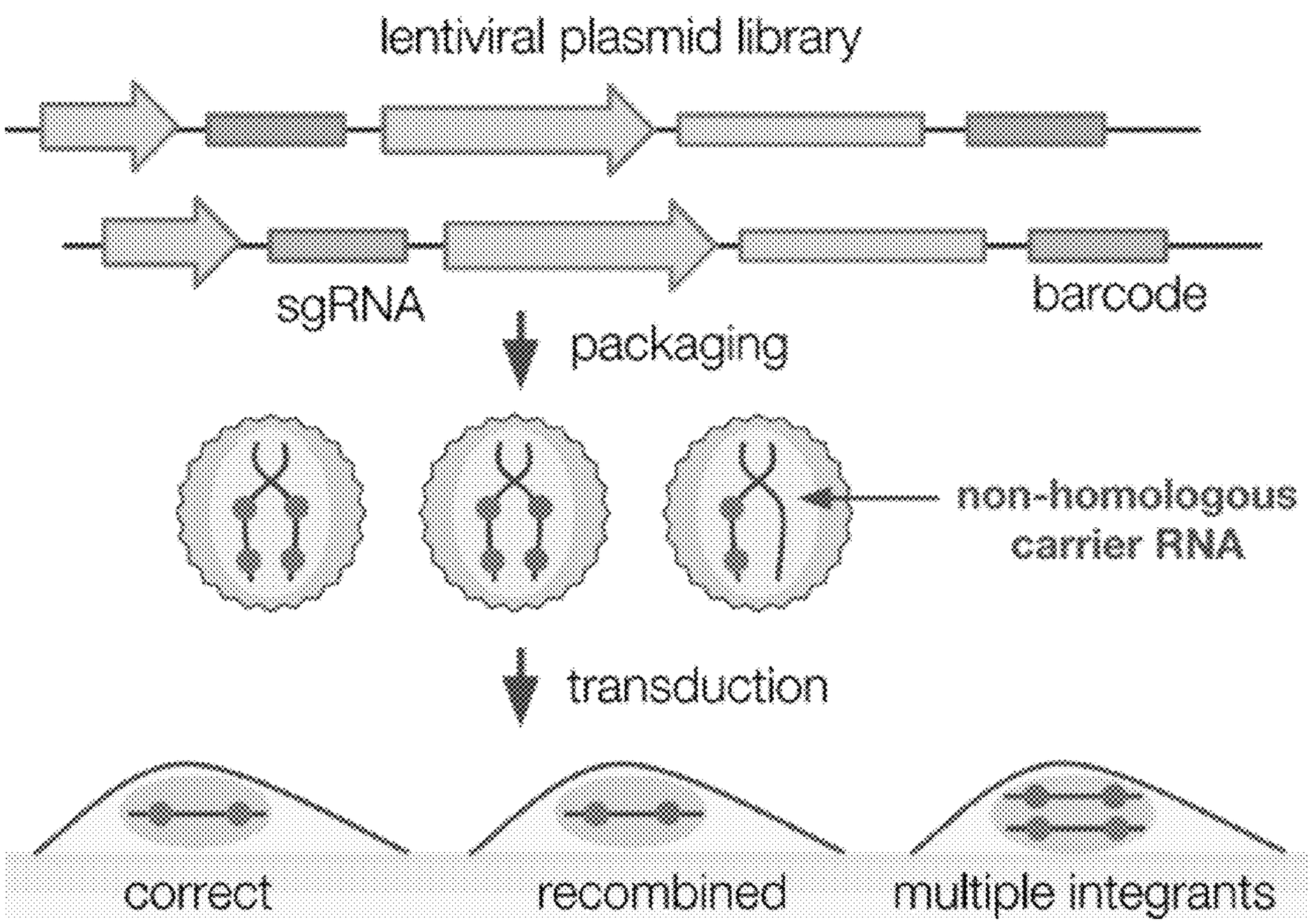
(57) **ABSTRACT**

The subject matter disclosed herein is generally directed to methods and compositions for stable transduction of target cells with libraries of genetic elements. The invention reduces intermolecular recombination between library elements and integration of multiple genetic elements.



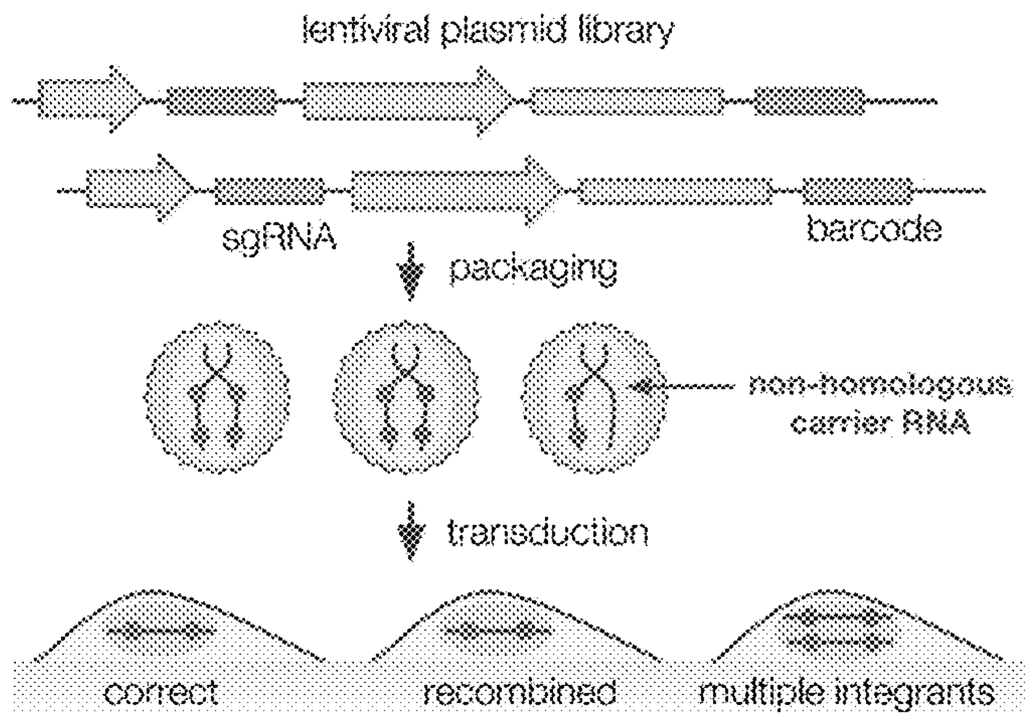

lentiviral plasmid library
sgRNA
barcode
packaging
non-homologous carrier RNA
transduction
correct
recombined
multiple integrants

FIG. 1

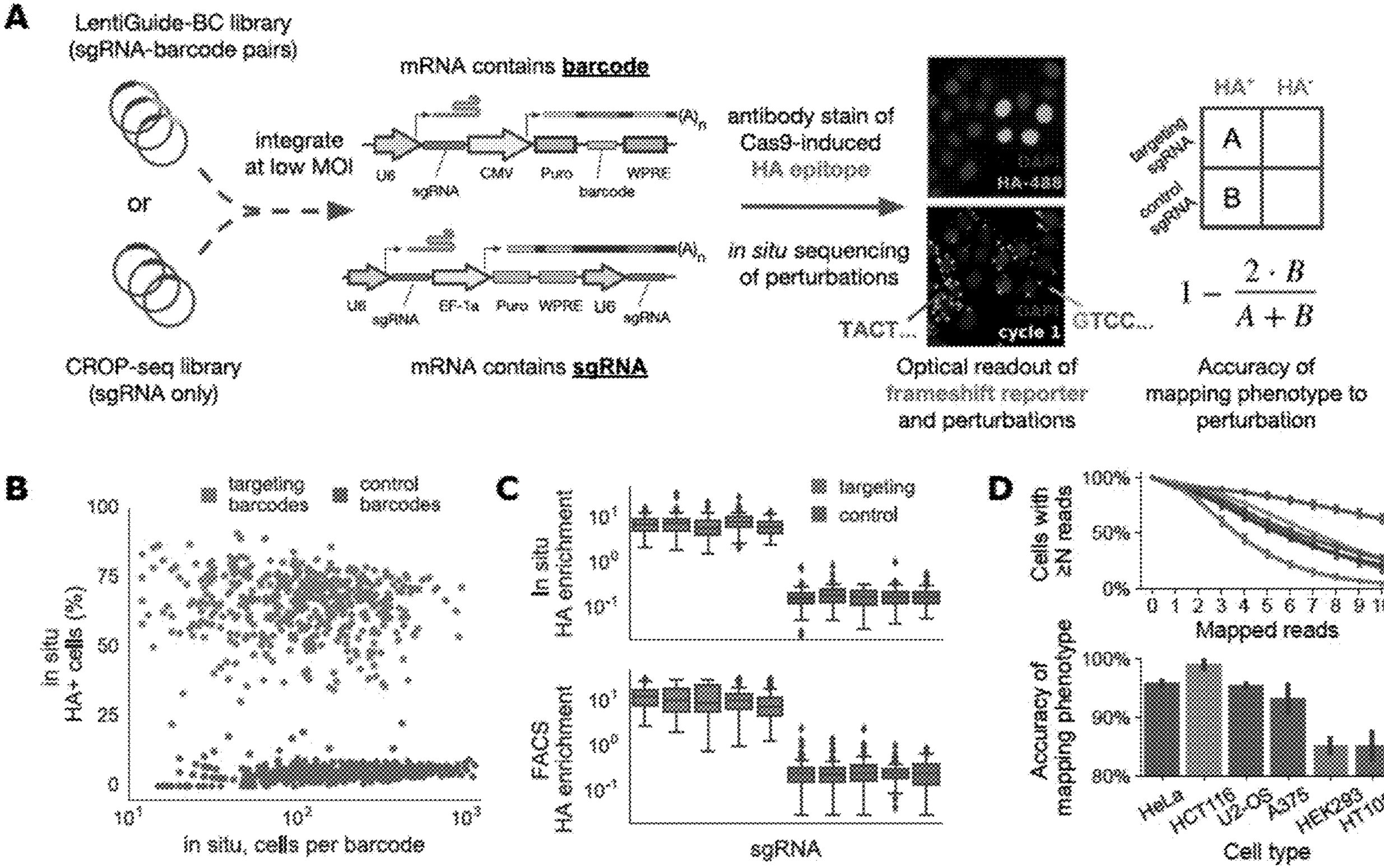

A
LentiGuide-BC library
(sgRNA-barcode pairs)
mRNA contains barcode
integrate
at low MOI
or
U6
sgRNA
CMV
Puro
WPRE
barcode
(A)n
antibody stain of
Cas9-induced
HA epitope
in situ sequencing
of perturbations
HA-488
cycle 1
TACT...
GTCC...
HA+
HA-
targeting sgRNA
control sgRNA
A
B
CROP-seq library
(sgRNA only)
mRNA contains sgRNA
EF-1a
Optical readout of
frameshift reporter
and perturbations
Accuracy of
mapping phenotype to
perturbation
B
targeting barcodes
control barcodes
in situ
HA+ cells (%)
in situ, cells per barcode
C
in situ
HA enrichment
FACS
HA enrichment
targeting
control
sgRNA
D
Cells with
≥N reads
Mapped reads
Accuracy of
mapping phenotype
HeLa
HCT116
U2-OS
A375
HEK293
HT1080
Cell type

FIG. 2

CO-PACKAGING TO MITIGATE INTERMOLECULAR RECOMBINATION

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a Continuation application of U.S. patent application Ser. No. 16/269,138, filed Feb. 6, 2019, which claims the benefit of U.S. Provisional Application No. 62/627,183, filed Feb. 6, 2018. The entire contents of the above-identified application are hereby fully incorporated herein by reference.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

[0002] This invention was made with government support under Grant Nos. HG009283 and HG006193 granted by National Institutes of Health. The government has certain rights in the invention.

REFERENCE TO AN ELECTRONIC SEQUENCE LISTING

[0003] The contents of the electronic sequence listing ("BROD-2465US-CON_ST26.xml", 1,986,453 bytes, created on Dec. 16, 2022) is herein incorporated by reference in its entirety.

TECHNICAL FIELD

[0004] The subject matter disclosed herein is generally directed to methods and compositions for stable transduction of target cells with libraries of genetic elements. The invention reduces intermolecular recombination between library elements and integration of multiple genetic elements.

BACKGROUND

[0005] Lentiviral vectors provide a convenient, scalable platform to deliver genetic perturbations to cells en masse and read out the identity of each perturbation by next-generation sequencing[1,2]. Certain screen modalities rely on the delivery of multiple sequences per lentiviral vector in order to probe gene interactions with combinations of perturbations or to encode the identity of each perturbation in an easily-detectable barcode sequence, such as in CRISPR-based single-cell gene expression screens[3-8]. However, these methods are highly susceptible to intermolecular recombination that scrambles engineered associations between the variable sequences. For screens where all variable elements are sequenced directly (e.g. targeted pairs of gene knockouts), recombination events can be detected and filtered out before statistical analysis[6,9]. However, in situations where certain functional sequences are not read out, such as when a barcode stands in as a proxy for a genetic perturbation, recombination can lead to mislabeled data and has been noted to decrease the statistical power of genetic screens at a given number of cells analyzed[10,11].

[0006] Intermolecular recombination can arise from the template-switching activity of the lentiviral reverse-transcriptase[16]. As the lentivirus capsid normally packages a dimer of RNA genomes, the effect persists even under dilute conditions where cells are infected by a single virion. The fraction of cells with recombined integrants depends on the distance between variable sequences and has been measured to exceed 30% for distances of >1 kb, which may occur when the sequences are separated by regulatory elements such as promoters, or used as 3' barcodes in an expressed transcript, where recombination events can lead to an effective scrambling of barcodes and perturbations, which may be referred to herein as barcode swapping[10-12].

SUMMARY

[0007] The invention provides improved lentiviral or retroviral systems with reduced intermolecular recombination between library elements and reduced integration of multiple genetic elements in a target cell.

[0008] In one aspect, the invention provides a non-naturally occurring lentiviral or retroviral system comprising a polynucleotide having at least a first engineered association and a second engineered association, wherein the system has reduced recombination activity, or template switching activity, or multiple integration activity.

[0009] In an embodiment, the engineered system comprises an inhibitor of recombination activity, or template switching activity, or multiple integration activity. In an embodiment, the inhibitor of template switching is a carrier polynucleotide. The carrier polynucleotide can be involved in or affect any aspect of lentiviral packaging, and functions to reduce recombination activity or template switching activity, or multiple integration. For example, in an embodiment of the invention, the carrier polynucleotide is packaged with or forms a heterodimer with the polynucleotide comprising the one or more engineered associations, but lacks sufficient homology such that recombination activity, template switching activity, or multiple integration activity is reduced or eliminated. In an embodiment of the invention, the reduction in recombination activity, template switching activity, or multiple integration activity can be 2×, 5×, 10×, 20×, 50×, 100×, 500×, 1000× or greater as compared to packaging without the carrier polynucleotide. In packaging reactions, carrier polynucleotides are usually in excess. In certain embodiments, the carrier polynucleotide to payload polynucleotide ratio in packaging is from 5:1 to 10:1 or from 10:1 to 20:1 or from 20:1 to 50:1, or from 50:1 to 100:1 or from 100:1 to 500:1, of from 500:1 to 1000:1 or greater.

[0010] In another embodiment, the inhibitor of recombination activity, or template switching activity, or multiple integration activity can be any carrier polynucleotide transfected into a packaging cell and present with the payload to be packaged, which carrier polynucleotide is not designed to be packaged. Such carriers include, without limitation, single and double stranded DNA, replicable and non-replicable plasmid type vectors, including prokaryotic and eukaryotic vectors. In a non-limiting example set forth herein, bacterial plasmid pUC19, which does not replicate in a packaging cell, is not transcribed, and is not designed to be packaged in a lentiviral particle, is demonstrated to inhibit recombination activity, template switching activity, or multiple integration activity.

[0011] In an embodiment, the inhibitor of recombination activity, or template switching activity, or multiple integration activity comprises a polynucleotide designed to hybridize with all or part of the 5' UTR, including but not limited to such regions as U5-PBS complex or the dimer initiation site (DIS).

[0012] In an embodiment, recombination activity, template switching activity, or multiple integration activity is reduced by rearranging elements of the payload polynucleotide. This includes without limitation, deletion of 5' UTR

elements and/or introduction of 5' UTR elements elsewhere in the sequence of the payload to be packaged. In an embodiment, introduction and/or relocation of the DIS provides lentivirus genomes (e.g., payloads) that package predominantly or completely as monomers.

[0013] In certain embodiments of the invention, recombination activity, template switching activity, or multiple integration activity is modulated by altering interaction of the payload with the capsid. In one embodiment, the lentivirus nucleocapsid (NC) protein is altered by mutating the zinc-finger region so as to disrupt NC-dependent dimerization.

[0014] In an embodiment of the invention, the system comprises a multiplicity of payload polynucleotides, each having at least a first engineered association and a second engineered association. The multiplicity of polynucleotides can be 2, 3, 4, 5, 6, 7, 8, 9, 10 or more and further any number of polynucleotides each having at least a first engineered association and a second engineered association.

[0015] In an embodiment of the invention, the first engineered association comprises a genetic perturbation. In an embodiment of the invention, both the first and the second engineered association each comprises a genetic perturbation. In an embodiment of the invention, the first engineered association comprises a genetic perturbation and the second engineered association comprises an identifier, such as but not limited to a unique molecular identifier. In an embodiment, the unique molecular identifier is a barcode.

[0016] In an embodiment of the invention, the carrier polynucleotide comprises or encodes non-recombinogenic RNA sequences or proteins that are capable of dimerizing with the polynucleotide having engineered associations. In certain embodiments, the RNA sequences or proteins disrupt recombination with the polynucleotide having engineered associations.

[0017] According to the invention the reduced recombination or template activity comprises reduced hairpin formation or dimerization through modification, knockdown or knockout of retroviral genomic RNA or retroviral protein involved in dimerization.

[0018] Further, in certain embodiments, the modification, knockdown or knockout of the retroviral genomic RNA retroviral protein comprises modification, knockdown or knockout of nucleocapsid (NC)-protein(s) or RNA for expression thereof or modification, knockdown or knockout of stem-loop I element (SLI) element or modification, knockdown or knockout of genomic RNA whereby U5.AUG pairing is prevented or modification, knockdown or knockout of a dimer initiation site (DIS).

[0019] In an embodiment of the invention, the polynucleotide sequence encoding one or more genetic perturbations encodes an over expressed gene, an RNAi based system, a zinc finger nuclease, a transcription activator-like effector nuclease (TALEN), a meganuclease, or a CRISPR-Cas system.

[0020] In another embodiment, the sequence encoding one or more genetic perturbations encodes a CRISPR-Cas9 system. In another embodiment, the sequence encoding one or more genetic perturbations encodes one or more guides.

[0021] In an aspect, the invention provides a method of preparing a lentiviral or retroviral system comprising a polynucleotide having at least a first engineered association and a second engineered association wherein the system has reduced recombination activity or template switching activity, or multiple integration activity. In an embodiment of the invention, the reduction can be 2×, 5×, 10×, 20×, 50×, 100×, 500×, 1000× or greater. In an embodiment, the method comprises packaging the polynucleotide with an inhibitor of template switching.

[0022] In an embodiment, the method comprises packaging the polynucleotide with a carrier polynucleotide. As set forth above, the carrier polynucleotide can be involved in or affect any aspect of lentiviral packaging and functions to reduce recombination activity or template switching activity, or multiple integration. In an embodiment of the invention, the method comprises packaging of a multiplicity of polynucleotides, each having at least a first engineered association and a second engineered association. The multiplicity of polynucleotides can be 2, 3, 4, 5, 6, 7, 8, 9, 10 or more and further any number of polynucleotides each having at least a first engineered association and a second engineered association.

[0023] In an embodiment of the invention, the method comprises genetic perturbation. In an embodiment of the invention, both the first and the second engineered association each comprises a genetic perturbation. In an embodiment of the invention the first engineered association comprises a genetic perturbation and the second engineered association comprises an identifier, such as but not limited to a unique molecular identifier. In an embodiment, the unique molecular identifier is a barcode. In an embodiment of the invention the method comprises use of non-recombinogenic RNA sequences or proteins that are capable of dimerizing with the polynucleotide having engineered associations.

[0024] According to the invention, the reduced recombination or template activity comprises reduced hairpin formation or dimerization through modification, knockdown or knockout of retroviral genomic RNA or retroviral protein involved in dimerization. Further, in certain embodiments, the modification, knockdown or knockout of the retroviral protein comprises modification, knockdown or knockout of nucleocapsid (NC)-protein(s) or RNA for expression thereof or modification, knockdown or knockout of stem-loop I element (SLI) element or modification, knockdown or knockout of genomic RNA whereby U5:AUG pairing is prevented or modification, knockdown or knockout of a dimer initiation site (DIS).

[0025] In an aspect, the invention provides a method of preparing a lentiviral or retroviral system comprising a polynucleotide having at least a first engineered association and a second engineered association wherein the system has reduced recombination activity or template switching activity, or multiple integration activity. In an embodiment of the invention, the reduction can be 2×, 5×, 10×, 20×, 50×, 100×, 500×, 1000× or greater. In an embodiment, the method comprises packaging the polynucleotide with an inhibitor of template switching.

[0026] In an embodiment, the method comprises packaging the polynucleotide with a carrier polynucleotide. As set forth above, the carrier polynucleotide can be involved in or affect any aspect of lentiviral packaging and function to reduce recombination activity or template switching activity, or multiple integration activity. In an embodiment of the invention, the method comprises packaging of a multiplicity of polynucleotides, each having at least a first engineered association and a second engineered association. The multiplicity of polynucleotides can be 2, 3, 4, 5, 6, 7, 8, 9, 10 or

more and further any number of polynucleotides each having at least a first engineered association and a second engineered association.

[0027] In an embodiment of the invention, the method comprises a genetic perturbation. In an embodiment of the invention, both the first and the second engineered association each comprises a genetic perturbation. In an embodiment of the invention, the first engineered association comprises a genetic perturbation and the second engineered association comprises an identifier, such as but not limited to a unique molecular identifier. In an embodiment, the unique molecular identifier is a barcode.

[0028] In an embodiment of the invention the method comprises use of non-recombinogenic RNA sequences or proteins that are capable of dimerizing with the polynucleotide having engineered associations. According to the invention, the reduced recombination or template activity comprises reduced hairpin formation or dimerization through modification, knockdown or knockout of retroviral genomic RNA or retroviral protein involved in dimerization.

[0029] Further, in certain embodiments, the modification, knockdown or knockout of the retroviral protein comprises modification, knockdown or knockout of nucleocapsid (NC)-protein(s) or RNA for expression thereof or modification, knockdown or knockout of stem-loop I element (SLI) element or modification, knockdown or knockout of genomic RNA whereby U5.AUG pairing is prevented or modification, knockdown or knockout of a dimer initiation site (DIS).

[0030] Screening using the CRISPR technology and method and systems of the invention is particularly advantageous because of its simplicity, specificity and versatility. For example genome-wide GeCKO and SAM libraries target every gene in the mouse or human genes and knock-out or transcriptionally activate each gene. Alternatively, libraries may be pathway-focused and screened under specific conditions such as by positive or negative selection, to identify important genes in a pathway. In an embodiment, a population of cells may be transfected with a library to knock out or activate certain genes, transfectants of interest identified on the basis of phenotypic screens, and cell products of the transfection identified by a unique molecular identifier originally associated with each gene knocked out, knocked down or activated. In certain embodiments, phenotypic screens identify gene expression profiles which may then be associated with an original transfectant. Generally in such embodiments, genetic elements for knock out, knock down, or activation are each associated in the library with an identifier, which can be but is not limited to a unique molecular identifier such as a barcode.

[0031] Lentiviral packaged libraries include particles containing heterodimers and recombinant heterodimers. Packaged heterodimers occur, for example, when two or more library members are contained in one cell of a packaging cell line and is accompanied by recombination or template switching in of the heterodimer. For example, a targeting library may be constructed such that in each library member, a gene targeting sequence such as a guide sequence of a CRISPR system is separated to some degree from an identifier element such as a barcode, but the intervening sequence is the same, and promotes recombination between library members when dimerized. In certain embodiments, the sequence intervening sequence common to the library members corresponds to the direct repeat that binds to a CRISPR protein. Recombination produces mispairing of guide sequences with barcodes, hence degrades information obtainable from the screen. The lentiviral systems described herein minimize recombination, providing lentivirus packages that are effectively monomeric. By "effectively monomeric" is meant that a library member is packaged as a monomer or in a manner that reduces or eliminates recombination. In certain embodiments, a library member, which is a polynucleotide having at least a first engineered association and a second engineered association, is packaged with a nucleic acid that is not recombinogenic, referred to herein as a stuffer. In certain non-limiting embodiments, a stuffer nucleic acid lacks any substantial homology with the polynucleotide having the first and second engineered association. In certain embodiments, a nucleic acid is provided in a packaging cell that is not packaged but reduces heterodimers and recombination thereof. The nucleic acid can be any replicable vector that need not produce a packageable polynucleotide. In an embodiment of the invention, the vector is pUC19.

[0032] Certain evidence has suggested that lentiviral genome dimerization normally occurs after RNA is packaged and virus particles are released. For example, 70S RNA dimers could not be isolated from infected cells and viral particles harvested upon formation contained monomeric RNA which dimerized minutes or hours after particle release. Also, dimerization of the RNA in the particles was blocked if the virus was solubilized with detergent. (Canaani et al., 1973, Proc. Natl. Acad. Sci. USA 72:401-405). In certain models, NC protein contributes to dimerization. For example, in one model, the NC protein after release from the Gag polyprotein, binds to each RNA and unfolds double-stranded structures near the 5' ends, allowing interstrand contacts to form. In this regard, there are observations that prevention of gag polyprotein cleavage by protease inactivation or mutation of NC results in virus particles that contain monomeric RNA. (Oertle and Spahr, 1990; Stewart et al., 1990, J Virol 64:5076-92; Dupraz et al., 1990).

[0033] Certain key nucleotides involved in the RNA dimerization event make up a palindromic sequence between the PBS and the major splice donor, and RNA sequences on both sides of this palindrome can form a stem-loop structure with the palindrome in the hairpin loop. Deletion of this stem-loop motif completely abolished dimerization of the 1 HIV-1 RNA fragment in vitro. Skripkin et al., 1994, Proc Natl Acad Sci USA 91:4945-4949.

[0034] Further, duplication of the DIS/DLS region in viral RNA causes production of virus particles containing partially monomeric RNAs without modifying any viral proteins and yields particles comparable in certain aspects to wild-type particles. Sakuragi et al., 2002, J. Virol. 76:959-967. The results indicate that RNA dimerization is not required for viral RNA packaging, virion maturation, and reverse transcription.

[0035] These and other aspects, objects, features, and advantages of the example embodiments will become apparent to those having ordinary skill in the art upon consideration of the following detailed description of illustrated example embodiments.

BRIEF DESCRIPTION OF THE DRAWINGS

[0036] An understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative

embodiments, in which the principles of the invention may be utilized, and the accompanying drawings of which:

[0037] FIG. **1**—Schematic of delivery of barcoded lentiviral plasmid library into target cells. Viral genomes containing sgRNAs and transcribed RNA barcodes, driven by U6 and EF1a promoters, are packaged into virions and integrated into target cells. Dimeric packaging of library plasmids may yield homodimeric or heterodimeric library associations or, in the case of co-packaging with a non-homologous carrier lentivirus (purple), a functionally monomeric virion Virions with two different library elements have the capacity for recombination between sgRNAs and barcodes as well as potential for integration of multiple perturbations into the target cell, whereas co-packaging with a non-homologous vector limits these alternatives.

[0038] FIG. **2**—An example method of constructing viral libraries using the methods described herein.

[0039] The figures herein are for illustrative purposes only and are not necessarily drawn to scale.

DETAILED DESCRIPTION OF THE EXAMPLE EMBODIMENTS

General Definitions

[0040] Unless defined otherwise, 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 pertains. Definitions of common terms and techniques in molecular biology may be found in Molecular Cloning: A Laboratory Manual, 2^{nd} edition (1989) (Sambrook, Fritsch, and Maniatis); Molecular Cloning: A Laboratory Manual, 4^{th} edition (2012) (Green and Sambrook); Current Protocols in Molecular Biology (1987) (F. M. Ausubel et al. eds.); the series Methods in Enzymology (Academic Press, Inc.): PCR 2: A Practical Approach (1995) (M. J. MacPherson, B. D. Hames, and G. R. Taylor eds.): Antibodies, A Laboratory Manual (1988) (Harlow and Lane, eds.): Antibodies A Laboratory Manual, 2^{nd} edition 2013 (E. A. Greenfield ed.); Animal Cell Culture (1987) (R. I. Freshney, ed.); Benjamin Lewin, Genes IX, published by Jones and Bartlet, 2008 (ISBN 0763752223); Kendrew et al. (eds.), The Encyclopedia of Molecular Biology, published by Blackwell Science Ltd., 1994 (ISBN 0632021829); Robert A. Meyers (ed.), Molecular Biology and Biotechnology: a Comprehensive Desk Reference, published by VCH Publishers, Inc., 1995 (ISBN 9780471185710); Singleton et al., Dictionary of Microbiology and Molecular Biology 2nd ed., J. Wiley & Sons (New York, N.Y. 1994), March, Advanced Organic Chemistry Reactions, Mechanisms and Structure 4th ed., John Wiley & Sons (New York, N.Y. 1992); and Marten H. Hofker and Jan van Deursen, Transgenic Mouse Methods and Protocols, 2^{nd} edition (2011).

[0041] As used herein, the singular forms "a", "an", and "the" include both singular and plural referents unless the context clearly dictates otherwise.

[0042] The term "optional" or "optionally" means that the subsequent described event, circumstance, or substituent may or may not occur, and that the description includes instances where the event or circumstance occurs and instances where it does not.

[0043] The recitation of numerical ranges by endpoints includes all numbers and fractions subsumed within the respective ranges, as well as the recited endpoints.

[0044] The terms "about" or "approximately" as used herein when referring to a measurable value such as a parameter, an amount, a temporal duration, and the like, are meant to encompass variations of and from the specified value, such as variations of +/−10% or less, +/−5% or less, +/−1% or less, and +/−0.1% or less of and from the specified value, insofar such variations are appropriate to perform in the disclosed invention. It is to be understood that the value to which the modifier "about" or "approximately" refers is itself also specifically, and preferably, disclosed.

[0045] As used herein, a "biological sample" may contain whole cells and/or live cells and/or cell debris. The biological sample may contain (or be derived from) a "bodily fluid". The present invention encompasses embodiments wherein the bodily fluid is selected from amniotic fluid, aqueous humour, vitreous humour, bile, blood serum, breast milk, cerebrospinal fluid, cerumen (earwax), chyle, chyme, endolymph, perilymph, exudates, feces, female ejaculate, gastric acid, gastric juice, lymph, mucus (including nasal drainage and phlegm), pericardial fluid, peritoneal fluid, pleural fluid, pus, rheum, saliva, sebum (skin oil), semen, sputum, synovial fluid, sweat, tears, urine, vaginal secretion, vomit and mixtures of one or more thereof. Biological samples include cell cultures, bodily fluids, cell cultures from bodily fluids. Bodily fluids may be obtained from a mammal organism, for example by puncture, or other collecting or sampling procedures.

[0046] The terms "subject," "individual," and "patient" are used interchangeably herein to refer to a vertebrate, preferably a mammal, more preferably a human. Mammals include, but are not limited to, murines, simians, humans, farm animals, sport animals, and pets. Tissues, cells and their progeny of a biological entity obtained in vivo or cultured in vitro are also encompassed.

[0047] As used herein, "engineered association" means a library member portion that comprises an engineered structural and/or functional part, including but not limited to a guide sequence for a CRISPR system, or a tag or identifier such as a unique molecular identifier (UMI) or barcode or other tracking element. The engineered structural or functional part is physically associated with the library member in that it is linked to nucleotides or other chemical parts of the library member. Two or more engineered associations are linked when they are comprised by a single polynucleotide or other monomeric molecule. A library polynucleotide comprising engineered associations may be referred to as a "payload" or "template."

[0048] Various embodiments are described hereinafter. It should be noted that the specific embodiments are not intended as an exhaustive description or as a limitation to the broader aspects discussed herein. One aspect described in conjunction with a particular embodiment is not necessarily limited to that embodiment and can be practiced with any other embodiment(s). Reference throughout this specification to "one embodiment", "an embodiment," "an example embodiment," means that a particular feature, structure or characteristic described in connection with the embodiment is included in at least one embodiment of the present invention. Thus, appearances of the phrases "in one embodiment," "in an embodiment," or "an example embodiment" in various places throughout this specification are not necessarily all referring to the same embodiment, but may. Furthermore, the particular features, structures or characteristics may be combined in any suitable manner, as would be

apparent to a person skilled in the art from this disclosure, in one or more embodiments. Furthermore, while some embodiments described herein include some but not other features included in other embodiments, combinations of features of different embodiments are meant to be within the scope of the invention. For example, in the appended claims, any of the claimed embodiments can be used in any combination.

[0049] All publications, published patent documents, and patent applications cited herein are hereby incorporated by reference to the same extent as though each individual publication, published patent document, or patent application was specifically and individually indicated as being incorporated by reference.

Overview

[0050] Retroviral systems, including lentivirus-based systems, can be pseudo-diploid, that is two viral genomes are packaged into each viral particle and are non-covalently linked. During viral genome replication, the reverse transcriptase can switch from one template to another when it synthesizes a DNA provirus from a dimeric RNA genome, and this process happens most frequently at homologous regions. The frequency of recombination may depend on the distance between two regions which has been estimated to be 2% every kilobase. Thus, when libraries of distinct vector sequence are packaged together, template switching could lead to recombination that randomly shuffles associations between sequences, such as associations between sequences encoding one or more genetic perturbations and unique molecular sequence, for example a unique molecular sequence that identifies the encoding perturbation.

[0051] Embodiments disclosed herein provide retroviral systems comprising modifications that mitigates those effects by reducing recombination or template switching activity. Further included are modified methods for retroviral vector packaging. The modified retroviral systems disclosed herein may be used for combinatorial screening of perturbations, including single cell screening.

Engineered Viral Systems

[0052] The present disclosure includes non-naturally engineered viral systems. In some examples, the non-naturally occurring engineered viral systems may be a lentiviral or retroviral system. The systems disclosed herein may comprise a first polynucleotide having at least a first and second engineered association. For ease of reference, the remaining disclosure will address systems with a first and second engineered association, but more than two engineered associations are also envisioned. One or more activities of the engineered systems may be reduced (e.g., as compared to a non-engineered counterpart system). Such activities may include recombination activity, or template switching activity, and multiple integration activity.

[0053] The engineered systems herein may comprise a multiplicity of polynucleotides. In certain embodiments, the retroviral system may comprise a multiplicity of first polynucleotides. The multiplicity of first polynucleotides may comprise different combinations of engineered associations. As used herein, the term "retroviral" is intended to encompass both retroviral and lentivirus-based systems. The first and second engineered association represent sequences that need to remain associated with one another throughout the life cycle of the polynucleotide. For example, the polynucleotide may be a vector and the first and second association encode elements that need to remain associated on the same polynucleotide for further downstream applications. In certain example embodiments, the first and engineered associations may be located 1 kb or greater apart on the polynucleotide sequence. In certain example embodiments, the engineered associations may be located 2 kb or greater apart on the polynucleotide sequence.

[0054] The retroviral system may comprise an inhibitor of recombination or template switching. In certain example embodiment, the retroviral system may further comprise a second polypeptide. The second polynucleotide may be a carrier polynucleotide comprising non-recombinogenic RNA sequences or sequences with limited homology to the first nucleotide or otherwise configured to impair or prevent homologous recombination with the first polynucleotide when packaged together within a viral particle. In another embodiment, the second polynucleotide may result in reduced hairpin formation or dimerization through modification, knockdown or knockout of retroviral genomic RNA or retroviral proteins involved in dimerization.

[0055] In certain example embodiments, the second polypeptide may be 2 kb to 10 kb in size. In certain example embodiments, the second polypeptide is 2.0 kb, 2.1 kb, 2.2 kb, 2.3 kb, 2.4 kb, 2.5 kb, 2.6 kb, 2.7 kb, 2.8 kb, 2.9 kb, 3.0 kb, 3.1 kb, 3.2 kb, 3.3 kb, 3.4 kb, 3.5 kb, 3.6 kb, 3.7 kb, 3.8 kb, 3.9 kb, 4.0 kb, 4.1 kb, 4.2 kb, 4.3 kb, 4.4 kb, 4.5 kb, 4.6 kb, 4.7 kb, 4.8 kb, 4.9 kb, 5.0 kb, 5.1 kb, 5.2 kb, 5.3 kb, 5.4 kb, 5.5 kb 5.6 kb, 5.7 kb, 5.8 kb, 5.9 kb, 6.0 kb, 6.1 kb, 6.2 kb, 6.3 kb, 6.4 kb, 6.5 kb, 6.6 kb, 6.7 kb, 6.8 kb, 6.9 kb, 7.0 kb, 7.1 kb, 7.2 kb, 7.3 kb, 7.4 kb, 7.5 kb, 7.6 kb, 7.7 kb, 7.8 kb, 7.9 kb, 8.0 kb, 8.1 kb, 8.2 kb, 8.3 kb, 8.4 kb, 8.5 kb, 8.6 kb, 8.7 kb, 8.8 kb, 8.9 kb, 9.0 kb, 9.1 kb, 9.2 kb, 9.3 kb, 9.4 kb, 9.5 kb, 9.6 kb, 9.7 kb, 9.8 kb, 9.9 kb, or 10.0 kb in size.

[0056] In certain example embodiments, the second polypeptide may be selected to have less than 60%, 59%, 58%, 57%, 56%, 55%, 54%, 53%, 52%, 51%, 50%, 49%, 48%, 47%, 46%, 45%, 44%, 43%, 42%, 41%, 40%, 39%, 38%, 37%, 36%, 35%, 34%, 33%, 32%, 31%, 30%, 29%, 28%, 27%, 26%, 25%, 24%, 23%, 22%, 21%, 20%, 19%, 18%, 17%, 16%, 15%, 14%, 13%, 12%, 11%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, or 1% complementarity to the first polynucleotide.

[0057] In certain example embodiments, the second polypeptide is a lentiviral vector. In certain example embodiments, the lentiviral vector has long terminal repeat to long terminal repeat distance (LTR-LTR distance) of 2.5 kb, 2.4 kb, 2.3 kb, 2.2 kb, 2.1 kb, 2.0 kb, 1.9 kb, 1.8 kb, 1.7 kb. 1.6 kb, 1.5 kb, 1.4 kb, 1.3 kb, 1.2 kb. 1.1 kb, or 1.0 kb.

[0058] In certain example embodiments, the lentiviral vector comprises one or more LTR mutations in one or both LTR regions that abrogate integration capability.

[0059] Other factors that may be considered in selecting or designing second polynucleotide include GC content, presence/absence of repeats, sequence signatures that affect DNA helix parameters, using supercoiled versus relaxed plasmids, nicked or un-nicked plasmids, methylated or non-methylated plasmids.

Retroviral Systems

[0060] The viral backbone of the retroviral system may be any retrovirus suitable for use in delivering expression constructs to cells. Example retroviral systems include

moloney murine leukemia virus (MoMuLV), feline immunodeficiency virus (FIV), HIV-1 based packaging systems (HIV), and lentiviral based systems. In certain example embodiments, the retroviral system is based on Moloney murine leukemia virus (MoMuLV), Harvey murine sarcoma virus (HaMuSV), murine mammary tumor virus (MuMTV), gibbon ape leukemia virus (GaLV) human immunodeficiency virus (HIV) and Rous Sarcoma Virus (RSV). (see, e.g., Buchscher et al, J. Virol. 66:2731-2739 (1992); Johann et al, J. Virol. 66: 1635-1640 (1992); Sommnerfelt et al, Virol. 176:58-59 (1990); Wilson et al, J. Virol. 63:2374-2378 (1989); Miller et al, J. Virol. 65:2220-2224 (1991); PCT/US94/05700).

[0061] Vectors that are based on HIV may retain <5% of the parental genome, and <25% of the genome may be incorporated into packaging constructs, which minimizes the possibility of the generation of revertant replication-competent HIV. The vector region may include sequences form the 5' and 3' LTRs of a lentivirus. In some instances, the vector domain includes the R and U5 sequences from the 5' LTR of a lentivirus and an inactivated or self-inactivating 3' LTR from a lentivirus. The LTR sequences may be LTR sequences from any lentivirus from any species. For example, they may be LTR sequences from HIV, SIV, FIV or BIV. Where desired, the packaged viral barcoded library may be made up of self-inactivating vectors that contain deletions of the regulatory elements in the downstream long-terminal-repeat sequence, eliminating transcription of the packaging signal that is required for vector mobilization. As such, the vector region may include an inactivated or self-inactivating 3' LTR. The 3' LTR may be made self-inactivating by any convenient method. For example, the U3 element of the 3' LTR may contain a deletion of its enhancer sequence, such as the TATA box, Sp1 and NF-kappa B sites. As a result of the self-inactivating 3' LTR, the provirus that is integrated into the host cell genome will comprise an inactivated 5' LTR. Optionally, the U3 sequence from the lentiviral 5' LTR may be replaced with a promoter sequence in the viral construct. This may increase the titer of virus recovered from the packaging cell line. An enhancer sequence may also be included. In certain aspects, the viral construct is a non-integrating lentiviral construct, where the construct does not integrate by virtue of having a defective (e.g., by site-specific mutation) or absent integrase gene Integrase-defective lentiviral vectors are described, e.g., in Banasik and McCray (2010) *Gene Therapy* 17(2):150-157.

[0062] In certain example embodiments, a lentivirus based system is used. Lentiviruses are members of the retrovirus family. Widely used retroviral vectors include those based upon murine leukemia virus (MuLV), gibbon ape leukemia virus (GaLV), Simian Immuno deficiency virus (SIV), human immuno deficiency virus (HIV), and combinations thereof (see, e.g., Buchscher et al, J. Virol. 66:2731-2739 (1992); Johann et al, J. Virol. 66: 1635-1640 (1992); Sommnerfelt et al, Virol. 176:58-59 (1990); Wilson et al, J. Virol. 63:2374-2378 (1989); Miller et al, J. Virol. 65:2220-2224 (1991); PCT/US94/05700).

[0063] The embodiments disclosed herein may also be useful in non-retroviral based systems, that are pseudo-diploid or otherwise known to have the same recombination and template-switching limitations of lentivirus and retrovirus systems disclosed herein.

Carrier Polynucleotides

[0064] The invention provides inhibitors of recombination activity, template switching activity, or multiple integration activity. In some cases, the engineered systems described herein comprise an inhibitor of template switching. In an embodiment, the inhibitor of template switching is a carrier polynucleotide. The carrier polynucleotide can be involved in or affect any aspect of lentiviral packaging, and functions to reduce recombination activity or template switching activity, or multiple integration. For example, in an embodiment of the invention, the carrier polynucleotide is packaged with or forms a heterodimer with the polynucleotide comprising the one or more engineered associations, but lacks sufficient homology such that recombination activity, template switching activity, or multiple integration activity is reduced or eliminated. In an embodiment of the invention, the reduction in recombination activity, template switching activity, or multiple integration activity can be 2×, 5×, 10×, 20×, 50×, 100×, 500×, 1000× or greater as compared to packaging without the carrier polynucleotide. In packaging reactions, carrier polynucleotides are usually in excess. In certain embodiments, the carrier polynucleotide to payload polynucleotide ratio in packaging is from 5:1 to 10:1 or from 10:1 to 20:1 or from 20:1 to 50:1, or from 50:1 to 100:1 or from 100:1 to 500:1, of from 500:1 to 1000:1 or greater.

[0065] In another embodiment, the inhibitor of recombination activity, or template switching activity, or multiple integration activity can be any carrier polynucleotide transfected into a packaging cell and present with the payload to be packaged, which carrier polynucleotide is not designed to be packaged. Such carriers include, without limitation, single and double stranded DNA, replicable and non-replicable plasmid type vectors, including prokaryotic and eukaryotic vectors. In a non-limiting example set forth herein, bacterial plasmid pUC19, which does not replicate in a packaging cell, is not transcribed, and is not designed to be packaged in a lentiviral particle, is demonstrated to inhibit recombination activity, template switching activity, or multiple integration activity.

[0066] In some embodiments, the carrier polynucleotide comprises or encodes one or more non-recombinogenic RNA sequences. Alternatively or additionally, the carrier polynucleotide may encode proteins that capable of dimerizing with the polynucleotide having engineered association.

[0067] Reduced recombination or template activity herein may comprise reduced hairpin formation or dimerization through modification, knockdown or knockout of retroviral genomic RNA or retroviral protein involved in dimerization. In some examples, the retroviral genomic RNA or retroviral protein comprises nucleocapsid (NC)-protein(s) or RNA encoding thereof, stem-loop I element (SLI), genomic RNA in which U5:AUG pairing is prevented, a dimer initiation site (DIS), or any combination thereof.

[0068] In an embodiment, the inhibitor of recombination activity, or template switching activity, or multiple integration activity comprises a polynucleotide designed to hybridize with all or part of the 5' UTR, including but not limited to such regions as U5-PBS complex or the dimer initiation site (DIS). In an embodiment, the inhibitor polynucleotide can be RNA produced concurrently with the payload or added to the payload prior to packaging. In an embodiment, the inhibitor polynucleotide can be synthetic. Tran et al., 2015, Retrovirology 12:83 reviews conserved determinants of lentiviral genome dimerization.

[0069] In an embodiment, recombination activity, template switching activity, or multiple integration activity is reduced by rearranging elements of the payload polynucleotide. This includes without limitation, deletion of 5' UTR elements and/or introduction of 5' UTR elements elsewhere in the sequence of the payload to be packaged. In an embodiment, introduction and/or relocation of the DIS provides lentivirus genomes (e.g., payloads) that package predominantly or completely as monomers. Sakuragi et al., 2002, J. Virol. 76:959-967 reports several HIV mutants comprising multiple and rearranged copies of viral E/DLS sequences. According to the invention, 5' UTR elements can be added and/or rearranged in payload genomes, taking care not to interrupt desired genetic elements (associations) provided therein.

[0070] In certain embodiments of the invention, recombination activity, template switching activity, or multiple integration activity is modulated by altering interaction of the payload with the capsid. In one embodiment, the lentivirus nucleocapsid (NC) protein is altered by mutating the zinc-finger region so as to disrupt NC-dependent dimerization. See, e.g., Tran et al., 2015, reviewing 5' UTR and NC features involved in dimerization.

Genetic Perturbations

[0071] In one example embodiment, the first polynucleotide may encode one or more genetic perturbations. The sequences encoding one or more genetic perturbations may comprise an overexpressed gene, siRNAs, microRNAs, regulatory RNAs, ribozymes, antisense RNAs, guide sequences, or a site-specific nuclease. The polynucleotides (e.g., polynucleotides with sequence encoding one or more genetic perturbations) may encode a site-specific nuclease such as, but not limited to, zinc-finger nuclease (ZFN), a transcription activator-like effector nuclease (TALENs) a CRISPR system, a component thereof, a portion thereof, or any combination thereof. Alternatively or additionally, the polynucleotides may encode one or more overexpressed genes, a RNAi based system, a component thereof, or a portion thereof. In some examples, the polynucleotides encode a CRISPR-Cas system or a component thereof. The CRISPR-Cas system may be a CRISPR-Cas9 system. In some cases, the polynucleotides encode one or more guide sequences.

[0072] Suitable site-specific nuclease systems are described in further detail below. The perturbation(s) may comprise single-order perturbations. The perturbation(s) may comprise combinatorial perturbations. The perturbations may include gene knock-outs, gene knock-ins, transpositions, inversions, and/or one or more nucleotide insertions, deletions, or substitutions.

[0073] In some cases, the polynucleotide comprises a first and a second engineered associations. The associations may comprise one or more genetic perturbations. For example, the first engineered association may comprise a first genetic perturbation and the second engineered association may comprise a second genetic perturbation.

TALENs

[0074] In certain embodiments, the sequence encoding the one or more genetic perturbation encodes a (modified) transcription activator-like effector nuclease (TALEN) system. Transcription activator-like effectors (TALEs) can be engineered to bind practically any desired DNA sequence. Exemplary methods of genome editing using the TALEN system can be found for example in Cermak T. Doyle E L. Christian M. Wang L. Zhang Y. Schmidt C, et al. Efficient design and assembly of custom TALEN and other TAL effector-based constructs for DNA targeting. Nucleic Acids Res. 2011; 39:e82; Zhang F. Cong L. Lodato S. Kosuri S. Church G M. Arlotta P Efficient construction of sequence-specific TAL effectors for modulating mammalian transcription. Nat Biotechnol. 2011; 29:149-153 and U.S. Pat. Nos. 8,450,471, 8,440,431 and 8,440,432, all of which are specifically incorporated by reference. By means of further guidance, and without limitation, naturally occurring TALEs or "wild type TALEs" are nucleic acid binding proteins secreted by numerous species of proteobacteria. TALE polypeptides contain a nucleic acid binding domain composed of tandem repeats of highly conserved monomer polypeptides that are predominantly 33, 34 or 35 amino acids in length and that differ from each other mainly in amino acid positions 12 and 13. In advantageous embodiments the nucleic acid is DNA. As used herein, the term "polypeptide monomers", or "TALE monomers" will be used to refer to the highly conserved repetitive polypeptide sequences within the TALE nucleic acid binding domain and the term "repeat variable di-residues" or "RVD" will be used to refer to the highly variable amino acids at positions 12 and 13 of the polypeptide monomers. As provided throughout the disclosure, the amino acid residues of the RVD are depicted using the IUPAC single letter code for amino acids. A general representation of a TALE monomer which is comprised within the DNA binding domain is X1-11-(X12X13)-X14-33 or 34 or 35, where the subscript indicates the amino acid position and X represents any amino acid. X12X13 indicate the RVDs. In some polypeptide monomers, the variable amino acid at position 13 is missing or absent and in such polypeptide monomers, the RVD consists of a single amino acid. In such cases the RVD may be alternatively represented as X*, where X represents X12 and (*) indicates that X13 is absent. The DNA binding domain comprises several repeats of TALE monomers and this may be represented as (X1-11-(X12X13)-X14-33 or 34 or 35)z, where in an advantageous embodiment, z is at least 5 to 40. In a further advantageous embodiment, z is at least 10 to 26. The TALE monomers have a nucleotide binding affinity that is determined by the identity of the amino acids in its RVD. For example, polypeptide monomers with an RVD of NI preferentially bind to adenine (A), polypeptide monomers with an RVD of NG preferentially bind to thymine (T), polypeptide monomers with an RVD of HD preferentially bind to cytosine (C) and polypeptide monomers with an RVD of NN preferentially bind to both adenine (A) and guanine (G). In yet another embodiment of the invention, polypeptide monomers with an RVD of IG preferentially bind to T. Thus, the number and order of the polypeptide monomer repeats in the nucleic acid binding domain of a TALE determines its nucleic acid target specificity. In still further embodiments of the invention, polypeptide monomers with an RVD of NS recognize all four base pairs and may bind to A, T, G or C. The structure and function of TALEs is further described in, for example, Moscou et al., Science 326:1501 (2009); Boch et al., Science 326:1509-1512 (2009); and Zhang et al., Nature Biotechnology 29:149-153 (2011), each of which is incorporated by reference in its entirety. In certain embodiments, targeting is affected by a polynucleic acid binding

TALEN fragment. In certain embodiments, the targeting domain comprises or consists of a catalytically inactive TALEN or nucleic acid binding fragment thereof.

Zn-Finger Nucleases

[0075] In certain embodiments, the sequence encoding one or more genetic perturbations comprises or consists of a (modified) zinc-finger nuclease (ZFN) system. The ZFN system uses artificial restriction enzymes generated by fusing a zinc finger DNA-binding domain to a DNA-cleavage domain that can be engineered to target desired DNA sequences. Exemplary methods of genome editing using ZFNs can be found for example in U.S. Pat. Nos. 6,534,261, 6,607,882, 6,746,838, 6,794,136, 6,824,978, 6,866,997, 6,933,113, 6,979,539, 7,013,219, 7,030,215, 7,220,719, 7,241,573, 7,241,574, 7,585,849, 7,595,376, 6,903,185, and 6,479,626, all of which are specifically incorporated by reference. By means of further guidance, and without limitation, artificial zinc-finger (ZF) technology involves arrays of ZF modules to target new DNA-binding sites in the genome. Each finger module in a ZF array targets three DNA bases. A customized array of individual zinc finger domains is assembled into a ZF protein (ZFP). ZFPs can comprise a functional domain. The first synthetic zinc finger nucleases (ZFNs) were developed by fusing a ZF protein to the catalytic domain of the Type IIS restriction enzyme FokI. (Kim, Y. G. et al., 1994, Chimeric restriction endonuclease, Proc. Natl. Acad. Sci. U.S.A. 91, 883-887; Kim, Y. G. et al., 1996, Hybrid restriction enzymes: zinc finger fusions to Fok I cleavage domain. Proc. Natl. Acad. Sci. U.S.A. 93, 1156-1160). Increased cleavage specificity can be attained with decreased off target activity by use of paired ZFN heterodimers, each targeting different nucleotide sequences separated by a short spacer. (Doyon, Y. et al., 2011, Enhancing zinc-finger-nuclease activity with improved obligate heterodimeric architectures. Nat. Methods 8, 74-79). ZFPs can also be designed as transcription activators and repressors and have been used to target many genes in a wide variety of organisms. In certain embodiments, the targeting domain comprises or consists of a nucleic acid binding zinc finger nuclease or a nucleic acid binding fragment thereof. In certain embodiments, the nucleic acid binding (fragment of) a zinc finger nuclease is catalytically inactive.

Meganuclease

[0076] In certain embodiments, the sequences encoding one or more genetic perturbations comprises a (modified) meganuclease, which are endodeoxyribonucleases characterized by a large recognition site (double-stranded DNA sequences of 12 to 40 base pairs). Exemplary method for using meganucleases can be found in U.S. Pat. Nos. 8,163,514; 8,133,697; 8,021,867; 8,119,361; 8,119,381; 8,124,369; and 8,129,134, which are specifically incorporated by reference. In certain embodiments, targeting is affected by a polynucleic acid binding meganuclease fragment. In certain embodiments, targeting is affected by a polynucleic acid binding catalytically inactive meganuclease (fragment). Accordingly in particular embodiments, the targeting domain comprises or consists of a nucleic acid binding meganuclease or a nucleic acid binding fragment thereof.

CRISPR-Cas Systems

[0077] In certain embodiments, the sequence encoding the one or more genetic perturbation encodes a (modified) CRISPR/Cas complex or system. General information on CRISPR/Cas Systems, components thereof, and delivery of such components, including methods, materials, delivery vehicles, vectors, particles, and making and using thereof, including as to amounts and formulations, as well as CRISPR/Cas-expressing eukaryotic cells, CRISPR/Cas expressing eukaryotes, such as a mouse, is described herein elsewhere. In certain embodiments, targeting is affected by an oligonucleic acid binding CRISPR protein fragment and/or a gRNA. In certain embodiments, targeting is affected by a nucleic acid binding catalytically inactive CRISPR protein (fragment). Accordingly in particular embodiments, the targeting domain comprises oligonucleic acid binding CRISPR protein or an oligonucleic acid binding fragment of a CRISPR protein and/or a gRNA.

[0078] As used herein, the term "Cas" generally refers to a (modified) effector protein of the CRISPR/Cas system or complex, and can be without limitation a (modified) Cas9, or other enzymes such as Cpf1, C2c1, C2c2, C2c3, group 29, or group 30 protein. The term "Cas" may be used herein interchangeably with the terms "CRISPR" protein, "CRISPR/Cas protein", "CRISPR effector", "CRISPR/Cas effector", "CRISPR enzyme", "CRISPR/Cas enzyme" and the like, unless otherwise apparent, such as by specific and exclusive reference to Cas9. It is to be understood that the term "CRISPR protein" may be used interchangeably with "CRISPR enzyme", irrespective of whether the CRISPR protein has altered, such as increased or decreased (or no) enzymatic activity, compared to the wild type CRISPR protein. Likewise, as used herein, in certain embodiments, where appropriate and which will be apparent to the skilled person, the term "nuclease" may refer to a modified nuclease wherein catalytic activity has been altered, such as having increased or decreased nuclease activity, or no nuclease activity at all, as well as nickase activity, as well as otherwise modified nuclease as defined herein elsewhere, unless otherwise apparent, such as by specific and exclusive reference to unmodified nuclease.

[0079] In some embodiments, the CRISPR effector protein is Cas9, Cpf1, C2c1, C2c2, or Cas13a, Cas13b, or Cas13c. In some embodiments, the CRISPR effector protein is a DNA-targeting CRISPR effector protein. In some embodiments, the CRISPR effector protein is a Type-II CRISPR effector protein such as Cas9. In some embodiments, the CRISPR effector protein is a Type-V CRISPR effector protein such as Cpf1 or C2cl. In some embodiments, the CRISPR effector protein is a RNA-targeting CRISPR effector protein. In some embodiments, the CRISPR effector protein is a Type-VI CRISPR effector protein such as Cas13a, Cas13b, or Cas13c.

[0080] In some embodiments, the CRISPR effector protein is a Cas9, for instance SaCas9, SpCas9, StCas9, CjCas9 and so forth—any ortholog is envisaged. In some embodiments, the CRISPR effector protein is a Cpf1, for instance AsCpf1, LbCpf1, FnCpf1 and so forth—any ortholog is envisaged. In certain embodiments, the targeting component as described herein according to the invention is a (endo)nuclease or a variant thereof having altered or modified activity (i.e. a modified nuclease, as described herein elsewhere). In certain embodiments, said nuclease is a targeted or site-specific or homing nuclease or a variant thereof having altered or modified activity. In certain embodiments, said nuclease or targeted/site-specific/homing nuclease is, comprises, consists essentially of, or consists of a (modified) CRISPR/Cas

system or complex, a (modified) Cas protein, a (modified) zinc finger, a (modified) zinc finger nuclease (ZFN), a (modified) transcription factor-like effector (TALE), a (modified) transcription factor-like effector nuclease (TALEN), or a (modified) meganuclease. In certain embodiments, said (modified) nuclease or targeted/site-specific/homing nuclease is, comprises, consists essentially of, or consists of a (modified) RNA-guided nuclease.

[0081] In particular embodiments, more particularly where the nuclease is a CRISPR protein, the targeting domain further comprises a guide molecule which targets a selected nucleic acid. For instance, in the context of the CRISPR/Cas system, the guide RNA is capable of hybridizing with a selected nucleic acid sequence. As used herein, "hybridization" or "hybridizing" refers to a reaction in which one or more polynucleotides react to form a complex that is stabilized via hydrogen bonding between the bases of the nucleotide residues. The hydrogen bonding may occur by Watson Crick base pairing, Hoogsteen binding, or in any other sequence specific manner. The complex may comprise two strands forming a duplex structure, three or more strands forming a multi stranded complex, a single self-hybridizing strand, or any combination of these. A hybridization reaction may constitute a step in a more extensive process, such as the initiation of PGR, or the cleavage of a polynucleotide by an enzyme. A sequence capable of hybridizing with a given sequence is referred to as the "complement" of the given sequence.

Guide Sequences

[0082] In certain example embodiments, one of the engineered associations may comprise one of the above Cas proteins. In another embodiment, one of the engineered associations may comprise a Cas protein and second engineered association may comprise a guide sequence. In yet another embodiment, the engineered associations may comprise two or more guide sequences. As used herein, the term "guide sequence" and "guide molecule" in the context of a CRISPR-Cas system, comprises any polynucleotide sequence having sufficient complementarity with a target nucleic acid sequence to hybridize with the target nucleic acid sequence and direct sequence-specific binding of a nucleic acid-targeting complex to the target nucleic acid sequence. The guide sequences made using the methods disclosed herein may be a full-length guide sequence, a truncated guide sequence, a full-length sgRNA sequence, a truncated sgRNA sequence, or an E+F sgRNA sequence. In some embodiments, the degree of complementarity of the guide sequence to a given target sequence, when optimally aligned using a suitable alignment algorithm, is about or more than about 50%, 60%, 75%, 80%, 85%, 90%, 95%, 97.5%, 99%, or more. In certain example embodiments, the guide molecule comprises a guide sequence that may be designed to have at least one mismatch with the target sequence, such that a RNA duplex formed between the guide sequence and the target sequence. Accordingly, the degree of complementarity is preferably less than 99%. For instance, where the guide sequence consists of 24 nucleotides, the degree of complementarity is more particularly about 96% or less. In particular embodiments, the guide sequence is designed to have a stretch of two or more adjacent mismatching nucleotides, such that the degree of complementarity over the entire guide sequence is further reduced. For instance, where the guide sequence consists of 24 nucleotides, the degree of complementarity is more particularly about 96% or less, more particularly, about 92% or less, more particularly about 88% or less, more particularly about 84% or less, more particularly about 80% or less, more particularly about 76% or less, more particularly about 72% or less, depending on whether the stretch of two or more mismatching nucleotides encompasses 2, 3, 4, 5, 6 or 7 nucleotides, etc. In some embodiments, aside from the stretch of one or more mismatching nucleotides, the degree of complementarity, when optimally aligned using a suitable alignment algorithm, is about or more than about 50%, 60%, 75%, 80%, 85%, 90%, 95%, 97.5%, 99%, or more. Optimal alignment may be determined with the use of any suitable algorithm for aligning sequences, non-limiting example of which include the Smith-Waterman algorithm, the Needleman-Wunsch algorithm, algorithms based on the Burrows-Wheeler Transform (e.g., the Burrows Wheeler Aligner), ClustalW, Clustal X, BLAT, Novoalign (Novocraft Technologies; available at www.novocraft.com), ELAND (Illumina, San Diego, CA), SOAP (available at soap.genomics.org.cn), and Maq (available at maq.sourceforge.net). The ability of a guide sequence (within a nucleic acid-targeting guide RNA) to direct sequence-specific binding of a nucleic acid-targeting complex to a target nucleic acid sequence may be assessed by any suitable assay. For example, the components of a nucleic acid-targeting CRISPR system sufficient to form a nucleic acid-targeting complex, including the guide sequence to be tested, may be provided to a host cell having the corresponding target nucleic acid sequence, such as by transfection with vectors encoding the components of the nucleic acid-targeting complex, followed by an assessment of preferential targeting (e.g., cleavage) within the target nucleic acid sequence, such as by Surveyor assay as described herein. Similarly, cleavage of a target nucleic acid sequence (or a sequence in the vicinity thereof) may be evaluated in a test tube by providing the target nucleic acid sequence, components of a nucleic acid-targeting complex, including the guide sequence to be tested and a control guide sequence different from the test guide sequence, and comparing binding or rate of cleavage at or in the vicinity of the target sequence between the test and control guide sequence reactions. Other assays are possible, and will occur to those skilled in the art. A guide sequence, and hence a nucleic acid-targeting guide RNA may be selected to target any target nucleic acid sequence.

[0083] In certain embodiments, the guide sequence or spacer length of the guide molecules is from 15 to 50 nt. In certain embodiments, the spacer length of the guide RNA is at least 15 nucleotides. In certain embodiments, the spacer length is from 15 to 17 nt, e.g., 15, 16, or 17 nt, from 17 to 20 nt, e.g., 17, 18, 19, or 20 nt, from 20 to 24 nt, e.g., 20, 21, 22, 23, or 24 nt, from 23 to 25 nt, e.g., 23, 24, or 25 nt, from 24 to 27 nt, e.g., 24, 25, 26, or 27 nt, from 27-30 nt, e.g., 27, 28, 29, or 30 nt, from 30-35 nt, e.g., 30, 31, 32, 33, 34, or 35 nt, or 35 nt or longer. In certain example embodiments, the guide sequence is 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39 40, 41, 42, 43, 44, 45, 46, 47 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 nt.

[0084] In some embodiments, the guide sequence is an RNA sequence of between 10 to 50 nt in length, but more particularly of about 20-30 nt advantageously about 20 nt,

23-25 nt or 24 nt. The guide sequence is selected so as to ensure that it hybridizes to the target sequence. This is described more in detail below. Selection can encompass further steps which increase efficacy and specificity.

[0085] In some embodiments, the guide sequence has a canonical length (e.g., about 15-30 nt) is used to hybridize with the target RNA or DNA. In some embodiments, a guide molecule is longer than the canonical length (e.g., >30 nt) is used to hybridize with the target RNA or DNA, such that a region of the guide sequence hybridizes with a region of the RNA or DNA strand outside of the Cas-guide target complex. This can be of interest where additional modifications, such deamination of nucleotides is of interest. In alternative embodiments, it is of interest to maintain the limitation of the canonical guide sequence length.

[0086] In some embodiments, the sequence of the guide molecule (direct repeat and/or spacer) is selected to reduce the degree secondary structure within the guide molecule. In some embodiments, about or less than about 75%, 50%, 40%, 30%, 25%, 20%, 15%, 10%, 5%, 1%, or fewer of the nucleotides of the nucleic acid-targeting guide RNA participate in self-complementary base pairing when optimally folded. Optimal folding may be determined by any suitable polynucleotide folding algorithm. Some programs are based on calculating the minimal Gibbs free energy. An example of one such algorithm is mFold, as described by Zuker and Stiegler (Nucleic Acids Res. 9 (1981), 133-148). Another example folding algorithm is the online webserver RNAfold, developed at Institute for Theoretical Chemistry at the University of Vienna, using the centroid structure prediction algorithm (see e.g., A. R. Gruber et al., 2008, Cell 106(1): 23-24; and P A Carr and G M Church, 2009, Nature Biotechnology 27(12): 1151-62).

[0087] In some embodiments, it is of interest to reduce the susceptibility of the guide molecule to RNA cleavage, such as to cleavage by Cas13. Accordingly, in particular embodiments, the guide molecule is adjusted to avoid cleavage by Cas13 or other RNA-cleaving enzymes.

[0088] In certain embodiments, the guide molecule comprises non-naturally occurring nucleic acids and/or non-naturally occurring nucleotides and/or nucleotide analogs, and/or chemically modifications. Preferably, these non-naturally occurring nucleic acids and non-naturally occurring nucleotides are located outside the guide sequence. Non-naturally occurring nucleic acids can include, for example, mixtures of naturally and non-naturally occurring nucleotides. Non-naturally occurring nucleotides and/or nucleotide analogs may be modified at the ribose, phosphate, and/or base moiety. In an embodiment of the invention, a guide nucleic acid comprises ribonucleotides and non-ribonucleotides. In one such embodiment, a guide comprises one or more ribonucleotides and one or more deoxyribonucleotides. In an embodiment of the invention, the guide comprises one or more non-naturally occurring nucleotide or nucleotide analog such as a nucleotide with phosphorothioate linkage, a locked nucleic acid (LNA) nucleotide comprising a methylene bridge between the 2' and 4' carbons of the ribose ring, or bridged nucleic acids (BNA). Other examples of modified nucleotides include 2'-O-methyl analogs, 2'-deoxy analogs, or 2'-fluoro analogs. Further examples of modified bases include, but are not limited to, 2-aminopurine, 5-bromo-uridine, pseudouridine, inosine, 7-methylguanosine. Examples of guide RNA chemical modifications include, without limitation, incorporation of 2'-O-methyl (M), 2'-O-methyl 3'phosphorothioate (MS), S-constrained ethyl(cEt), or 2'-O-methyl 3'thioPACE (MSP) at one or more terminal nucleotides. Such chemically modified guides can comprise increased stability and increased activity as compared to unmodified guides, though on-target vs. off-target specificity is not predictable. (See, Hendel, 2015, Nat Biotechnol. 33(9):985-9, doi: 10.1038/nbt.3290, published online 29 Jun. 2015 Ragdarm et al., 0215, *PNAS*, E7110-E7111; Allerson et al., *J. Med. Chem.* 2005, 48:901-904; Bramsen et al., *Front. Genet.,* 2012, 3:154; Deng et al., *PNAS,* 2015, 112:11870-11875; Sharma et al., *Med Chem Comm.,* 2014, 5:1454-1471; Hendel et al., *Nat. Biotechnol.* (2015) 33(9): 985-989; Li et al., *Nature Biomedical Engineering,* 2017, 1, 0066 DOI:10.1038/s41551-017-0066). In some embodiments, the 5' and/or 3' end of a guide RNA is modified by a variety of functional moieties including fluorescent dyes, polyethylene glycol, cholesterol, proteins, or detection tags. (See Kelly et al., 2016, *J. Biotech.* 233: 74-83). In certain embodiments, a guide comprises ribonucleotides in a region that binds to a target RNA and one or more deoxyribonucleotides and/or nucleotide analogs in a region that binds to Cas13. In an embodiment of the invention, deoxyribonucleotides and/or nucleotide analogs are incorporated in engineered guide structures, such as, without limitation, stem-loop regions, and the seed region. For Cas13 guide, in certain embodiments, the modification is not in the 5'-handle of the stem-loop regions. Chemical modification in the 5'-handle of the stem-loop region of a guide may abolish its function (see Li, et al., *Nature Biomedical Engineering,* 2017, 1:0066). In certain embodiments, at least 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, 35, 40, 45, 50, or 75 nucleotides of a guide is chemically modified. In some embodiments, 3-5 nucleotides at either the 3' or the 5' end of a guide is chemically modified. In some embodiments, only minor modifications are introduced in the seed region, such as 2'-F modifications. In some embodiments, 2'-F modification is introduced at the 3' end of a guide. In certain embodiments, three to five nucleotides at the 5' and/or the 3' end of the guide are chemically modified with 2'-O-methyl (M), 2'-O-methyl 3' phosphorothioate (MS), S-constrained ethyl(cEt), or 2'-O-methyl 3' thioPACE (MSP). Such modification can enhance genome editing efficiency (see Hendel et al., *Nat. Biotechnol.* (2015) 33(9): 985-989). In certain embodiments, all of the phosphodiester bonds of a guide are substituted with phosphorothioates (PS) for enhancing levels of gene disruption. In certain embodiments, more than five nucleotides at the 5' and/or the 3' end of the guide are chemically modified with 2'-O-Me, 2'-F or S-constrained ethyl(cEt). Such chemically modified guide can mediate enhanced levels of gene disruption (see Ragdarm et al., 0215, *PNAS*, E7110-E7111). In an embodiment of the invention, a guide is modified to comprise a chemical moiety at its 3' and/or 5' end. Such moieties include, but are not limited to amine, azide, alkyne, thio, dibenzocyclooctyne (DBCO), or Rhodamine. In certain embodiment, the chemical moiety is conjugated to the guide by a linker, such as an alkyl chain. In certain embodiments, the chemical moiety of the modified guide can be used to attach the guide to another molecule, such as DNA, RNA, protein, or nanoparticles. Such chemically modified guide can be used to identify or enrich cells genetically edited by a CRISPR system (see Lee et al., *eLife,* 2017, 6:e25312, DOI:10.7554).

[0089] In some embodiments, the modification to the guide is a chemical modification, an insertion, a deletion or a split. In some embodiments, the chemical modification includes, but is not limited to, incorporation of 2'-O-methyl (M) analogs, 2'-deoxy analogs, 2-thiouridine analogs, N6-methyladenosine analogs, 2'-fluoro analogs, 2-aminopurine, 5-bromo-uridine, pseudouridine (Ψ), N1-methylpseudouridine (melΨ), 5-methoxyuridine (5moU), inosine, 7-methylguanosine, 2'-O-methyl 3'phosphorothioate (MS), S-constrained ethyl(cEt), phosphorothioate (PS), or 2'-O-methyl 3'thioPACE (MSP). In some embodiments, the guide comprises one or more of phosphorothioate modifications. In certain embodiments, at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 nucleotides of the guide are chemically modified. In certain embodiments, one or more nucleotides in the seed region are chemically modified. In certain embodiments, one or more nucleotides in the 3'-terminus are chemically modified. In certain embodiments, none of the nucleotides in the 5'-handle is chemically modified. In some embodiments, the chemical modification in the seed region is a minor modification, such as incorporation of a 2'-fluoro analog. In a specific embodiment, one nucleotide of the seed region is replaced with a 2'-fluoro analog. In some embodiments, 5 to 10 nucleotides in the 3'-terminus are chemically modified. Such chemical modifications at the 3'-terminus of the Cas13 CrRNA may improve Cas13 activity. In a specific embodiment, 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 nucleotides in the 3'-terminus are replaced with 2'-fluoro analogues. In a specific embodiment, 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 nucleotides in the 3'-terminus are replaced with 2'-O-methyl (M) analogs.

[0090] In some embodiments, the loop of the 5'-handle of the guide is modified. In some embodiments, the loop of the 5'-handle of the guide is modified to have a deletion, an insertion, a split, or chemical modifications. In certain embodiments, the modified loop comprises 3, 4, or 5 nucleotides. In certain embodiments, the loop comprises the sequence of UCUU, UUUU, UAUU, or UGUU.

[0091] In some embodiments, the guide molecule forms a stemloop with a separate non-covalently linked sequence, which can be DNA or RNA. In particular embodiments, the sequences forming the guide are first synthesized using the standard phosphoramidite synthetic protocol (Herdewijn, P., ed., Methods in Molecular Biology Col 288, Oligonucleotide Synthesis: Methods and Applications, Humana Press, New Jersey (2012)). In some embodiments, these sequences can be functionalized to contain an appropriate functional group for ligation using the standard protocol known in the art (Hermanson, G. T., Bioconjugate Techniques, Academic Press (2013)). Examples of functional groups include, but are not limited to, hydroxyl, amine, carboxylic acid, carboxylic acid halide, carboxylic acid active ester, aldehyde, carbonyl, chlorocarbonyl, imidazolylcarbonyl, hydrozide, semicarbazide, thio semicarbazide, thiol, maleimide, haloalkyl, sufonyl, ally, propargyl, diene, alkyne, and azide. Once this sequence is functionalized, a covalent chemical bond or linkage can be formed between this sequence and the direct repeat sequence. Examples of chemical bonds include, but are not limited to, those based on carbamates, ethers, esters, amides, imines, amidines, aminotrizines, hydrozone, disulfides, thioethers, thioesters, phosphorothioates, phosphorodithioates, sulfonamides, sulfonates, fulfones, sulfoxides, ureas, thioureas, hydrazide, oxime, triazole, photolabile linkages, C—C bond forming groups such as Diels-Alder cyclo-addition pairs or ring-closing metathesis pairs, and Michael reaction pairs.

[0092] In some embodiments, these stem-loop forming sequences can be chemically synthesized. In some embodiments, the chemical synthesis uses automated, solid-phase oligonucleotide synthesis machines with 2'-acetoxyethyl orthoester (2'-ACE) (Scaringe et al., J. Am. Chem. Soc. (1998) 120: 11820-11821; Scaringe, Methods Enzymol. (2000) 317: 3-18) or 2'-thionocarbamate (2'-TC) chemistry (Dellinger et al., J. Am. Chem. Soc. (2011) 133: 11540-11546; Hendel et al., Nat. Biotechnol. (2015) 33:985-989).

[0093] In certain embodiments, the guide molecule comprises (1) a guide sequence capable of hybridizing to a target locus and (2) a tracr mate or direct repeat sequence whereby the direct repeat sequence is located upstream (i.e., 5') from the guide sequence. In a particular embodiment the seed sequence (i.e. the sequence essential critical for recognition and/or hybridization to the sequence at the target locus) of th guide sequence is approximately within the first 10 nucleotides of the guide sequence.

[0094] In a particular embodiment the guide molecule comprises a guide sequence linked to a direct repeat sequence, wherein the direct repeat sequence comprises one or more stem loops or optimized secondary structures. In particular embodiments, the direct repeat has a minimum length of 16 nts and a single stem loop. In further embodiments the direct repeat has a length longer than 16 nts, preferably more than 17 nts, and has more than one stem loops or optimized secondary structures. In particular embodiments the guide molecule comprises or consists of the guide sequence linked to all or part of the natural direct repeat sequence. A typical Type V or Type VI CRISPR-cas guide molecule comprises (in 3' to 5' direction or in 5' to 3' direction): a guide sequence a first complimentary stretch (the "repeat"), a loop (which is typically 4 or 5 nucleotides long), a second complementary stretch (the "anti-repeat" being complementary to the repeat), and a poly A (often poly U in RNA) tail (terminator). In certain embodiments, the direct repeat sequence retains its natural architecture and forms a single stem loop. In particular embodiments, certain aspects of the guide architecture can be modified, for example by addition, subtraction, or substitution of features, whereas certain other aspects of guide architecture are maintained. Preferred locations for engineered guide molecule modifications, including but not limited to insertions, deletions, and substitutions include guide termini and regions of the guide molecule that are exposed when complexed with the CRISPR-Cas protein and/or target, for example the stemloop of the direct repeat sequence.

[0095] In particular embodiments, the stem comprises at least about 4 bp comprising complementary X and Y sequences, although stems of more, e.g., 5, 6, 7, 8, 9, 10, 11 or 12 or fewer, e.g., 3, 2, base pairs are also contemplated. Thus, for example X2-10 and Y2-10 (wherein X and Y represent any complementary set of nucleotides) may be contemplated. In one aspect, the stem made of the X and Y nucleotides, together with the loop will form a complete hairpin in the overall secondary structure; and this may be advantageous and the amount of base pairs can be any amount that forms a complete hairpin. In one aspect, any complementary X:Y basepairing sequence (e.g., as to length) is tolerated, so long as the secondary structure of the entire guide molecule is preserved. In one aspect, the loop

that connects the stem made of X:Y basepairs can be any sequence of the same length (e.g., 4 or 5 nucleotides) or longer that does not interrupt the overall secondary structure of the guide molecule. In one aspect, the stemloop can further comprise, e.g. an MS2 aptamer. In one aspect, the stem comprises about 5-7 bp comprising complementary X and Y sequences, although stems of more or fewer basepairs are also contemplated. In one aspect, non-Watson Crick basepairing is contemplated, where such pairing otherwise generally preserves the architecture of the stemloop at that position.

[0096] In particular embodiments the natural hairpin or stemloop structure of the guide molecule is extended or replaced by an extended stemloop. It has been demonstrated that extension of the stem can enhance the assembly of the guide molecule with the CRISPR-Cas proten (Chen et al. Cell. (2013); 155(7): 1479-1491). In particular embodiments the stem of the stemloop is extended by at least 1, 2, 3, 4, 5 or more complementary basepairs (i.e. corresponding to the addition of 2, 4, 6, 8, 10 or more nucleotides in the guide molecule). In particular embodiments these are located at the end of the stem, adjacent to the loop of the stemloop.

[0097] In particular embodiments, the susceptibility of the guide molecule to RNAses or to decreased expression can be reduced by slight modifications of the sequence of the guide molecule which do not affect its function. For instance, in particular embodiments, premature termination of transcription, such as premature transcription of U6 Pol-III, can be removed by modifying a putative Pol-III terminator (4 consecutive U's) in the guide molecules sequence. Where such sequence modification is required in the stemloop of the guide molecule, it is preferably ensured by a basepair flip.

[0098] In a particular embodiment the direct repeat may be modified to comprise one or more protein-binding RNA aptamers. In a particular embodiment, one or more aptamers may be included such as part of optimized secondary structure. Such aptamers may be capable of binding a bacteriophage coat protein as detailed further herein.

[0099] In some embodiments, the guide molecule forms a duplex with a target RNA comprising at least one target cytosine residue to be edited. Upon hybridization of the guide RNA molecule to the target RNA, the cytidine deaminase binds to the single strand RNA in the duplex made accessible by the mismatch in the guide sequence and catalyzes deamination of one or more target cytosine residues comprised within the stretch of mismatching nucleotides.

[0100] A guide sequence, and hence a nucleic acid-targeting guide RNA may be selected to target any target nucleic acid sequence. The target sequence may be mRNA.

[0101] In certain embodiments, the target sequence should be associated with a PAM (protospacer adjacent motif) or PFS (protospacer flanking sequence or site); that is, a short sequence recognized by the CRISPR complex. Depending on the nature of the CRISPR-Cas protein, the target sequence should be selected such that its complementary sequence in the DNA duplex (also referred to herein as the non-target sequence) is upstream or downstream of the PAM. In the embodiments of the present invention where the CRISPR-Cas protein is a Cas13 protein, the complementary sequence of the target sequence is downstream or 3' of the PAM or upstream or 5' of the PAM. The precise sequence and length requirements for the PAM differ depending on the Cas13 protein used, but PAMs are typically 2-5 base pair sequences adjacent the protospacer (that is, the target sequence). Examples of the natural PAM sequences for different Cas13 orthologues are provided herein below and the skilled person will be able to identify further PAM sequences for use with a given Cas13 protein.

[0102] Further, engineering of the PAM Interacting (PI) domain may allow programing of PAM specificity, improve target site recognition fidelity, and increase the versatility of the CRISPR-Cas protein, for example as described for Cas9 in Kleinstiver B P et al. Engineered CRISPR-Cas9 nucleases with altered PAM specificities. Nature. 2015 Jul. 23; 523 (7561):481-5. doi: 10.1038/nature14592. As further detailed herein, the skilled person will understand that Cas13 proteins may be modified analogously.

[0103] In particular embodiment, the guide is an escorted guide. By "escorted" is meant that the CRISPR-Cas system or complex or guide is delivered to a selected time or place within a cell, so that activity of the CRISPR-Cas system or complex or guide is spatially or temporally controlled. For example, the activity and destination of the 3 CRISPR-Cas system or complex or guide may be controlled by an escort RNA aptamer sequence that has binding affinity for an aptamer ligand, such as a cell surface protein or other localized cellular component. Alternatively, the escort aptamer may for example be responsive to an aptamer effector on or in the cell, such as a transient effector, such as an external energy source that is applied to the cell at a particular time.

[0104] The escorted CRISPR-Cas systems or complexes may have a guide molecule with a functional structure designed to improve guide molecule structure, architecture, stability, genetic expression, or any combination thereof. Such a structure can include an aptamer.

[0105] Aptamers are biomolecules that can be designed or selected to bind tightly to other ligands, for example using a technique called systematic evolution of ligands by exponential enrichment (SELEX; Tuerk C, Gold L: "Systematic evolution of ligands by exponential enrichment: RNA ligands to bacteriophage T4 DNA polymerase." Science 1990, 249:505-510). Nucleic acid aptamers can for example be selected from pools of random-sequence oligonucleotides, with high binding affinities and specificities for a wide range of biomedically relevant targets, suggesting a wide range of therapeutic utilities for aptamers (Keefe, Anthony D., Supriya Pai, and Andrew Ellington. "Aptamers as therapeutics." Nature Reviews Drug Discovery 9.7 (2010): 537-550). These characteristics also suggest a wide range of uses for aptamers as drug delivery vehicles (Levy-Nissenbaum, Etgar, et al. "Nanotechnology and aptamers: applications in drug delivery." Trends in biotechnology 26.8 (2008): 442-449; and, Hicke B J, Stephens A W. "Escort aptamers: a delivery service for diagnosis and therapy." J Clin Invest 2000, 106:923-928.). Aptamers may also be constructed that function as molecular switches, responding to a que by changing properties, such as RNA aptamers that bind fluorophores to mimic the activity of green fluorescent protein (Paige, Jeremy S., Karen Y. Wu, and Samie R. Jaffrey. "RNA mimics of green fluorescent protein." Science 333.6042 (2011): 642-646). It has also been suggested that aptamers may be used as components of targeted siRNA therapeutic delivery systems, for example targeting cell

surface proteins (Zhou, Jiehua, and John J. Rossi. "Aptamer-targeted cell-specific RNA interference." Silence 1.1 (2010): 4).

[0106] Accordingly, in particular embodiments, the guide molecule is modified, e.g., by one or more aptamer(s) designed to improve guide molecule delivery, including delivery across the cellular membrane, to intracellular compartments, or into the nucleus. Such a structure can include, either in addition to the one or more aptamer(s) or without such one or more aptamer(s), moiety(ies) so as to render the guide molecule deliverable, inducible or responsive to a selected effector. The invention accordingly comprehends a guide molecule that responds to normal or pathological physiological conditions, including without limitation pH, hypoxia, O_2 concentration, temperature, protein concentration, enzymatic concentration, lipid structure, light exposure, mechanical disruption (e.g. ultrasound waves), magnetic fields, electric fields, or electromagnetic radiation.

[0107] Light responsiveness of an inducible system may be achieved via the activation and binding of cryptochrome-2 and CIB1. Blue light stimulation induces an activating conformational change in cryptochrome-2, resulting in recruitment of its binding partner CIB1. This binding is fast and reversible, achieving saturation in <15 sec following pulsed stimulation and returning to baseline<15 min after the end of stimulation. These rapid binding kinetics result in a system temporally bound only by the speed of transcription/translation and transcript/protein degradation, rather than uptake and clearance of inducing agents. Cryptochrome-2 activation is also highly sensitive, allowing for the use of low light intensity stimulation and mitigating the risks of phototoxicity. Further, in a context such as the intact mammalian brain, variable light intensity may be used to control the size of a stimulated region, allowing for greater precision than vector delivery alone may offer.

[0108] The disclosure contemplates energy sources such as electromagnetic radiation, sound energy or thermal energy to induce the guide. Advantageously, the electromagnetic radiation is a component of visible light. In a preferred embodiment, the light is a blue light with a wavelength of about 450 to about 495 nm. In an especially preferred embodiment, the wavelength is about 488 nm. In another preferred embodiment, the light stimulation is via pulses. The light power may range from about 0-9 mW/cm^2. In a preferred embodiment, a stimulation paradigm of as low as 0.25 sec every 15 sec should result in maximal activation.

[0109] The chemical or energy sensitive guide may undergo a conformational change upon induction by the binding of a chemical source or by the energy allowing it act as a guide and have the Cas13 CRISPR-Cas system or complex function. The invention can involve applying the chemical source or energy so as to have the guide function and the Cas13 CRISPR-Cas system or complex function; and optionally further determining that the expression of the genomic locus is altered.

[0110] There are several different designs of this chemical inducible system: 1. ABI-PYL based system inducible by Abscisic Acid (ABA) (see, e.g., stke.sciencemag.org/cgi/content/abstract/sigtrans; 4/164/rs2), 2. FKBP-FRB based system inducible by rapamycin (or related chemicals based on rapamycin) (see, e.g., www.nature.com/nmeth/journal/v2/n6/full/nmeth763.html), 3. GID1-GAI based system inducible by Gibberellin (GA) (see, e.g., nature.com/nchembio/journal/v8/n5/full/nchembio.922.html).

[0111] A chemical inducible system can be an estrogen receptor (ER) based system inducible by 4-hydroxytamoxifen (4OHT) (see, e.g., //www.pnas.org/content/104/3/1027.abstract). A mutated ligand-binding domain of the estrogen receptor called ERT2 translocates into the nucleus of cells upon binding of 4-hydroxytamoxifen. In further embodiments of the invention any naturally occurring or engineered derivative of any nuclear receptor, thyroid hormone receptor, retinoic acid receptor, estrogen receptor, estrogen-related receptor, glucocorticoid receptor, progesterone receptor, androgen receptor may be used in inducible systems analogous to the ER based inducible system.

[0112] Another example inducible system is based on the design using Transient receptor potential (TRP) ion channel based system inducible by energy, heat or radio-wave (see, e.g., sciencemag.org/content/336/6081/604). These TRP family proteins respond to different stimuli, including light and heat. When this protein is activated by light or heat, the ion channel will open and allow the entering of ions such as calcium into the plasma membrane. This influx of ions will bind to intracellular ion interacting partners linked to a polypeptide including the guide and the other components of the Cas13 CRISPR-Cas complex or system, and the binding will induce the change of sub-cellular localization of the polypeptide, leading to the entire polypeptide entering the nucleus of cells. Once inside the nucleus, the guide protein and the other components of the Cas13 CRISPR-Cas complex will be active and modulating target gene expression in cells.

[0113] While light activation may be an advantageous embodiment, sometimes it may be disadvantageous especially for in vivo applications in which the light may not penetrate the skin or other organs. In this instance, other methods of energy activation are contemplated, in particular, electric field energy and/or ultrasound which have a similar effect.

[0114] Electric field energy is preferably administered substantially as described in the art, using one or more electric pulses of from about 1 Volt/cm to about 10 kVolts/cm under in vivo conditions. Instead of or in addition to the pulses, the electric field may be delivered in a continuous manner. The electric pulse may be applied for between 1 μs and 500 milliseconds, preferably between 1 μs and 100 milliseconds. The electric field may be applied continuously or in a pulsed manner for 5 about minutes.

[0115] As used herein, 'electric field energy' is the electrical energy to which a cell is exposed. Preferably the electric field has a strength of from about 1 Volt/cm to about 10 kVolts/cm or more under in vivo conditions (see WO97/49450).

[0116] As used herein, the term "electric field" includes one or more pulses at variable capacitance and voltage and including exponential and/or square wave and/or modulated wave and/or modulated square wave forms. References to electric fields and electricity should be taken to include reference the presence of an electric potential difference in the environment of a cell. Such an environment may be set up by way of static electricity, alternating current (AC), direct current (DC), etc., as known in the art. The electric field may be uniform, non-uniform or otherwise, and may vary in strength and/or direction in a time dependent manner.

[0117] Single or multiple applications of electric field, as well as single or multiple applications of ultrasound are also possible, in any order and in any combination. The ultra-

sound and/or the electric field may be delivered as single or multiple continuous applications, or as pulses (pulsatile delivery).

[0118] Electroporation has been used in both in vitro and in vivo procedures to introduce foreign material into living cells. With in vitro applications, a sample of live cells is first mixed with the agent of interest and placed between electrodes such as parallel plates. Then, the electrodes apply an electrical field to the cell/implant mixture. Examples of systems that perform in vitro electroporation include the Electro Cell Manipulator ECM600 product, and the Electro Square Porator T820, both made by the BTX Division of Genetronics, Inc (see U.S. Pat. No. 5,869,326).

[0119] The known electroporation techniques (both in vitro and in vivo) function by applying a brief high voltage pulse to electrodes positioned around the treatment region. The electric field generated between the electrodes causes the cell membranes to temporarily become porous, whereupon molecules of the agent of interest enter the cells. In known electroporation applications, this electric field comprises a single square wave pulse on the order of 1000 V/cm, of about 100 .mu.s duration. Such a pulse may be generated, for example, in known applications of the Electro Square Porator T820.

[0120] Preferably, the electric field has a strength of from about 1 V/cm to about 10 kV/cm under in vitro conditions. Thus, the electric field may have a strength of 1 V/cm, 2 V/cm, 3 V/cm, 4 V/cm, 5 V/cm, 6 V/cm, 7 V/cm, 8 V/cm, 9 V/cm, 10 V/cm, 20 V/cm, 50 V/cm, 100 V/cm, 200 V/cm, 300 V/cm, 400 V/cm, 500 V/cm, 600 V/cm, 700 V/cm, 800 V/cm, 900 V/cm, 1 kV/cm, 2 kV/cm, 5 kV/cm, 10 kV/cm, 20 kV/cm, 50 kV/cm or more. More preferably from about 0.5 kV/cm to about 4.0 kV/cm under in vitro conditions. Preferably the electric field has a strength of from about 1 V/cm to about 10 kV/cm under in vivo conditions. However, the electric field strengths may be lowered where the number of pulses delivered to the target site are increased. Thus, pulsatile delivery of electric fields at lower field strengths is envisaged.

[0121] Preferably the application of the electric field is in the form of multiple pulses such as double pulses of the same strength and capacitance or sequential pulses of varying strength and/or capacitance. As used herein, the term "pulse" includes one or more electric pulses at variable capacitance and voltage and including exponential and/or square wave and/or modulated wave/square wave forms.

[0122] Preferably the electric pulse is delivered as a waveform selected from an exponential wave form, a square wave form, a modulated wave form and a modulated square wave form.

[0123] A preferred embodiment employs direct current at low voltage. Thus, Applicants disclose the use of an electric field which is applied to the cell, tissue or tissue mass at a field strength of between 1V/cm and 20V/cm, for a period of 100 milliseconds or more, preferably 15 minutes or more.

[0124] Ultrasound is advantageously administered at a power level of from about 0.05 W/cm^2 to about 100 W/cm^2. Diagnostic or therapeutic ultrasound may be used, or combinations thereof.

[0125] As used herein, the term "ultrasound" refers to a form of energy which consists of mechanical vibrations the frequencies of which are so high they are above the range of human hearing. Lower frequency limit of the ultrasonic spectrum may generally be taken as about 20 kHz. Most diagnostic applications of ultrasound employ frequencies in the range 1 and 15 MHz' (From Ultrasonics in Clinical Diagnosis, P. N. T. Wells, ed., 2nd. Edition, Publ. Churchill Livingstone [Edinburgh, London & NY, 1977]).

[0126] Ultrasound has been used in both diagnostic and therapeutic applications. When used as a diagnostic tool ("diagnostic ultrasound"), ultrasound is typically used in an energy density range of up to about 100 mW/cm^2 (FDA recommendation), although energy densities of up to 750 mW/cm^2 have been used. In physiotherapy, ultrasound is typically used as an energy source in a range up to about 3 to 4 W/cm^2 (WHO recommendation). In other therapeutic applications, higher intensities of ultrasound may be employed, for example, HIFU at 100 W/cm up to 1 kW/cm^2 (or even higher) for short periods of time. The term "ultrasound" as used in this specification is intended to encompass diagnostic, therapeutic, and focused ultrasound.

[0127] Focused ultrasound (FUS) allows thermal energy to be delivered without an invasive probe (see Morocz et al 1998 Journal of Magnetic Resonance Imaging Vol. 8, No. 1, pp. 136-142). Another form of focused ultrasound is high intensity focused ultrasound (HIFU) which is reviewed by Moussatov et al in Ultrasonics (1998) Vol. 36, No. 8, pp. 893-900 and TranHuuHue et al in Acustica (1997) Vol. 83, No. 6, pp. 1103-1106.

[0128] Preferably, a combination of diagnostic ultrasound and a therapeutic ultrasound is employed. This combination is not intended to be limiting, however, and the skilled reader will appreciate that any variety of combinations of ultrasound may be used. Additionally, the energy density, frequency of ultrasound, and period of exposure may be varied.

[0129] Preferably the exposure to an ultrasound energy source is at a power density of from about 0.05 to about 100 Wcm^{-2}. Even more preferably, the exposure to an ultrasound energy source is at a power density of from about 1 to about 15 Wcm^{-2}.

[0130] Preferably the exposure to an ultrasound energy source is at a frequency of from about 0.015 to about 10.0 MHz. More preferably the exposure to an ultrasound energy source is at a frequency of from about 0.02 to about 5.0 MHz or about 6.0 MHz. Most preferably, the ultrasound is applied at a frequency of 3 MHz.

[0131] Preferably the exposure is for periods of from about 10 milliseconds to about 60 minutes. Preferably the exposure is for periods of from about 1 second to about 5 minutes. More preferably, the ultrasound is applied for about 2 minutes. Depending on the particular target cell to be disrupted, however, the exposure may be for a longer duration, for example, for 15 minutes.

[0132] Advantageously, the target tissue is exposed to an ultrasound energy source at an acoustic power density of from about 0.05 Wcm^{-2} to about 10 Wcm^{-2} with a frequency ranging from about 0.015 to about 10 MHz (see WO 98/52609). However, alternatives are also possible, for example, exposure to an ultrasound energy source at an acoustic power density of above 100 Wcm^{-2}, but for reduced periods of time, for example, 1000 Wcm^{-2} for periods in the millisecond range or less.

[0133] Preferably the application of the ultrasound is in the form of multiple pulses; thus, both continuous wave and pulsed wave (pulsatile delivery of ultrasound) may be employed in any combination. For example, continuous wave ultrasound may be applied, followed by pulsed wave

ultrasound, or vice versa. This may be repeated any number of times, in any order and combination. The pulsed wave ultrasound may be applied against a background of continuous wave ultrasound, and any number of pulses may be used in any number of groups.

[0134] Preferably, the ultrasound may comprise pulsed wave ultrasound. In a highly preferred embodiment, the ultrasound is applied at a power density of 0.7 Wcm-2 or 1.25 Wcm-2 as a continuous wave. Higher power densities may be employed if pulsed wave ultrasound is used.

[0135] Use of ultrasound is advantageous as, like light, it may be focused accurately on a target. Moreover, ultrasound is advantageous as it may be focused more deeply into tissues unlike light. It is therefore better suited to whole-tissue penetration (such as but not limited to a lobe of the liver) or whole organ (such as but not limited to the entire liver or an entire muscle, such as the heart) therapy. Another important advantage is that ultrasound is a non-invasive stimulus which is used in a wide variety of diagnostic and therapeutic applications. By way of example, ultrasound is well known in medical imaging techniques and, additionally, in orthopedic therapy. Furthermore, instruments suitable for the application of ultrasound to a subject vertebrate are widely available and their use is well known in the art.

[0136] In particular embodiments, the guide molecule is modified by a secondary structure to increase the specificity of the CRISPR-Cas system and the secondary structure can protect against exonuclease activity and allow for 5' additions to the guide sequence also referred to herein as a protected guide molecule.

[0137] In one aspect, the invention provides for hybridizing a "protector RNA" to a sequence of the guide molecule, wherein the "protector RNA" is an RNA strand complementary to the 3' end of the guide molecule to thereby generate a partially double-stranded guide RNA. In an embodiment of the invention, protecting mismatched bases (i.e. the bases of the guide molecule which do not form part of the guide sequence) with a perfectly complementary protector sequence decreases the likelihood of target RNA binding to the mismatched basepairs at the 3' end. In particular embodiments of the invention, additional sequences comprising an extended length may also be present within the guide molecule such that the guide comprises a protector sequence within the guide molecule. This "protector sequence" ensures that the guide molecule comprises a "protected sequence" in addition to an "exposed sequence" (comprising the part of the guide sequence hybridizing to the target sequence). In particular embodiments, the guide molecule is modified by the presence of the protector guide to comprise a secondary structure such as a hairpin. Advantageously there are three or four to thirty or more, e.g., about 10 or more, contiguous base pairs having complementarity to the protected sequence, the guide sequence or both. It is advantageous that the protected portion does not impede thermodynamics of the CRISPR-Cas system interacting with its target. By providing such an extension including a partially double stranded guide molecule, the guide molecule is considered protected and results in improved specific binding of the CRISPR-Cas complex, while maintaining specific activity.

[0138] In particular embodiments, use is made of a truncated guide (tru-guide), i.e. a guide molecule which comprises a guide sequence which is truncated in length with respect to the canonical guide sequence length. As described by Nowak et al. (Nucleic Acids Res (2016) 44 (20): 9555-9564), such guides may allow catalytically active CRISPR-Cas enzyme to bind its target without cleaving the target RNA. In particular embodiments, a truncated guide is used which allows the binding of the target but retains only nickase activity of the CRISPR-Cas enzyme.

[0139] In certain example embodiments, the system may comprise a first guide sequence and a second guide sequence such as used in paired nickase system or self-inactivating systems. Paired nickase systems are used, for example, to minimize off-target effects. Typically, guides are designed in pairs and used with a nickase to introduce two nicks, one on each strand, into a DNA duplex, each nick targeted to adjacent but different sequences of a genomic locus. In an embodiment, the guides are expressed from the same promoter. In and embodiment, the guides are in tandem. In such embodiments, the guides are designed to work together, encoded on a single polynucleotide, and packaged together. By reducing or eliminating recombination or template switching activity, the invention improves the performance of multiplexed nickase systems comprising two or more guide pairs (i.e., targeting two or more genetic loci). In a self-inactivating (SIN) system two or more loci are targeted. One target comprises, for example, a genomic locus intended to be modified and the second target comprises a locus associated with a CRISPR system component whereby the function of the CRISPR system may be targeted. In certain SIN systems, it will be desired to maintain the linkage of a guide that targets the genomic locus with the guide that targets the CRISPR component. Example self-inactivating systems are disclosed in WO/2015/070083, WO/2015/089354, and WO/2015/089351. Example tandem guide systems are disclosed in WO/2014/204724, WO/2014/093622, and WO/2014/204725.

Unique Molecular Sequence

[0140] In certain example embodiments, one of the engineered associations may be a unique molecular identifier. The unique molecular identifier may be a random nucleotide sequence that uniquely identifies the polynucleotide and/or the other engineered associations encoded on the first polynucleotide. In certain example embodiment, the unique molecular sequence may be a barcode. The term "barcode" as used herein refers to a short sequence of nucleotides (for example, DNA or RNA) that is used as an identifier for an associated molecule, such as a target molecule and/or target nucleic acid, or as an identifier of the source of an associated molecule, such as a cell-of-origin. A barcode may also refer to any unique, non-naturally occurring, nucleic acid sequence that may be used to identify the originating source of a nucleic acid fragment. Although it is not necessary to understand the mechanism of an invention, it is believed that the barcode sequence provides a high-quality individual read of a barcode associated with a single cell, a viral vector, labeling ligand (e.g., an aptamer), protein, shRNA, sgRNA or cDNA such that multiple species can be sequenced together.

[0141] Barcoding may be performed based on any of the compositions or methods disclosed in patent publication WO 2014047561 A1, Compositions and methods for labeling of agents, incorporated herein in its entirety. In certain embodiments barcoding uses an error correcting scheme (T. K. Moon, Error Correction Coding: Mathematical Methods and Algorithms (Wiley, New York, ed. 1, 2005)). Not being

bound by a theory, amplified sequences from single cells can be sequenced together and resolved based on the barcode associated with each cell.

[0142] In preferred embodiments, sequencing is performed using unique molecular identifiers (UMI). The term "unique molecular identifiers" (UMI) as used herein refers to a sequencing linker or a subtype of nucleic acid barcode used in a method that uses molecular tags to detect and quantify unique amplified products. A UMI is used to distinguish effects through a single clone from multiple clones. The term "clone" as used herein may refer to a single mRNA or target nucleic acid to be sequenced. The UMI may also be used to determine the number of transcripts that gave rise to an amplified product, or in the case of target barcodes as described herein, the number of binding events. In preferred embodiments, the amplification is by PCR or multiple displacement amplification (MDA).

[0143] In certain embodiments, an UMI with a random sequence of between 4 and 20 base pairs is added to a template, which is amplified and sequenced. In preferred embodiments, the UMI is added to the 5' end of the template. Sequencing allows for high resolution reads, enabling accurate detection of true variants. As used herein, a "true variant" will be present in every amplified product originating from the original clone as identified by aligning all products with a UMI. Each clone amplified will have a different random UMI that will indicate that the amplified product originated from that clone. Background caused by the fidelity of the amplification process can be eliminated because true variants will be present in all amplified products and background representing random error will only be present in single amplification products (See e.g., Islam S. et al., 2014. Nature Methods No: 11, 163-166). Not being bound by a theory, the UMI's are designed such that assignment to the original can take place despite up to 4-7 errors during amplification or sequencing. Not being bound by a theory, an UMI may be used to discriminate between true barcode sequences.

[0144] Unique molecular identifiers can be used, for example, to normalize samples for variable amplification efficiency. For example, in various embodiments, featuring a solid or semisolid support (for example a hydrogel bead), to which nucleic acid barcodes (for example a plurality of barcodes sharing the same sequence) are attached, each of the barcodes may be further coupled to a unique molecular identifier, such that every barcode on the particular solid or semisolid support receives a distinct unique molecule identifier. A unique molecular identifier can then be, for example, transferred to a target molecule with the associated barcode, such that the target molecule receives not only a nucleic acid barcode, but also an identifier unique among the identifiers originating from that solid or semisolid support.

[0145] A nucleic acid barcode or UMI can have a length of at least, for example, 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, 35, 40, 45, 50, 60, 70, 80, 90, or 100 nucleotides, and can be in single- or double-stranded form. Target molecule and/or target nucleic acids can be labeled with multiple nucleic acid barcodes in combinatorial fashion, such as a nucleic acid barcode concatemer. Typically, a nucleic acid barcode is used to identify a target molecule and/or target nucleic acid as being from a particular discrete volume, having a particular physical property (for example, affinity, length, sequence, etc.), or having been subject to certain treatment conditions. Target molecule and/or target nucleic acid can be associated with multiple nucleic acid barcodes to provide information about all of these features (and more). Each member of a given population of UMIs, on the other hand, is typically associated with (for example, covalently bound to or a component of the same molecule as) individual members of a particular set of identical, specific (for example, discreet volume-, physical property-, or treatment condition-specific) nucleic acid barcodes. Thus, for example, each member of a set of origin-specific nucleic acid barcodes, or other nucleic acid identifier or connector oligonucleotide, having identical or matched barcode sequences, may be associated with (for example, covalently bound to or a component of the same molecule as) a distinct or different UMI.

[0146] As disclosed herein, unique nucleic acid identifiers may be used to label the target molecules and/or target nucleic acids, for example origin-specific barcodes and the like. The nucleic acid identifiers, nucleic acid barcodes, can include a short sequence of nucleotides that can be used as an identifier for an associated molecule, location, or condition. In certain embodiments, the nucleic acid identifier further includes one or more unique molecular identifiers and/or barcode receiving adapters. A nucleic acid identifier can have a length of about, for example, 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, 35, 40, 45, 50, 60, 70, 80, 90, or 100 base pairs (bp) or nucleotides (nt). In certain embodiments, a nucleic acid identifier can be constructed in combinatorial fashion by combining randomly selected indices (for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 indexes). Each such index is a short sequence of nucleotides (for example, DNA, RNA, or a combination thereof) having a distinct sequence. An index can have a length of about, for example, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 bp or nt. Nucleic acid identifiers can be generated, for example, by split-pool synthesis methods, such as those described, for example, in International Patent Publication Nos. WO 2014/047556 and WO 2014/143158, each of which is incorporated by reference herein in its entirety.

[0147] One or more nucleic acid identifiers (for example a nucleic acid barcode) can be attached, or "tagged," to a target molecule. This attachment can be direct (for example, covalent or noncovalent binding of the nucleic acid identifier to the target molecule) or indirect (for example, via an additional molecule). Such indirect attachments may, for example, include a barcode bound to a specific-binding agent that recognizes a target molecule. In certain embodiments, a barcode is attached to protein G and the target molecule is an antibody or antibody fragment. Attachment of a barcode to target molecules (for example, proteins and other biomolecules) can be performed using standard methods well known in the art. For example, barcodes can be linked via cysteine residues (for example, C-terminal cysteine residues). In other examples, barcodes can be chemically introduced into polypeptides (for example, antibodies) via a variety of functional groups on the polypeptide using appropriate group-specific reagents (see for example www.drmr.com/abcon). In certain embodiments, barcode tagging can occur via a barcode receiving adapter associate with (for example, attached to) a target molecule, as described herein.

[0148] Target molecules can be optionally labeled with multiple barcodes in combinatorial fashion (for example,

using multiple barcodes bound to one or more specific binding agents that specifically recognizing the target molecule), thus greatly expanding the number of unique identifiers possible within a particular barcode pool. In certain embodiments, barcodes are added to a growing barcode concatemer attached to a target molecule, for example, one at a time. In other embodiments, multiple barcodes are assembled prior to attachment to a target molecule. Compositions and methods for concatemerization of multiple barcodes are described, for example, in International Patent Publication No. WO 2014/047561, which is incorporated herein by reference in its entirety.

[0149] In some embodiments, a nucleic acid identifier (for example, a nucleic acid barcode) may be attached to sequences that allow for amplification and sequencing (for example, SBS3 and P5 elements for Illumina sequencing). In certain embodiments, a nucleic acid barcode can further include a hybridization site for a primer (for example, a single-stranded DNA primer) attached to the end of the barcode. For example, an origin-specific barcode may be a nucleic acid including a barcode and a hybridization site for a specific primer. In particular embodiments, a set of origin-specific barcodes includes a unique primer specific barcode made, for example, using a randomized oligo type NNNNNNNNNNNN.

[0150] A nucleic acid identifier can further include a unique molecular identifier and/or additional barcodes specific to, for example, a common support to which one or more of the nucleic acid identifiers are attached. Thus, a pool of target molecules can be added, for example, to a discrete volume containing multiple solid or semisolid supports (for example, beads) representing distinct treatment conditions (and/or, for example, one or more additional solid or semisolid support can be added to the discreet volume sequentially after introduction of the target molecule pool), such that the precise combination of conditions to which a given target molecule was exposed can be subsequently determined by sequencing the unique molecular identifiers associated with it.

[0151] Labeled target molecules and/or target nucleic acids associated origin-specific nucleic acid barcodes (optionally in combination with other nucleic acid barcodes as described herein) can be amplified by methods known in the art, such as polymerase chain reaction (PCR). For example, the nucleic acid barcode can contain universal primer recognition sequences that can be bound by a PCR primer for PCR amplification and subsequent high-throughput sequencing. In certain embodiments, the nucleic acid barcode includes or is linked to sequencing adapters (for example, universal primer recognition sequences) such that the barcode and sequencing adapter elements are both coupled to the target molecule. In particular examples, the sequence of the origin specific barcode is amplified, for example using PCR. In some embodiments, an origin-specific barcode further comprises a sequencing adaptor. In some embodiments, an origin-specific barcode further comprises universal priming sites. A nucleic acid barcode (or a concatemer thereof), a target nucleic acid molecule (for example, a DNA or RNA molecule), a nucleic acid encoding a target peptide or polypeptide, and/or a nucleic acid encoding a specific binding agent may be optionally sequenced by any method known in the art, for example, methods of high-throughput sequencing, also known as next generation sequencing or deep sequencing. A nucleic acid target molecule labeled with a barcode (for example, an origin-specific barcode) can be sequenced with the barcode to produce a single read and/or contig containing the sequence, or portions thereof, of both the target molecule and the barcode. Exemplary next generation sequencing technologies include, for example, Illumina sequencing, Ion Torrent sequencing, 454 sequencing, SOLiD sequencing, and nanopore sequencing amongst others. In some embodiments, the sequence of labeled target molecules is determined by non-sequencing based methods. For example, variable length probes or primers can be used to distinguish barcodes (for example, origin-specific barcodes) labeling distinct target molecules by, for example, the length of the barcodes, the length of target nucleic acids, or the length of nucleic acids encoding target polypeptides. In other instances, barcodes can include sequences identifying, for example, the type of molecule for a particular target molecule (for example, polypeptide, nucleic acid, small molecule, or lipid). For example, in a pool of labeled target molecules containing multiple types of target molecules, polypeptide target molecules can receive one identifying sequence, while target nucleic acid molecules can receive a different identifying sequence. Such identifying sequences can be used to selectively amplify barcodes labeling particular types of target molecules, for example, by using PCR primers specific to identifying sequences specific to particular types of target molecules. For example, barcodes labeling polypeptide target molecules can be selectively amplified from a pool, thereby retrieving only the barcodes from the polypeptide subset of the target molecule pool.

[0152] A nucleic acid barcode can be sequenced, for example, after cleavage, to determine the presence, quantity, or other feature of the target molecule. In certain embodiments, a nucleic acid barcode can be further attached to a further nucleic acid barcode. For example, a nucleic acid barcode can be cleaved from a specific-binding agent after the specific-binding agent binds to a target molecule or a tag (for example, an encoded polypeptide identifier element cleaved from a target molecule), and then the nucleic acid barcode can be ligated to an origin-specific barcode. The resultant nucleic acid barcode concatemer can be pooled with other such concatemers and sequenced. The sequencing reads can be used to identify which target molecules were originally present in which discrete volumes.

Libraries and Cell Lines

[0153] The compositions of the present invention further include libraries comprising a multiplicity of the retroviral systems disclosed herein. A number of libraries may be used in accordance with the present invention, including but not limited to, normalized and non-normalized libraries for sense and antisense expression; libraries selected for specific chromosomes or regions of chromosomes (e.g. as comprised in YACs or BACs), which would be possible by inclusion of the f1 origin; and libraries derived from a tissue source; and genomic libraries.

[0154] In some cases, the compositions herein comprise a viral expression library. The viral expression library may comprise viral particles, wherein each viral particle comprises a polynucleotide having engineered associations comprising a sequence encoding one or more genetic perturbations and a unique molecular sequence clone, and one or

more polypeptides that comprise non-recombinogenic RNA sequences, or proteins that are capable of dimerizing with the polynucleotide.

[0155] The libraries employed in embodiments of the subject methods can be produced using any convenient protocol. According to certain embodiments, preparing the libraries includes combining polynucleotide having a first engineered association and a second engineered association with a vector construct comprising a vector domain of vector sequence under conditions sufficient to produce transfection plasmids which, upon transfection of a packaging cell, result in the production of viral particles containing the polynucleotide as part of genomic nucleic acids encapsidated in viral protein shells. To prepare the product transfection plasmids used for transfection, a polynucleotide may be inserted into a vector nucleic acid, where any suitable protocol may be employed. Examples of suitable protocols include but are not limited to: DNA ligase mediated joining, recombination enzyme mediate joining, Gateway® cloning technology (Life Technologies, Carlsbad, Calif.), and the like.

[0156] The resultant product transfection plasmids may then be used to transfect a suitable packaging cell line for production of library viral particles. The packaging cell line provides the viral proteins that are required in trans for the packaging of the viral genomic RNA into viral particles. The packaging cell line may be any cell line that is capable of expressing retroviral proteins, including HEK293, HeLa, D17, MDCK, BHK, NIH3T3, CHO, CrFK, and Cf2Th. In some embodiments, the construct is used together with a viral reporter construct which may comprise one or more reporter genes under the control of a constitutive or conditional promoter. The packaging cell line may stably express necessary viral proteins. Such a packaging cell line is described, for example, in U.S. Pat. No. 6,218,181 Alternatively, a packaging cell line may be transiently transfected with plasmids comprising nucleic acids that encode the necessary viral proteins. In another embodiment, a packaging cell line that does not stably express the necessary viral proteins is co-transfected with two or more plasmids. One of the plasmids comprises the viral construct comprising the polynucleotide. The other plasmid(s) comprises nucleic acids encoding the proteins necessary to allow the cells to produce functional virus that is able to infect the desired host cell. The packaging cell line may not express envelope gene products. In this case, the packaging cell line will package the viral genome into particles that lack an envelope protein. As the envelope protein is responsible, in part, for the host range of the viral particles, the viruses preferably are pseudotyped. A "pseudotyped" retrovirus is a retroviral particle having an envelope protein that is from a virus other than the virus from which the RNA genome is derived. The envelope protein may be from a different retrovirus or a ion-retrovirus. One envelope protein is the vesicular stomatitis virus G (VSV-G) protein. Thus, the packaging cell line may be transfected with a plasmid that includes sequences encoding a membrane-associated protein, such as VSV-G, that will permit entry of the virus into a target cell. One of skill in the art can choose an appropriate pseudo type specific and/or more efficient for the target cell used. In addition to conferring a specific host range, a chosen pseudotype may permit the virus to be concentrated to a very high titer. Viruses alternatively can be pseudotyped with ecotropic envelope proteins that limit infection to a specific species.

[0157] The compositions of the present invention further include retrovirus particles derived from said first and second polynucleotides and other packaging vectors needed to form a complete viral particle. Such retrovirus particles are produced by the transfection of the polynucleotides and/or packaging vectors into retroviral cell packaging cell lines. Thus stably transfected cell lines comprising said sequences are also within the scope of the invention disclosed herein. The compositions of the invention further include provirus sequences derived from the retrovirus particles. The provirus sequences may be present in an integrated form within the genome of a recipient cell, or may be present in a free, circularized form. An integrated provirus is produced upon infection of a recipient cell, wherein the infection leads to the production an integration into the cell genome of the provirus nucleic acid sequence. The circularized provirus sequence may generally be produced upon excision of the integrated provirus from the recipient cell genome.

[0158] The compositions of the present invention still further include cells containing the retroviral systems disclosed herein, whether the packaging cell lines or recipient cell lines. Additionally, the present invention includes transgenic animals containing the retroviral systems disclosed herein, including preferably animals containing retroviral systems form which sequences (sense or antisense) are expressed in one or more cells.

Methods for Making Lentiviral System

[0159] In one aspect, the embodiments disclosed herein are directed to methods of preparing a lentiviral or retroviral system comprising a polynucleotide having engineered associations comprising a sequence encoding one or more genetic perturbations and a unique molecular sequence wherein the system has reduced recombination or template switching activity. The methods may comprise packaging the polynucleotide with a modulator of one or more activities of the system. The modulator may be an inhibitor of recombination or template switching activity. For example, the modular may be an inhibitor of template switching. In one embodiment, polynucleotides encoding the one or more genetic perturbation and associated unique molecular sequence are cloned into a suitable lentiviral or retroviral vector ("targeting vector"). Suitable vectors include, for example, pBA571 (Addgene Cat #85968), pMJ114 (Addgene Cat #85995), pMJ179 (Addgene Cat #85996), pMJ117 (Addgene Cat #85997). Carrier plasmids are likewise selected. The carrier plasmids do not include sequences encoding the one or more genetic perturbations or the unique molecular sequence. Instead carrier plasmids are selected to comprise non-recombinogenic sequences or encode proteins that are capable of dimerizing with the polynucleotide of sequence. Example carrier polynucleotides include pr_H2b-BFB (encoding a histone subunit tagged with blue fluorescent protein) and pLX_TRC131_LacZ (control vector used in ORF screens). In certain embodiments, the carrier plasmid may comprise a lentiviral or retroviral plasmid that has been modified to be non-integrating. For example, a lentiviral vector may be made non-integrating by mutating the 5' long terminal repeat (LTR) and having a short LTR to LTR distance of 2.1 kb. Example proteins that are capable of dimerizing are disclosed in retroviral nucleoproteins (NC). The target vector and carrier may then be introduced along with standard lentiviral or retroviral packaging plasmids that encode remaining elements need for full viral particle pro-

duction into a packaging cell lines to generate a viral clone library, each clone comprising a different target vector and one or more carrier vectors. The target vector may be diluted in a composition with one or more carrier vectors prior to introduction in the packaging cell line. In certain example embodiments, the target vector is diluted in a solution comprising one or more carrier vectors prior to introduction into the packaging cell line at a dilution of 1:10, 1:20, 1:30, 1:40, 1:50, 1:60, 1:70, 1:80, 1:90, 1:100, 1:200, 1:300, 1:400, 1:500, 1:600, 1:700, 1:800, 1:900, 1:1000, 1:2000, 1:3000, 1:4000, or 1:5000.

[0160] Also provided herein include a cell or cell line for the viral systems herein. The cell or cell line may be used for producing viral particles. In some cases, the compositions may comprise a cell or cell line for producing viral particles comprising a set of polynucleotide constructs such that the viral particles comprise polynucleotides having engineered associations comprising a sequence encoding one or more genetic perturbations and a unique molecular sequence clone, and one or more polypeptides that comprise non-recombinogenic RNA sequences, or proteins that are capable of dimerizing with the polynucleotide.

Genetic Screens

[0161] In some embodiments, the present disclosure includes methods for screening cells for genetic perturbations. The methods may comprise one or more of: (i) providing (e.g., culturing) a cell or population of cells in one or more discrete volumes; introducing the system described herein, such that each cell receives one or more polynucleotides each having at least one genetic perturbation and a unique identifier; detecting genomic, genetic, proteomic, epigenetic and/or phenotypic differences in single cells; and identifying the at least one genetic perturbation in each cell based on the unique identifier.

[0162] In one aspect, the present invention provides for a method of reconstructing a cellular network or circuit, comprising introducing at least 1, 2, 3, 4 or more single-order or combinatorial perturbations to a plurality of cells in a population of cells, wherein each cell in the plurality of the cells receives at least 1 perturbation; measuring comprising: detecting genomic, genetic, proteomic, epigenetic and/or phenotypic differences in single cells compared to one or more cells that did not receive any perturbation, and detecting the perturbation(s) in single cells; and determining measured differences relevant to the perturbations by applying a model accounting for co-variates to the measured differences, whereby intercellular and/or intracellular networks or circuits are inferred. The measuring in single cells may comprise single cell sequencing. The single cell sequencing may comprise cell barcodes, whereby the cell-of-origin of each RNA is recorded. The single cell sequencing may comprise unique molecular identifiers (UMI), whereby the capture rate of the measured signals, such as transcript copy number or probe binding events, in a single cell is determined. The model may comprise accounting for the capture rate of measured signals, whether the perturbation actually perturbed the cell (phenotypic impact), the presence of subpopulations of either different cells or cell states, and/or analysis of matched cells without any perturbation.

[0163] The single-order or combinatorial perturbations may comprise 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, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100 perturbations. The perturbation(s) may target genes in a pathway or intracellular network.

[0164] The measuring may comprise detecting the transcriptome of each of the single cells. The perturbation(s) may comprise one or more genetic perturbation(s). The perturbation(s) may comprise one or more epigenetic or epigenomic perturbation(s). At least one perturbation may be introduced with RNAi- or a CRISPR-Cas system. At least one perturbation may be introduced via a chemical agent, biological agent, an intracellular spatial relationship between two or more cells, an increase or decrease of temperature, addition or subtraction of energy, electromagnetic energy, or ultrasound.

[0165] The cell(s) may comprise a cell in a model non-human organism, a model non-human mammal that expresses a Cas protein, a mouse that expresses a Cas protein, a mouse that expresses Cpf1, a cell in vivo or a cell ex vivo or a cell in vitro. The cell(s) may also comprise a human cell.

[0166] The measuring or measured differences may comprise measuring or measured differences of DNA, RNA, protein, or post translational modification; or measuring or measured differences of protein or post translational modification correlated to RNA and/or DNA level(s).

[0167] The perturbing or perturbation(s) may comprise(s) genetic perturbing. The perturbing or perturbation(s) may comprise(s) single-order perturbations. The perturbing or perturbation(s) may comprise(s) combinatorial perturbations. The perturbing or perturbation(s) may comprise gene knock-down, gene knock-out, gene activation, gene insertion, or regulatory element deletion. The perturbation may result in a change. The perturbing or perturbation(s) may comprise genome-wide perturbation. The perturbing or perturbation(s) may comprise performing CRISPR-Cas-based perturbation. The perturbing or perturbation(s) may comprise performing pooled single or combinatorial CRISPR-Cas-based perturbation with a genome-wide library of sgRNAs. The perturbations may be of a selected group of targets based on similar pathways or network of targets.

[0168] The perturbing or perturbation(s) may comprises performing pooled combinatorial CRISPR-Cas-based perturbation with a genome-wide library of sgRNAs. Each sgRNA may be associated with a unique perturbation barcode. Each sgRNA may be co-delivered with a reporter mRNA comprising the unique perturbation barcode (or sgRNA perturbation barcode).

[0169] The perturbing or perturbation(s) may comprise subjecting the cell to an increase or decrease in temperature. The perturbing or perturbation(s) may comprise subjecting the cell to a chemical agent. The perturbing or perturbation (s) may comprise subjecting the cell to a biological agent. The biological agent may be a toll like receptor agonist or cytokine. The perturbing or perturbation(s) may comprise subjecting the cell to a chemical agent, biological agent and/or temperature increase or decrease across a gradient.

[0170] The cell may be in a microfluidic system. The cell may be in a droplet. The population of cells may be sequenced by using microfluidics to partition each individual cell into a droplet containing a unique barcode, thus allowing a cell barcode to be introduced.

[0171] The perturbing or perturbation(s) may comprise transforming or transducing the cell or a population that includes and from which the cell is isolated with one or more genomic sequence-perturbation constructs that perturbs a genomic sequence in the cell. The sequence-perturbation construct may be a viral vector, preferably a lentivirus vector. The perturbing or perturbation(s) may comprise multiplex transformation or transduction with a plurality of genomic sequence-perturbation constructs.

[0172] In another aspect, or in alternative embodiments of aspects described herein, the present invention provides for a method wherein proteins or transcripts expressed in single cells are determined in response to a perturbation, wherein the proteins or transcripts are detected in the single cells by binding of more than one labeling ligand comprising an oligonucleotide tag, and wherein the oligonucleotide tag comprises a unique constituent identifier (UCI) specific for a target protein or transcript. The single cells may be fixed in discrete particles. The discrete particles may be washed and sorted, such that cell barcodes may be added, e.g. sgRNA perturbation barcodes as described above. The oligonucleotide tag and sgRNA perturbation barcode may comprise a universal ligation handle sequence, whereby a unique cell barcode may be generated by split-pool ligation. The labeling ligand may comprise an oligonucleotide label comprising a regulatory sequence configured for amplification by T7 polymerase. The labeling ligands may comprise oligonucleotide sequences configured to hybridize to a transcript specific region. Not being bound by a theory, both proteins and RNAs may be detected after perturbation. The oligonucleotide label may further comprise a photocleavable linker. The oligonucleotide label may further comprise a restriction enzyme site between the labeling ligand and unique constituent identifier (UCI). The ligation handle may comprise a restriction site for producing an overhang complementary with a first index sequence overhang, and wherein the method further comprises digestion with a restriction enzyme. The ligation handle may comprise a nucleotide sequence complementary with a ligation primer sequence and wherein the overhang complementary with a first index sequence overhang is produced by hybridization of the ligation primer to the ligation handle. The method may further comprise quantitating the relative amount of UCI sequence associated with a first cell to the amount of the same UCI sequence associated with a second cell, whereby the relative differences of a cellular constituent between cell(s) are determined. The labeling ligand may comprise an antibody or an antibody fragment. The antibody fragment may be a nanobody, Fab, Fab', (Fab')2, Fv, ScFv, diabody, triabody, tetrabody, Bis-scFv, minibody, Fab2, or Fab3 fragment. The labeling ligand may comprise an aptamer. The labeling ligand may be a nucleotide sequence complementary to a target sequence.

[0173] Single cell sequencing may comprise whole transcriptome amplification.

[0174] The method in aspects of the invention may comprise comparing an RNA profile of the perturbed cell with any mutations in the cell to also correlate phenotypic or transcriptome profile and genotypic profile.

[0175] In another aspect, or in alternative embodiments of aspects described herein, the present invention provides for a method comprising determining genetic interactions by causing a set of P genetic perturbations in single cells of the population of cells, wherein the method comprises: determining, based upon random sampling, a subset of π genetic perturbations from the set of P genetic perturbations; performing said subset of π genetic perturbations in a population of cells; performing single-cell molecular profiling of the population of genetically perturbed cells; inferring, from the results and based upon the random sampling, single-cell molecular profiles for the set of P genetic perturbations in cells. The method may further comprise from the results, determining genetic interactions. The method may further comprise confirming genetic interactions determined with additional genetic manipulations.

[0176] The set of P genetic perturbations or said subset of π genetic perturbations may comprise single-order genetic perturbations. The set of P genetic perturbations or said subset of π genetic perturbations may comprise combinatorial genetic perturbations. The genetic perturbation may comprise gene knock-down, gene knock-out, gene activation, gene insertion, or regulatory element deletion. The set of P genetic perturbations or said subset of π genetic perturbations may comprise genome-wide perturbations. The set of P genetic perturbations or said subset of π genetic perturbations may comprise k-order combinations of single genetic perturbations, wherein k is an integer ranging from 2 to 15, and wherein the method comprises determining k-order genetic interactions. The set of P genetic perturbations may comprise combinatorial genetic perturbations, such as k-order combinations of single-order genetic perturbations, wherein k is an integer ranging from 2 to 15, and wherein the method comprises determining j-order genetic interactions, with $j<k$.

[0177] The method in aspects of this invention may comprise performing RNAi- or CRISPR-Cas-based perturbation. The method may comprise an array-format or pool-format perturbation. The method may comprise pooled single or combinatorial CRISPR-Cas-based perturbation with a genome-wide library of sgRNAs. The method may comprise pooled combinatorial CRISPR-Cas-based perturbation with a genome-wide library of sgRNAs.

[0178] The random sampling may comprise matrix completion, tensor completion, compressed sensing, or kernel learning. The random sampling may comprise matrix completion, tensor completion, or compressed sensing, and wherein π is of the order of log P.

[0179] The cell may comprise a eukaryotic cell. The eukaryotic cell may comprise a mammalian cell. The mammalian cell may comprise a human cell. The cell may be from a population comprising 10^2 to 10^8 cells and DNA or RNA or protein or post translational modification measurements or variables per cell comprise 50 or more.

[0180] The perturbation of the population of cells may be performed in vivo. The perturbation of the population of cells may be performed ex vivo and the population of cells may be adoptively transferred to a subject. The population of cells may comprise tumor cells. The method may comprise a lineage barcode associated with single cells, whereby the lineage or clonality of single cells may be determined.

[0181] The perturbing may be across a library of cells to thereby obtain RNA level and/or optionally protein level, whereby cell-to-cell circuit data at genomic or transcript or expression level is determined. The library of cells may comprise or is from a tissue sample. The tissue sample may comprise or is from a biopsy from a mammalian subject. The mammalian subject may comprise a human subject. The

biopsy may be from a tumor. The method may further comprise reconstructing cell-to-cell circuits.

[0182] The method may comprise measuring open chromatin and may comprise fragmenting chromatin inside isolated intact nuclei from a cell, adding universal primers at cutting sites, and uniquely tagging DNA that originated from the cell.

[0183] The method may comprise measuring protein and RNA levels and may comprise CyTOF.

[0184] In another aspect, the present invention provides for a method of determining any combination of protein detection, RNA detection, open chromatin detection, protein-protein interactions, protein-RNA interactions, or protein-DNA interactions comprising any of the preceding methods.

[0185] In another aspect, the present invention provides for a method for screening compounds or agents capable of modifying a cellular network or circuit comprising performing any method as described herein, wherein perturbing further comprises exposing the cell to each compound or agent.

[0186] In another aspect, the present invention provides for a method of identifying a therapeutic, and to a therapeutic identified by the method described herein.

[0187] In another aspect, the present invention provides a method of reconstructing a cellular network or circuit, comprising introducing at least 1, 2, 3, 4 or more single-order or combinatorial perturbations to each cell in a population of cells; measuring genomic, genetic and/or phenotypic differences of each cell and coupling combinatorial perturbations with measured differences to infer intercellular and/or intracellular networks or circuits. The single-order or combinatorial perturbations can comprise 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, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98 or 99 or massively parallel perturbations. The perturbation(s) can comprise one or more genetic perturbation. The perturbation(s) can comprise one or more epigenetic or epigenomic perturbation. The perturbation can be introduced with RNAi- or a CRISPR-Cas system. For example, reference is also made to Dahlman et al., Nature Biotechnology (2015) doi:10.1038/nbt.3390 Published online 5 Oct. 2015 to allow efficient orthogonal genetic and epigenetic manipulation. Dahlman et al., Nature Biotechnology (2015) doi:10.1038/nbt.3390 have developed a CRISPR-based method that uses catalytically active Cas9 and distinct single guide (sgRNA) constructs to knock out and activate different genes in the same cell. These sgRNAs, with 14- to 15-bp target sequences and MS2 binding loops, can activate gene expression using an active *Streptococcus pyogenes* Cas9 nuclease, without inducing double-stranded breaks. Dahlman et al., Nature Biotechnology (2015) doi:10.1038/nbt.3390 use these 'dead RNAs' to perform orthogonal gene knockout and transcriptional activation in human cells.

[0188] The at least one perturbation can be introduced via a chemical agent, an intracellular spatial relationship between two or more cells, an increase or decrease of temperature, addition or subtraction of energy, electromagnetic energy, or ultrasound. The cell can comprise a cell in a model non-human organism, a model non-human mammal that expresses a Cas protein, a mouse that expresses a Cas protein, a cell in vivo or a cell ex vivo or a cell in vitro. The measuring or measured differences can comprise measuring or measured differences of DNA, RNA, protein, or post translational modification; or measuring or measured differences of protein or post translational modification correlated to RNA and/or DNA level(s). The method can include sequencing, and prior to sequencing: perturbing and isolating a single cell with at least one labeling ligand specific for binding at one or more target RNA transcripts or isolating a single cell with at least one labeling ligand specific for binding at one or more target RNA transcripts and perturbing the cell; and/or lysing the cell under conditions wherein the labeling ligand binds to the target RNA transcript(s).

[0189] The method in aspects of this invention may also include, prior to sequencing perturbing and isolating a single cell with at least one labeling ligand specific for binding at one or more target RNA transcripts or isolating a single cell with at least one labeling ligand specific for binding at one or more target RNA transcripts and perturbing the cell; and lysing the cell under conditions wherein the labeling ligand binds to the target RNA transcript(s). The perturbing and isolating a single cell may be with at least one labeling ligand specific for binding at one or more target RNA transcripts. The isolating a single cell may be with at least one labeling ligand specific for binding at one or more target RNA transcripts and perturbing the cell.

[0190] The perturbing of the present invention may involve genetic perturbing, single-order genetic perturbations or combinatorial genetic perturbations. The perturbing may also involve gene knock-down, gene knock-out, gene activation, gene insertion or regulatory element deletion. The perturbation may be genome-wide perturbation. The perturbation may be performed by RNAi- or CRISPR-Cas-based perturbation, performed by pooled single or combinatorial CRISPR-Cas-based perturbation with a genome-wide library of sgRNAs or performing pooled combinatorial CRISPR-Cas-based perturbation with a genome-wide library of sgRNAs.

[0191] In addition to loss-of-function (LOF) mutations, embodiments disclosed herein may also be used to modulate transcription without modifying genomic sequences. For example, inactive Cas9 (dCas9) can be catalytically fused to transcriptional activation and repression domains. CRISPR activation (CRISPRa) and CRISPR inhibition (CRISPRi) can be achieved by direct fusion or recruitment of activation and repression domains, such as VP64 and KRAB, respectively. Methods for setting up GOF and LOF genetic screens are described in detail in Joung et al. Nat Protoc. 2017 April: 12(4): 828-863.

[0192] Methods and tools for genome-scale screening of perturbations in single cells using CRISPR-Cas9 have been described, herein referred to as perturb-seq (see e.g., Dixit et al., "Perturb-Seq: Dissecting Molecular Circuits with Scalable Single-Cell RNA Profiling of Pooled Genetic Screens" 2016, Cell 167, 1853-1866; Adamson et al., "A Multiplexed Single-Cell CRISPR Screening Platform Enables Systematic Dissection of the Unfolded Protein Response" 2016, Cell 167, 1867-1882; and International publication serial number WO/2017/075294). The present invention is compatible with perturb-seq, such that lentiviral vectors targeting genes for perturbation may be identified and assigned to the proteomic and gene expression readouts of single cells based on transcripts encoding for guide sequence specific

barcodes. The present invention can be used to prevent recombination during packaging lentiviral libraries that may shuffle associations between guide sequences and barcode transcripts, thus greatly improving phenotypic readouts associated with a perturbation.

Methods for Reducing Intermolecular Recombination

[0193] In some embodiments, the present disclosure provides methods for reducing intermolecular recombination with a lentiviral genome plasmid of interest in a library (e.g., lentiviral library). The methods may comprise mixing the lentiviral genome plasmid of interest with a lentiviral carrier plasmid and packaging the mixture. The lentiviral carrier plasmid may comprise a non-integrating lentiviral vector, a non-recombinogenic lentiviral vector, or a combination thereof. The library herein may comprise a barcode library, a plurality of guide polynucleotides, a plurality of sgRNAs, or any combination thereof.

[0194] The lentiviral genome plasmid of interest and the lentiviral carrier plasmid may be mixed at a suitable ratio. The ratio of the lentiviral genome plasmid of interest to the lentiviral carrier plasmid may be at least 1:1, 2:1, 10:1, 20:1, 30:1, 40:1, 50:1, 60:1, 70:1, 60:1, 70:1, 80:1, 90:1, 100:1, 120:1, 150:1, or 200:1.

[0195] The invention is further described in the following examples, which do not limit the scope of the invention described in the claims.

EXAMPLES

Example 1

[0196] Lentiviral vectors provide a convenient, scalable platform to deliver genetic perturbations to cells en masse and read out the identity of each perturbation by next-generation sequencing[1,2]. There is increasing interest in screening approaches reliant on the delivery of multiple library elements to each cell, for example, in CRISPR-based single-cell gene expression screens[3-8]. Such approaches facilitate the study of genetic interactions by probing cells with combinations of perturbations or convenient detection of perturbations by readout of a barcode sequence. However, the goal of accurately delivering a single integrated library variant per cell is complicated by aspects of lentiviral delivery.

[0197] Lentiviral virions normally contain two copies of the viral genome. During standard lentivirus production, transfection of packaging cells with multiple plasmids generates virions containing two distinct library elements, which can then lead to intermolecular recombination that shuffles variable library sequences ("barcode swapping"). Together with the inadvertent integration of multiple variants in individual target cells, this process has the effect of reducing the sensitivity of pooled screens. For screens where all library elements are read out (e.g. targeted pairs of gene knockouts), recombination events can be detected and filtered out before statistical analysis[6,9]. However, in situations where functional library elements are not sequenced directly, but are rather inferred via a linked barcode, recombination or multiple integration can lead to mislabeled data and has been noted to decrease the statistical power of genetic screens at a given number of cells analyzed[10,11].

[0198] Recombination can arise from the template-switching activity of the lentiviral reverse-transcriptase[12]. As the lentivirus capsid normally packages a dimer of RNA genomes, intermolecular recombination could in principle occur in target cells infected by a single virion. The fraction of target cells with recombined integrants depends on the distance between variable sequences and has been measured to exceed 30% for distances greater than 1 kb[11]. Such wide spacing of library elements is common when the elements are separated by regulatory sequences or when an element is used as a 3' barcode in an expressed transcript[10,11,13].

[0199] To quantify the frequencies of barcode swapping and multiple integration events, we performed clonal analysis of target cells transduced with a library of CRISPR sgRNA and transcribed barcode elements separated by >1.7 kb. Similar to other groups, Applicant found that standard lentiviral packaging results in substantial (>30%) barcode swapping between library elements. Applicant further observed that an unexpectedly high number of target cells had multiple library variants integrated into their genomes even when transduced at low multiplicity-of-infection (MOI). Here Applicant shows that by diluting the perturbation library plasmid with sufficient excess of carrier plasmid in the packaging step, Applicant was able to substantially reduce barcode swaps (<4%) and attenuate the rate of multiple integrations several-fold. Altogether, this co-packaging strategy constitutes a simple solution to improve data quality for genetic screens without constraining library vector design or necessitating individual ("arrayed") packaging of library element.

Results

[0200] In order to test the feasibility of barcoding a U6-driven sgRNA with a short sequence located in the 3' UTR of a Pol II-driven resistance transcript, Applicant individually cloned 8 lentiviral plasmids with different sgRNA-barcode pairs and transduced HeLa cells at an MOI<5%, pooling either before or after lentiviral packaging. After flow sorting and clonally expanding single cells, Applicant analyzed the sgRNA and barcode sequences present in each clone using next-generation sequencing (Methods). Applicant observed that pooled lentiviral packaging resulted in barcode swaps in 37% of clones with a single detected integration, whereas no swapping was detected between individually packaged lentiviral genome sequences (Table 1). Similar results were obtained when packaging a library of 400 barcodes (cloned as a pool) using the standard protocol. Applicant reports barcode swapping rates as the functional and measurable outcome of recombination. Overall, the results are consistent with observations by a number of groups and precautionary comments published in some of the first examples of pooled single-cell gene expression screens[10,11,14].

[0201] The standard pooled lentivirus packaging protocol calls for transfecting the packaging cell line with the lentiviral perturbation library and associated packaging plasmids needed to produce virus (Methods). The present clonal analysis of target cells transduced by virus produced in this manner revealed not only barcode swaps but also a higher occurrence of multiple integrants per cell than predicted by a Poisson model of independent integration events, even at MOI below 5%. The presence of multiple genomic integrants even at limiting virus dilutions could be explained by the ability of a single virion to integrate both packaged genomes, or non-independence of integration probability across target cells, possibly as a result of differences in cell state.

[0202] Hypothesizing that recombination and multiple integration events are driven by co-packaging of two RNA genomes per lentiviral capsid[13] and co-delivery of multiple genomes to individual target cells, Applicant tested dilution of the perturbation library plasmids in unrelated carrier plasmids as a means of mitigating both of these undesired effects. Three lentiviral plasmids were evaluated as carriers, including two integration-capable vectors (pR_H2B-BFP

encoding a histone subunit tagged with blue fluorescent protein, and pLX_TRC313LacZ, a control vector used in ORF screens). In addition, Applicant tested a non-integrating lentiviral vector with a mutated 5' long terminal repeat (LTR) and a short LTR-LTR distance of 2.1 kb in hopes of avoiding unnecessary genomic integrations[15]. All three carriers tested reduced recombination rates to 0-4%. Interestingly, Applicant found that while it was necessary to use the integrating carrier plasmids in 1000-fold excess over the perturbation library, the non-integrating carrier plasmid reduced barcode swaps to the same extent at a dilution of only 1:10, perhaps due to enhanced expression of the shorter LTR-LTR transcript in the packaging cell line. Furthermore, co-packaging with a non-homologous lentiviral vector also limited instances of multiple distinct integrations, likely due to a reduction in the probability that two perturbation library variants enter the target cell.

ished viral titer, Applicant was able to transduce a library of 1,000 perturbations with 300-fold cell coverage.

[0205] Applicant also explored whether recombination events hypothetically occurring in the packaging cell line could be reduced by shortening packaging times. The time from transfection to harvesting viral supernatant was reduced from 48 h to 11 h, a decrease in barcode swapping was not observed, consistent with a model where most of the recombination occurs in the target cells.

TABLE 1

Clonal analysis of lentiviral packaging strategies for barcoded perturbation libraries. Individual transduced cells were isolated by flow sorting and clonally expanded prior to genomic DNA extraction and examination of sgRNA and barcode identity by next-generation sequencing. Each clone was classified by the number of observed integrations, with single integrants further subdivided by whether the sgRNA matched the associated barcode. A recombination rate (rightmost column) was estimated by dividing the number of recombined single integrants by the total number of cells with a single integration. Standard packaging refers to transfection of the pooled perturbation library alone with packaging plasmids (pMD2.G and psPAX2); for arrayed packaging, each library element was individually co-transfected with packaging plasmids for production of a pure population of virions that was subsequently pooled. Carrier plasmids come in three varieties: non-lentiviral (pUC19), integrating lentiviral (pR_H2B-BFP and pLX_TRC313_LacZ) and non-integrating lentiviral (pR_LG). Finally, a quick harvest (11 hours) of the packaged lentivirus was also explored; for all other conditions, virus was packaged for 48 hours.

Packaging condition	# of barcodes	# of cell clones analyzed	Single integration, correct association	Single integration, barcode swap	Multiple integration	Estimated barcode swap rate	Relative titer
arrayed	8	48	46 (95.8%)	0 (0.0%)	2 (4.2%)	0%	100%
standard	8	61	34 (55.7%)	20 (32.8%)	7 (11.5%)	37.0%	100%
standard	400	28	16 (57.1%)	8 (28.6%)	4 (14.3%)	33.3%	100%
10x dilution in pR_LG	400	68	67 (98.5%)	1 (1.5%)	0 (0.0%)	1.5%	1%
1000x dilution in pR_H2B-BFP	8	61	59 (96.7%)	0 (0.0%)	2 (3.3%)	0%	1%
1000x dilution in pLX_TRC313_LacZ	400	53	50 (94.3%)	2 (3.8%)	1 (1.9%)	3.8%	1%
100x dilution in pLX_TRC313_Lacz	400	16	12 (75.0%)	1 (6.2%)	3 (18.8%)	7.7%	3%
1000x dilution in pUC19	8	45	35 (77.8%)	2 (4.4%)	8 (17.8%)	5.4%	1%
standard, quick harvest (11 h)	8	51	28 (54.9%)	17 (33.3%)	6 (11.8%)	37.8%	3%

[0203] Applicant also tested dilution in a non-lentiviral carrier plasmid, pUC19, hypothesizing that stringent dilution of the perturbation library could reduce the number of library variants in each packaging cell to one or fewer and minimize the risk that heterodimeric virions are produced. This strategy was found to decrease the recombination rate to 6%. However, Applicant still observed 18% of cell clones with greater than one integrated library variant, consistent with the correlated infection hypothesis and indicating that lentiviral plasmids may be a better choice of carrier material.

[0204] A limitation of this dilution strategy is a 100-fold decrease in titer relative to lentivirus prepared with the non-diluted perturbation library, measured by counting the number of cell colonies surviving after antibiotic selection. To investigate die trade-off between titer and unwanted lentiviral effects, Applicant titrated the dilution ratio of one of the integrating lentiviral carrier plasmids (pLX_TRC3_13 LacZ) but found that 100-fold excess did not show the desired performance, with 25% of colonies showing barcode swaps or multiple integrants. Nevertheless, even with dimin-

[0206] In the context of genetic screens, lentiviral co-packaging can greatly reduce barcode swaps and decrease the background of multiple integrants without constraining library vector design or necessitating individual packaging of library elements. The latter approach was used by Adamson et al. to avoid recombination in a single-cell gene expression screen but is limited in scalability[14]. Datlinger et al. developed a --specialized CROP-seq vector in which the sgRNA is itself transcribed by Pol II and captured in a 3' RNA-seq protocol, obviating the need for an additional barcode and eliminating concerns about recombination[5]. However, this approach requires locating the perturbation within the 3' LTR and is not generalizable to some types of screens (e.g. paired perturbation screens, or screens of regulatory elements monitored via transcribed barcodes)[16]. By addressing both recombination and multiple integration, co-packaged lentiviral libraries have the potential to improve the accuracy of perturbation barcoding and boost the sensitivity of screens that deliver library constructs with multiple variable elements.

[0207] Applicant chose to employ clonal analysis of the genomic integrants by next-generation sequencing to achieve sensitive and unbiased detection of perturbation library elements with single-cell resolution. As Applicant amplified each variable sequence in a separate PCR reaction, this approach is not subject to artifacts resulting from PCR-based recombination. Moreover, the readout does not depend on events subsequent to integration and antibiotic selection, such as detection of a fluorescent marker or

perturbation of cellular phenotype that may be confounded by multiple integrations. However, clonal analysis is practically limited to the scale of 100-1000 clones per sequencing run, making it better suited for high-confidence measurements of undesired integration events than for systematic optimization across many test conditions.

[0208] Under the standard assumption of a zero-truncated Poisson distribution of lentiviral integrations, one would expect a multiple integration rate below 2.5% when transducing cells at an MOI below 5%. However, despite working in this range for our infections, the measured multiple integration rate was greater than 10%, suggesting that, at least in our HeLa cell system, lentiviral integrations detected after antibiotic selection are correlated and do not follow a zero-truncated Poisson distribution as is commonly assumed[17]. It is likely that multiple integration background is a persistent noise source in genetic screens utilizing lentivirus, with an effect that depends on the particular system. A lack of statistical independence between integration events underscores the need to maintain high representation of library elements in transduced cells in order to average over technical and biological noise.

[0209] Decreased viral titer is a potential drawback to the dilute co-packaging approach. Here, Applicant opted to perform clonal analysis under stringent dilution conditions, which minimized recombination but exacerbated the viral titer issue. For example, using the integration-defective pR_LG 1:10 co-packaging condition, Applicant was able to generate 10,000 HeLa colonies per mL of viral supernatant. At this titer, 35 mL of viral supernatant would be sufficient for one replicate of a screen involving 1,000 perturbations with 300 initially infected cells per library element. The cost of tissue culture and transfection reagents to generate 35 mL of viral supernatant is currently orders of magnitude smaller than the cost of preparing and sequencing single-cell gene expression libraries covering 1,000 perturbations and does not thus pose a limit to the achievable scale of the screen. On the other hand, this titer may be prohibitive for a genome-wide CRISPR screen reading out enrichment of more than 50,000 sgRNAs by amplicon sequencing. Ultimately, any particular screen will exhibit an optimal trade-off between degradation of data quality by lentiviral recombination and loss of titer due to co-packaging with a carrier plasmid, and the user may select an appropriate level of dilution to balance these effects.

[0210] The ability to minimize both recombination and multiple integrations by diluting the transfer vector in another lentiviral plasmid supports the hypothesis that RNA dimerization during lentiviral packaging is involved in these undesired outcomes. In the case of dilution with excess lentiviral carrier plasmid, most library genomes are likely packaged with a non-homologous carrier genome such that the frequency of virions containing two library variants is substantially reduced. Meanwhile, limiting dilution with a non-lentiviral carrier plasmid may reduce the likelihood that two library variants are transfected into the same cell for packaging, hence preventing two different library RNA genomes from dimerizing. Both of these approaches mitigate the potential for template switching and recombination between two different library genomes in the target cells.

[0211] Alternative approaches to control recombination include directly inhibiting the template-switching activity of the viral reverse transcriptase in the transduced cells or biasing packaging to a single genome per virion by modifying the RNA sequence or proteins involved in dimerization[18]. Such efforts could potentially address both the effects of recombination and multiple genomic integrations without a corresponding loss in titer due to dilution.

[0212] Methods

[0213] Single cell clonal analysis of integrated sgRNAs and barcodes was performed by transducing a lentiviral library into a target cell population, selecting with antibiotic, sorting and expanding single cells, and separately PCR-amplifying and deep sequencing the sgRNA and barcode sequences from each expanded colony. All cell lines were transduced at an MOI<5%, determined by counting the fraction of cells surviving antibiotic selection.

[0214] Lentivirus was prepared following published methods[19]. All cell culture used Dulbecco's Modified Eagle's Medium supplemented with 10% FBS (GE Life Sciences SH30070.03T), 100 units/mL penicillin, and 100 μg/mL streptomycin. A 4:3:2 ratio by mass of packaging plasmids pMD2.G (Addgene 12259) and psPAX2 (Addgene 12260), and library transfer vector pLas (Supplementary Sequence 1, lentiviral backbone derived from Addgene 61427) was transfected into 293FT cells (Thermo Fisher R70007) using Lipofectamine 2000 (Invitrogen 11668019). Fresh media was exchanged 4 h after transfection. At 24 h post-transfection, 2 mM caffeine (Sigma-Aldrich C0750) was added, and at 48 h post-transfection lentiviral supernatant was filtered through 0.45 m cellulose acetate filters (VWR 28145-481), frozen at −80° C., and thawed immediately before use. HeLa cells (a gift from Dr. Iain Cheeseman's lab) were infected by mixing lentiviral supernatant with 8 μg/mL polybrene (Sigma-Aldrich 107689-10G) and centrifuging at 1000 g for 2 h at 33° C. At 6 h post-infection, media was exchanged, and at 24 h post-infection cells were passaged into media containing 300 μg/mL zeocin (Thermo Fisher R25001) and selected for one week. Single cells were sorted into 96-well plates and clonally expanded. More than 90% of wells with cell growth contained single colonies, determined by visual inspection. These expanded clones were analyzed by extracting gDNA, separately amplifying sgRNA and barcode sequences by PCR, and deep sequencing the amplicons (Illumina MiniSeq).

[0215] Sequence data from each colony were analyzed by matching reads to known sgRNAs within an allowed edit distance of 2 bases and barcodes within an allowed edit distance of 1 base to accommodate errors in oligo synthesis (Supplementary Table 1). Sequences with fewer than 30 reads or a read fraction below 10% were discarded. Multiple integration events were defined by the presence of more than one sgRNA or more than one barcode sequence. Single integration with barcode swapping was defined as detection of one sgRNA and one barcode cognate to a different sgRNA. We report the frequency of observed barcode swapping events, which does not include multiple integration of the same library element, recombination between two identical library elements, or secondary recombination events that restore the original sgRNA-barcode pairing.

[0216] sgRNA vector sequences and vector details are provided below in Table 2. (Pred sgRNA identified as SEQ ID NOs: 1-945) (Required "match" sequences identified as SEQ ID NOs: 946-1573)

TABLE 2

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, individually packaged	20170608	T1	B09	pL43	83.80%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	3540
pLas, individually packaged	20170608	T1	B09	sgRNA	92.70%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	356
pLas, individually packaged	20170608	T1	B12	pL43	87.40%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	3955
pLas, individually packaged	20170608	T1	B12	sgRNA	96.00%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	924
pLas, individually packaged	20170608	T1	C09	pL43	95.70%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	3707
pLas, individually packaged	20170608	T1	C09	sgRNA	95.80%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	1451
pLas, individually packaged	20170608	T1	C10	pL43	95.70%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	4431
pLas, individually packaged	20170608	T1	C10	sgRNA	93.60%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	904
pLas, individually packaged	20170608	T1	C12	pL43	94.40%	TCCACCGGCGA AAGAGATCC	FALSE	2	CAATCGG	4541
pLas, individually packaged	20170608	T1	C12	sgRNA	94.40%	TCCACCGGCGA AAGAGATCC	FALSE	2	TCCACCGGCGAA AGAGATCC	34
pLas, individually packaged	20170608	T1	D09	pL43	96.00%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	4873
pLas, individually packaged	20170608	T1	D09	sgRNA	94.90%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	806
pLas, individually packaged	20170608	T1	D11	pL43	10.60%	TCATATTACGAG TCAGTAGG	TRUE	3	AGAGAGA	493
pLas, individually packaged	20170608	T1	D11	pL43	85.30%	AGAGCACTGCA CTCCTTCA	FALSE	3	CCAGTTA	3980
pLas, individually packaged	20170608	T1	D11	sgRNA	87.60%	AGAGCACTGCA CTCCTTCA	FALSE	3	AGAGCACTGCAC TCCTTCA	212
pLas, individually packaged	20170608	T1	D12	pL43	94.80%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	4567
pLas, individually packaged	20170608	T1	D12	sgRNA	94.60%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	1346
pLas, individually packaged	20170608	T1	E10	pL43	95.10%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA	4585

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, individually packaged	20170608	T1	E10	sgRNA	95.70%	CCAGTACAAAC CTACCTACG	FALSE	2	CCAGTACAAACC TACCTACG	425
pLas, individually packaged	20170608	T1	E11	pL43	94.70%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	4781
pLas, individually packaged	20170608	T1	E11	sgRNA	95.50%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	233
pLas, individually packaged	20170608	T1	E12	pL43	94.20%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	4257
pLas, individually packaged	20170608	T1	E12	sgRNA	95.80%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	1084
pLas, individually packaged	20170608	T1	F10	pL43	94.70%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	3828
pLas, individually packaged	20170608	T1	F10	sgRNA	93.30%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	532
pLas, individually packaged	20170608	T1	F11	pL43	47.30%	CCTGCAACGGG ACTAGTTGG	FALSE	4	CGTCATA	2137
pLas, individually packaged	20170608	T1	F11	pL43	48.40%	ATACAACTGCTT GCAACAGG	FALSE	4	ATTCCGA	2184
pLas, individually packaged	20170608	T1	F11	sgRNA	46.70%	ATACAACTGCTT GCAACAGG	FALSE	4	ATACAACTGCTT GCAACAGG	314
pLas, individually packaged	20170608	T1	F11	sgRNA	46.80%	CCTGCAACGGG ACTAGTTGG	FALSE	4	CCTGCAACGGGA CTAGTTGG	315
pLas, individually packaged	20170608	T1	F12	pL43	95.60%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	4409
pLas, individually packaged	20170608	T1	F12	sgRNA	95.30%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	843
pLas, individually packaged	20170608	T1	G09	pL43	79.80%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	2743
pLas, individually packaged	20170608	T1	G09	sgRNA	94.10%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	434
pLas, individually packaged	20170608	T1	G12	pL43	90.80%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA	4450
pLas, individually packaged	20170608	T1	G12	sgRNA	94.60%	CCAGTACAAAC CTACCTACG	FALSE	2	CCAGTACAAACC TACCTACG	945
pLas, individually packaged	20170608	T1	H09	pL43	95.20%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	4742

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, individually packaged	20170608	T1	H09	sgRNA	95.90%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	1368
pLas, individually packaged	20170608	T1	H10	pL43	95.60%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	4531
pLas, individually packaged	20170608	T1	H10	sgRNA	95.60%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	900
pLas, individually packaged	20170608	T1	H11	pL43	86.10%	TCCACCGGCGA AAGAGATCC	FALSE	2	CAATCGG	3570
pLas, individually packaged	20170608	T1	H11	sgRNA	94.80%	TCCACCGGCGA AAGAGATCC	FALSE	2	TCCACCGGCGAA AGAGATCC	2455
pLas, individually packaged	20170608	T1	H12	pL43	80.90%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	3032
pLas, individually packaged	20170608	T1	H12	sgRNA	87.80%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	1155
pLas, individually packaged	20170608	T2	B01	pL43	43.50%	AGAGCACTGCA CTCCTTCA	FALSE	4	CCAGTTA	1799
pLas, individually packaged	20170608	T2	B01	pL43	53.90%	TCATATTACGAG TCAGTAGG	FALSE	4	AGAGAGA	2225
pLas, individually packaged	20170608	T2	B01	sgRNA	46.70%	AGAGCACTGCA CTCCTTCA	FALSE	4	AGAGCACTGCAC TCCTTCA	293
pLas, individually packaged	20170608	T2	B01	sgRNA	48.70%	TCATATTACGAG TCAGTAGG	FALSE	4	TCATATTACGAGT CAGTAGG	306
pLas, individually packaged	20170608	T2	B02	pL43	96.60%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	4180
pLas, individually packaged	20170608	T2	B02	sgRNA	95.10%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	874
pLas, individually packaged	20170608	T2	B03	pL43	96.90%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	4136
pLas, individually packaged	20170608	T2	B03	sgRNA	95.80%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	877
pLas, individually packaged	20170608	T2	B04	pL43	96.00%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	3368
pLas, individually packaged	20170608	T2	B04	sgRNA	93.70%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	388
pLas, individually packaged	20170608	T2	C01	pL43	96.50%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	3512

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, individually packaged	20170608	T2	C01	sgRNA	96.50%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	599
pLas, individually packaged	20170608	T2	C02	pL43	94.50%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	3691
pLas, individually packaged	20170608	T2	C02	sgRNA	95.50%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	764
pLas, individually packaged	20170608	T2	C03	pL43	96.90%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	4307
pLas, individually packaged	20170608	T2	C03	sgRNA	93.80%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	405
pLas, individually packaged	20170608	T2	C04	pL43	97.20%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	4177
pLas, individually packaged	20170608	T2	C04	sgRNA	96.30%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	235
pLas, individually packaged	20170608	T2	D01	pL43	97.00%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	3954
pLas, individually packaged	20170608	T2	D01	sgRNA	95.90%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	352
pLas, individually packaged	20170608	T2	D02	pL43	94.30%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	3606
pLas, individually packaged	20170608	T2	D02	sgRNA	96.00%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	1285
pLas, individually packaged	20170608	T2	D03	pL43	95.50%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	3714
pLas, individually packaged	20170608	T2	D03	sgRNA	94.80%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	1102
pLas, individually packaged	20170608	T2	D04	pL43	94.70%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA	3834
pLas, individually packaged	20170608	T2	D04	sgRNA	94.00%	CCAGTACAAAC CTACCTACG	FALSE	2	CCAGTACAAACC TACCTACG	299
pLas, individually packaged	20170608	T2	E01	pL43	97.00%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	3354
pLas, individually packaged	20170608	T2	E01	sgRNA	93.60%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	497
pLas, individually packaged	20170608	T2	E02	pL43	96.10%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	3865

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, individually packaged	20170608	T2	E02	sgRNA	94.60%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	881
pLas, individually packaged	20170608	T2	E03	pL43	97.00%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	3574
pLas, individually packaged	20170608	T2	E03	sgRNA	95.00%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	498
pLas, individually packaged	20170608	T2	E04	pL43	96.50%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	4290
pLas, individually packaged	20170608	T2	E04	sgRNA	95.30%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	505
pLas, individually packaged	20170608	T2	F01	pL43	96.60%	TCCACCGGCGA AAGAGATCC	FALSE	2	CAATCGG	4255
pLas, individually packaged	20170608	T2	F01	sgRNA	94.60%	TCCACCGGCGA AAGAGATCC	FALSE	2	TCCACCGGCGAA AGAGATCC	905
pLas, individually packaged	20170608	T2	F02	pL43	97.30%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	4292
pLas, individually packaged	20170608	T2	F02	sgRNA	96.50%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	625
pLas, individually packaged	20170608	T2	F03	pL43	97.40%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	4249
pLas, individually packaged	20170608	T2	F03	sgRNA	93.70%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	328
pLas, individually packaged	20170608	T2	F04	pL43	96.90%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	3725
pLas, individually packaged	20170608	T2	F04	sgRNA	95.10%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	254
pLas, individually packaged	20170608	T2	G01	pL43	97.20%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	4241
pLas, individually packaged	20170608	T2	G01	sgRNA	95.10%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	1193
pLas, individually packaged	20170608	T2	G02	pL43	97.60%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	4452
pLas, individually packaged	20170608	T2	G02	sgRNA	94.60%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	712
pLas, individually packaged	20170608	T2	G03	pL43	97.50%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	4061

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, individually packaged	20170608	T2	G03	sgRNA	95.40%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	536
pLas, individually packaged	20170608	T2	G04	pL43	96.90%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	3959
pLas, individually packaged	20170608	T2	G04	sgRNA	96.20%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	179
pLas, individually packaged	20170608	T2	H01	pL43	97.20%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	4232
pLas, individually packaged	20170608	T2	H01	sgRNA	95.20%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	1226
pLas, individually packaged	20170608	T2	H02	pL43	96.30%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	3553
pLas, individually packaged	20170608	T2	H02	sgRNA	95.80%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	1508
pLas, individually packaged	20170608	T2	H03	pL43	97.40%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA	4423
pLas, individually packaged	20170608	T2	H03	sgRNA	96.60%	CCAGTACAAAC CTACCTACG	FALSE	2	CCAGTACAAACC TACCTACG	1501
pLas, individually packaged	20170608	T2	H04	pL43	97.70%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	4444
pLas, individually packaged	20170608	T2	H04	sgRNA	96.40%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	862
pLas, standard_8	20170608	T3	A01	pL43	38.30%	AGTAGTCCGGG ATATCAGCG	FALSE	5	CCTCTTC	916
pLas, standard_8	20170608	T3	A01	pL43	51.20%	ATACAACTGCTT GCAACAGG	FALSE	5	ATTCCGA	1222
pLas, standard_8	20170608	T3	A01	sgRNA	14.30%	AGAGCACTGCA CTCCTTCA	TRUE	5	AGAGCACTGCAC TCCTTCA	314
pLas, standard_8	20170608	T3	A01	sgRNA	29.50%	AGTAGTCCGGG ATATCAGCG	FALSE	5	AGTAGTCCGGGA TATCAGCG	648
pLas, standard_8	20170608	T3	A01	sgRNA	49.80%	ATACAACTGCTT GCAACAGG	FALSE	5	ATACAACTGCTT GCAACAGG	1094
pLas, standard_8	20170608	T3	A02	pL43	97.10%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	4458
pLas, standard_8	20170608	T3	A02	sgRNA	95.20%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	1199
pLas, standard_8	20170608	T3	A03	pL43	96.70%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	3846
pLas, standard_8	20170608	T3	A03	sgRNA	96.00%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	3791
pLas, standard_8	20170608	T3	A04	pL43	12.90%	AGAGCACTGCA CTCCTTCA	TRUE	3	AGGCTCT	202

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, standard_8	20170608	T3	A04	pL43	75.50%	AGAGCACTGCA CTCCTTCA	TRUE	3	CCAGTTA	1184
pLas, standard_8	20170608	T3	A04	sgRNA	95.50%	TCATATTACGAG TCAGTAGG	TRUE	3	TCATATTACGAGT CAGTAGG	3631
pLas, standard_8	20170608	T3	A05	pL43	94.30%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	3658
pLas, standard_8	20170608	T3	A05	sgRNA	92.60%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	312
pLas, standard_8	20170608	T3	A06	pL43	22.20%	CCTGCAACGGG ACTAGTTGG	TRUE	5	CGTCATA	1003
pLas, standard_8	20170608	T3	A06	pL43	23.50%	ATACAACTGCTT GCAACAGG	FALSE	5	ATTCCGA	1062
pLas, standard_8	20170608	T3	A06	pL43	51.50%	TCCACCGGCGA AAGAGATCC	FALSE	5	CAATCGG	2328
pLas, standard_8	20170608	T3	A06	sgRNA	37.00%	ATACAACTGCTT GCAACAGG	FALSE	5	ATACAACTGCTT GCAACAGG	125
pLas, standard_8	20170608	T3	A06	sgRNA	57.40%	TCCACCGGCGA AAGAGATCC	FALSE	5	TCCACCGGCGAA AGAGATCC	194
pLas, standard_8	20170608	T3	A07	pL43	97.60%	CCTGCAACGGG ACTAGTTGG	TRUE	2	CGTCATA	3824
pLas, standard_8	20170608	T3	A07	sgRNA	95.00%	AGTAGTCCGGG ATATCAGCG	TRUE	2	AGTAGTCCGGGA TATCAGCG	1558
pLas, standard_8	20170608	T3	A08	pL43	91.30%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	2460
pLas, standard_8	20170608	T3	A08	sgRNA	91.30%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	2853
pLas, standard_8	20170608	T3	B01	pL43	91.50%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	2732
pLas, standard_8	20170608	T3	B01	sgRNA	95.70%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	3419
pLas, standard_8	20170608	T3	B02	pL43	97.30%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA CCAGTACAAACC	4877
pLas, standard_8	20170608	T3	B02	sgRNA	96.20%	CCAGTACAAAC CTACCTACG	FALSE	2	TACCTACG	403
pLas, standard_8	20170608	T3	B03	pL43	67.90%	TCCACCGGCGA AAGAGATCC	TRUE	2	CAATCGG	1752
pLas, standard_8	20170608	T3	B03	sgRNA	93.20%	ATACAACTGCTT GCAACAGG	TRUE	2	ATACAACTGCTT GCAACAGG	743
pLas, standard_8	20170608	T3	B04	pL43	96.50%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	4275
pLas, standard_8	20170608	T3	B04	sgRNA	95.10%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	447
pLas, standard_8	20170608	T3	B05	pL43	97.00%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	3946
pLas, standard_8	20170608	T3	B05	sgRNA	96.40%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	986
pLas, standard_8	20170608	T3	B06	pL43	96.50%	AGTAGTCCGGG ATATCAGCG	TRUE	2	CCTCTTC	3955

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, standard_8	20170608	T3	B06	sgRNA	95.30%	ATACAACTGCTT GCAACAGG	TRUE	2	ATACAACTGCTT GCAACAGG	1075
pLas, standard_8	20170608	T3	B07	pL43	96.50%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	4415
pLas, standard_8	20170608	T3	B07	sgRNA	96.70%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG	652
pLas, standard_8	20170608	T3	B08	pL43	45.70%	AGTAGTCCGGG ATATCAGCG	FALSE	4	ACGCGACC CCTCTTC	1938
pLas, standard_8	20170608	T3	B08	pL43	51.40%	AGAGCACTGCA CTCCTTCA	FALSE	4	CCAGTTA	2177
Las, standard_8	20170608	T3	B08	sgRNA	47.90%	AGAGCACTGCA CTCCTTCA	FALSE	4	AGAGCACTGCAC TCCTTCA	512
pLas, standard_8	20170608	T3	B08	sgRNA	47.90%	AGTAGTCCGGG ATATCAGCG	FALSE	4	AGTAGTCCGGGA TATCAGCG	513
pLas, standard_8	20170608	T3	C01	pL43	97.10%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	5003
pLas, standard_8	20170608	T3	C01	sgRNA	96.40%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	782
pLas, standard_8	20170608	T3	C02	pL43	95.60%	CCAGTACAAAC CTACCTACG	TRUE	2	AAGAGGA	4832
pLas, standard_8	20170608	T3	C02	sgRNA	95.90%	CCTGCAACGGG ACTAGTTGG	TRUE	2	CCTGCAACGGGA CTAGTTGG	1433
pLas, standard_8	20170608	T3	C03	pL43	96.80%	CCTGCAACGGG ACTAGTTGG	TRUE	2	CGTCATA	5059
pLas, standard_8	20170608	T3	C03	sgRNA	95.40%	AGTAGTCCGGG ATATCAGCG	TRUE	2	AGTAGTCCGGGA TATCAGCG	638
pLas, standard_8	20170608	T3	C04	pL43	97.20%	CCTGCAACGGG ACTAGTTGG	TRUE	2	CGTCATA	4324
pLas, standard_8	20170608	T3	C04	sgRNA	95.30%	TCATATTACGAG TCAGTAGG	TRUE	2	TCATATTACGAGT CAGTAGG	323
pLas, standard_8	20170608	T3	C05	pL43	97.10%	TCCACCGGCGA AAGAGATCC	FALSE	2	CAATCGG	4711
pLas, standard_8	20170608	T3	C05	sgRNA	94.40%	TCCACCGGCGA AAGAGATCC	FALSE	2	TCCACCGGCGAA AGAGATCC	1218
pLas, standard_8	20170608	T3	C06	pL43	94.60%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	4576
pLas, standard_8	20170608	T3	C06	sgRNA	96.30%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	949
pLas, standard_8	20170608	T3	C07	pL43	93.00%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA	3743
pLas, standard_8	20170608	T3	C07	sgRNA	95.20%	CCAGTACAAAC CTACCTACG	FALSE	2	CCAGTACAAACC TACCTACG	758
pLas, standard_8	20170608	T3	C08	pL43	95.40%	CCAGTACAAAC CTACCTACG	TRUE	2	AAGAGGA	4504
pLas, standard_8	20170608	T3	C08	sgRNA	95.40%	CCTGCAACGGG ACTAGTTGG	TRUE	2	CCTGCAACGGGA CTAGTTGG	577
pLas, standard_8	20170608	T3	D01	pL43	96.00%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	4673
pLas, standard_8	20170608	T3	D01	sgRNA	94.90%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	691

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, standard_8	20170608	T3	D02	pL43	96.20%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	5213
pLas, standard_8	20170608	T3	D02	sgRNA	96.10%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	724
pLas, standard_8	20170608	T3	D03	pL43	59.90%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	1526
pLas, standard_8	20170608	T3	D03	sgRNA	94.70%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	622
pLas, standard_8	20170608	T3	D04	pL43	95.00%	TCCACCGGCGA AAGAGATCC	FALSE	2	CAATCGG	4568
pLas, standard_8	20170608	T3	D04	sgRNA	95.20%	TCCACCGGCGA AAGAGATCC	FALSE	2	TCCACCGGCGAA AGAGATCC	239
pLas, standard_8	20170608	T3	D05	pL43	96.50%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	4945
pLas, standard_8	20170608	T3	D05	sgRNA	96.90%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	409
pLas, standard_8	20170608	T3	D06	pL43	96.50%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	4165
pLas, standard_8	20170608	T3	D06	sgRNA	94.60%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	591
pLas, standard_8	20170608	T3	D07	pL43	96.80%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA	4170
pLas, standard_8	20170608	T3	D07	sgRNA	96.80%	CCAGTACAAAC CTACCTACG	FALSE	2	CCAGTACAAACC TACCTACG	605
pLas, standard_8	20170608	T3	D08	pL43	48.30%	CCTGCAACGGG ACTAGTTGG	FALSE	4	CGTCATA	2156
pLas, standard_8	20170608	T3	D08	pL43	48.90%	TCATATTACGAG TCAGTAGG	FALSE	4	AGAGAGA	2180
pLas, standard_8	20170608	T3	D08	sgRNA	45.20%	TCATATTACGAG TCAGTAGG	FALSE	4	TCATATTACGAGT CAGTAGG	150
pLas, standard_8	20170608	T3	D08	sgRNA	49.40%	CCTGCAACGGG ACTAGTTGG	FALSE	4	CCTGCAACGGGA CTAGTTGG	164
pLas, standard_8	20170608	T3	E01	pL43	93.70%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	3427
pLas, standard_8	20170608	T3	E01	sgRNA	94.20%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	1096
pLas, standard_8	20170608	T3	E02	pL43	44.00%	AGAGCACTGCA CTCCTTCA	FALSE	4	CCAGTTA	1441
pLas, standard_8	20170608	T3	E02	pL43	52.70%	ATACAACTGCTT GCAACAGG	FALSE	4	ATTCCGA	1726
pLas, standard_8	20170608	T3	E02	sgRNA	45.10%	ATACAACTGCTT GCAACAGG	FALSE	4	ATACAACTGCTT GCAACAGG	208
pLas, standard_8	20170608	T3	E02	sgRNA	48.60%	AGAGCACTGCA CTCCTTCA	FALSE	4	AGAGCACTGCAC TCCTTCA	224
pLas, standard_8	20170608	T3	E03	pL43	97.40%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	3657
pLas, standard_8	20170608	T3	E03	sgRNA	95.50%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	385

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, standard_8	20170608	T3	E04	pL43	97.20%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	3853
pLas, standard_8	20170608	T3	E04	sgRNA	95.10%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	254
pLas, standard_8	20170608	T3	E05	pL43	96.60%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	3585
pLas, standard_8	20170608	T3	E05	sgRNA	97.30%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	655
pLas, standard_8	20170608	T3	E06	pL43	97.60%	TCATATTACGAG TCAGTAGG	TRUE	2	AGAGAGA	3875
pLas, standard_8	20170608	T3	E06	sgRNA	92.90%	ATACAACTGCTT GCAACAGG	TRUE	2	ATACAACTGCTT GCAACAGG	262
pLas, standard_8	20170608	T3	E07	pL43	97.10%	ATACAACTGCTT GCAACAGG	TRUE	2	ATTCCGA	3665
pLas, standard_8	20170608	T3	E07	sgRNA	94.50%	AGAGCACTGCA CTCCTTCA	TRUE	2	AGAGCACTGCAC TCCTTCA	241
pLas, standard_8	20170608	T3	E08	pL43	95.40%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	3312
pLas, standard_8	20170608	T3	E08	sgRNA	95.40%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	248
pLas, standard_8	20170608	T3	F01	pL43	97.10%	CCAGTACAAAC CTACCTACG	TRUE	2	AAGAGGA	4357
pLas, standard_8	20170608	T3	F01	sgRNA	94.70%	AGAGCACTGCA CTCCTTCA	TRUE	2	AGAGCACTGCAC TCCTTCA	1724
pLas, standard_8	20170608	T3	F03	pL43	97.00%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	4167
pLas, standard_8	20170608	T3	F03	sgRNA	95.40%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	740
pLas, standard_8	20170608	T3	F04	pL43	96.70%	AGAGCACTGCA CTCCTTCA	TRUE	2	CCAGTTA	4419
pLas, standard_8	20170608	T3	F04	sgRNA	96.20%	CCTGCAACGGG ACTAGTTGG	TRUE	2	CCTGCAACGGGA CTAGTTGG	332
pLas, standard_8	20170608	T3	F05	pL43	96.70%	AGAGCACTGCA CTCCTTCA	TRUE	2	CCAGTTA	4215
pLas, standard_8	20170608	T3	F05	sgRNA	96.20%	CCTGCAACGGG ACTAGTTGG	TRUE	2	CCTGCAACGGGA CTAGTTGG	833
pLas, standard_8	20170608	T3	F06	pL43	96.80%	CGCCGCCCCCG GACGCGACC	TRUE	2	CATGCGT	3523
pLas, standard_8	20170608	T3	F06	sgRNA	95.50%	CCTGCAACGGG ACTAGTTGG	TRUE	2	CCTGCAACGGGA CTAGTTGG	231
pLas, standard_8	20170608	T3	F07	pL43	95.90%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	3831
pLas, standard_8	20170608	T3	F07	sgRNA	96.00%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	697
pLas, standard_8	20170608	T3	F08	pL43	96.50%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	3858
pLas, standard_8	20170608	T3	F08	sgRNA	94.60%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	1214

TABLE 2-continued

condition	date	plate	well	pat-tern	frac-tion	pred sgRNA	soli-tary	matches per sample	match	count
pLas, standard_8	20170608	T3	G01	pL43	96.80%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	4622
pLas, standard_8	20170608	T3	G01	sgRNA	94.10%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	1423
pLas, standard_8	20170608	T3	G02	pL43	46.40%	CCAGTACAAAC CTACCTACG	FALSE	3	AAGAGGA	2320
pLas, standard_8	20170608	T3	G02	PL43	51.00%	TCATATTACGAG TCAGTAGG	TRUE	3	AGAGAGA	2550
pLas, standard_8	20170608	T3	G02	sgRNA	95.50%	CCAGTACAAAC CTACCTACG	FALSE	3	CCAGTACAAACC TACCTACG	612
pLas, standard_8	20170608	T3	G05	pL43	96.60%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	3919
pLas, standard_8	20170608	T3	G05	sgRNA	95.80%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	2747
pLas, standard_8	20170608	T3	G06	pL43	95.30%	ATACAACTGCTT GCAACAGG	TRUE	2	ATTCCGA	4219
pLas, standard_8	20170608	T3	G06	sgRNA	94.70%	AGAGCACTGCA CTCCTTCA	TRUE	2	AGAGCACTGCAC TCCTTCA	1060
pLas, standard_8	20170608	T3	G07	pL43	96.90%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	4940
pLas, standard_8	20170608	T3	G07	sgRNA	94.90%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	991
pLas, standard_8	20170608	T3	G08	pL43	97.50%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	4771
pLas, standard_8	20170608	T3	G08	sgRNA	95.50%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	1030
pLas, standard_8	20170608	T3	H01	pL43	97.10%	CCTGCAACGGG ACTAGTTGG	TRUE	2	CGTCATA	4412
pLas, standard_8	20170608	T3	H01	sgRNA	95.00%	ATACAACTGCTT GCAACAGG	TRUE	2	ATACAACTGCTT GCAACAGG	830
pLas, standard_8	20170608	T3	H02	pL43	96.60%	ATACAACTGCTT GCAACAGG	TRUE	2	ATTCCGA	4004
pLas, standard_8	20170608	T3	H02	sgRNA	95.00%	AGAGCACTGCA CTCCTTCA	TRUE	2	AGAGCACTGCAC TCCTTCA	1371
pLas, standard_8	20170608	T3	H03	pL43	96.90%	TCCACCGGCGA AAGAGATCC	TRUE	2	CAATCGG	3486
pLas, standard_8	20170608	T3	H03	sgRNA	92.90%	ATACAACTGCTT GCAACAGG	TRUE	2	ATACAACTGCTT GCAACAGG	39
pLas, standard_8	20170608	T3	H04	pL43	97.80%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	4240
pLas, standard_8	20170608	T3	H04	sgRNA	94.60%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	227
pLas, standard_8	20170608	T3	H05	pL43	97.30%	TCATATTACGAG TCAGTAGG	TRUE	2	AGAGAGA	4390
pLas, standard_8	20170608	T3	H05	sgRNA	95.90%	CCTGCAACGGG ACTAGTTGG	TRUE	2	CCTGCAACGGGA CTAGTTGG	375
pLas, standard_8	20170608	T3	H06	pL43	30.90%	AGAGCACTGCA CTCCTTCA	TRUE	3	AGGCTCT	715

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, standard_8	20170608	T3	H06	pL43	62.70%	ATACAACTGCTT GCAACAGG	FALSE	3	ATTCCGA	1451
pLas, standard_8	20170608	T3	H06	sgRNA	95.00%	ATACAACTGCTT GCAACAGG	FALSE	3	ATACAACTGCTT GCAACAGG	3966
pLas, standard_8	20170608	T3	H07	pL43	97.30%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	4431
pLas, standard_8	20170608	T3	H07	sgRNA	95.00%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	707
pLas, standard_8	20170608	T3	H08	pL43	97.60%	AGAGCACTGCA CTCCTTCA	TRUE	2	CCAGTTA	4408
pLas, standard_8	20170608	T3	H08	sgRNA	94.20%	ATACAACTGCTT GCAACAGG	TRUE	2	ATACAACTGCTT GCAACAGG	1007
pLas + pR_H2B-BFP (1:1000)	20170608	T4	A05	pL43	97.50%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	4557
pLas + pR_H2B-BFP (1:1000)	20170608	T4	A05	sgRNA	94.40%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	1303
pLas + pR_H2B-BFP (1:1000)	20170608	T4	A06	pL43	97.40%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	4231
pLas + pR_H2B-BFP (1:1000)	20170608	T4	A06	sgRNA	96.40%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	1004
pLas + pR_H2B-BFP (1:1000)	20170608	T4	A07	pL43	97.00%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	4116
pLas + pR_H2B-BFP (1:1000)	20170608	T4	A07	sgRNA	94.60%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	823
pLas + pR_H2B-BFP (1:1000)	20170608	T4	A08	pL43	97.60%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	3955
pLas + pR_H2B-BFP (1:1000)	20170608	T4	A08	sgRNA	90.90%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	765
pLas + pR_H2B-BFP (1:1000)	20170608	T4	A09	pL43	93.70%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA	3001
pLas + pR_H2B-BFP (1:1000)	20170608	T4	A09	sgRNA	95.60%	CCAGTACAAAC CTACCTACG	FALSE	2	CCAGTACAAACC TACCTACG	5907
pLas + pR_H2B-BFP (1:1000)	20170608	T4	A10	pL43	96.70%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	4527
pLas + pR_H2B-BFP (1:1000)	20170608	T4	A10	sgRNA	95.00%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	906
pLas + pR_H2B-BFP (1:1000)	20170608	T4	A11	pL43	97.40%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	4269
pLas + pR_H2B-BFP (1:1000)	20170608	T4	A11	sgRNA	96.30%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	1234

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pR_H2B-BFP (1:1000)	20170608	T4	A12	pL43	92.50%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	3147
pLas + pR_H2B-BFP (1:1000)	20170608	T4	A12	sgRNA	94.80%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	3223
pLas + pR_H2B-BFP (1:1000)	20170608	T4	B05	pL43	97.20%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	3990
pLas + pR_H2B-BFP (1:1000)	20170608	T4	B05	sgRNA	95.70%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	902
pLas + pR_H2B-BFP (1:1000)	20170608	T4	B06	pL43	95.80%	TCCACCGGCGA AAGAGATCC	FALSE	2	CAATCGG	3985
pLas + pR_H2B-BFP (1:1000)	20170608	T4	B06	sgRNA	94.60%	TCCACCGGCGA AAGAGATCC	FALSE	2	TCCACCGGCGAA AGAGATCC	821
pLas + pR_H2B-BFP (1:1000)	20170608	T4	B07	pL43	94.00%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	3237
pLas + pR_H2B-BFP (1:1000)	20170608	T4	B07	sgRNA	95.40%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	2166
pLas + pR_H2B-BFP (1:1000)	20170608	T4	B08	pL43	96.20%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA	4316
pLas + pR_H2B-BFP (1:1000)	20170608	T4	B08	sgRNA	94.40%	CCAGTACAAAC CTACCTACG	FALSE	2	CCAGTACAAACC TACCTACG	1056
pLas + pR_H2B-BFP (1:1000)	20170608	T4	B09	pL43	68.70%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	2349
pLas + pR_H2B-BFP (1:1000)	20170608	T4	B09	sgRNA	94.90%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	1363
pLas + pR_H2B-BFP (1:1000)	20170608	T4	B10	pL43	90.00%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	3146
pLas + pR_H2B-BFP (1:1000)	20170608	T4	B10	sgRNA	94.90%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	259
pLas + pR_H2B-BFP (1:1000)	20170608	T4	B11	pL43	90.00%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	3920
pLas + pR_H2B-BFP (1:1000)	20170608	T4	B11	sgRNA	95.10%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	409
pLas + pR_H2B-BFP (1:1000)	20170608	T4	B12	pL43	79.40%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	3303
pLas + pR_H2B-BFP (1:1000)	20170608	T4	B12	sgRNA	93.20%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	547

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pR_H2B-BFP (1:1000)	20170608	T4	C05	pL43	96.40%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	3254
pLas + pR_H2B-BFP (1:1000)	20170608	T4	C05	sgRNA	94.70%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	1888
pLas + pR_H2B-BFP (1:1000)	20170608	T4	C06	pL43	96.40%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	3564
pLas + pR_H2B-BFP (1:1000)	20170608	T4	C06	sgRNA	96.70%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	231
pLas + pR_H2B-BFP (1:1000)	20170608	T4	C07	pL43	96.30%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	4010
pLas + pR_H2B-BFP (1:1000)	20170608	T4	C07	sgRNA	95.30%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	1061
pLas + pR_H2B-BFP (1:1000)	20170608	T4	C08	pL43	93.40%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	3041
pLas + pR_H2B-BFP (1:1000)	20170608	T4	C08	sgRNA	94.70%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	537
pLas + pR_H2B-BFP (1:1000)	20170608	T4	C09	pL43	94.60%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	3373
pLas + pR_H2B-BFP (1:1000)	20170608	T4	C09	sgRNA	94.70%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	1522
pLas + pR_H2B-BFP (1:1000)	20170608	T4	C10	pL43	94.70%	TCCACCGGCGA AAGAGATCC	FALSE	2	CAATCGG	3893
pLas + pR_H2B-BFP (1:1000)	20170608	T4	C10	sgRNA	92.90%	TCCACCGGCGA AAGAGATCC	FALSE	2	TCCACCGGCGAA AGAGATCC	1347
pLas + pR_H2B-BFP (1:1000)	20170608	T4	C11	pL43	83.40%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	2594
pLas + pR_H2B-BFP (1:1000)	20170608	T4	C11	sgRNA	95.80%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	1086
pLas + pR_H2B-BFP (1:1000)	20170608	T4	C12	pL43	92.90%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	3721
pLas + pR_H2B-BFP (1:1000)	20170608	T4	C12	sgRNA	95.90%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	635
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D05	pL43	96.20%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	3267
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D05	sgRNA	93.90%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	962

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D06	pL43	96.80%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA	4031
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D06	sgRNA	96.20%	CCAGTACAAAC CTACCTACG	FALSE	2	CCAGTACAAACC TACCTACG	410
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D07	pL43	97.00%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA	3789
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D07	sgRNA	96.70%	CCAGTACAAAC CTACCTACG	FALSE	2	CCAGTACAAACC TACCTACG	232
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D08	pL43	94.40%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	3480
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D08	sgRNA	94.80%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	921
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D09	pL43	95.90%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	3652
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D09	sgRNA	95.10%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	501
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D10	pL43	85.60%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	2837
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D10	sgRNA	94.20%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	3426
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D11	pL43	11.50%	TCCACCGGCGA AAGAGATCC	TRUE	6	CAATCGG	259
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D11	pL43	12.70%	AGAGCACTGCA CTCCTTCA	FALSE	6	AGGCTCT	285
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D11	pL43	17.10%	AGAGCACTGCA CTCCTTCA	FALSE	6	CCAGTTA	385
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D11	pL43	19.90%	CCAGTACAAAC CTACCTACG	TRUE	6	AAGAGGA	447
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D11	pL43	27.90%	TCATATTACGAG TCAGTAGG	TRUE	6	AGAGAGA	628
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D11	sgRNA	94.40%	AGAGCACTGCA CTCCTTCA	FALSE	6	AGAGCACTGCAC TCCTTCA	4967
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D12	pL43	91.10%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	3688
pLas + pR_H2B-BFP (1:1000)	20170608	T4	D12	sgRNA	96.30%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	678

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pR_H2B-BFP (1:1000)	20170608	T4	E05	pL43	96.60%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	3289
pLas + pR_H2B-BFP (1:1000)	20170608	T4	E05	sgRNA	95.60%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	1545
pLas + pR_H2B-BFP (1:1000)	20170608	T4	E06	pL43	97.10%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	4055
pLas + pR_H2B-BFP (1:1000)	20170608	T4	E06	sgRNA	95.30%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	763
pLas + pR_H2B-BFP (1:1000)	20170608	T4	E07	pL43	97.00%	TCCACCGGCGA AAGAGATCC	FALSE	2	CAATCGG	4106
pLas + pR_H2B-BFP (1:1000)	20170608	T4	E07	sgRNA	93.70%	TCCACCGGCGA AAGAGATCC	FALSE	2	TCCACCGGCGAA AGAGATCC	298
pLas + pR_H2B-BFP (1:1000)	20170608	T4	E08	pL43	95.50%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	4002
pLas + pR_H2B-BFP (1:1000)	20170608	T4	E08	sgRNA	98.30%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	116
pLas + pR_H2B-BFP (1:1000)	20170608	T4	E09	pL43	89.30%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	2769
pLas + pR_H2B-BFP (1:1000)	20170608	T4	E09	sgRNA	95.10%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	741
pLas + pR_H2B-BFP (1:1000)	20170608	T4	E10	pL43	88.50%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	3852
pLas + pR_H2B-BFP (1:1000)	20170608	T4	E10	sgRNA	96.00%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	819
pLas + pR_H2B-BFP (1:1000)	20170608	T4	E11	pL43	89.60%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	3194
pLas + pR_H2B-BFP (1:1000)	20170608	T4	E11	sgRNA	97.00%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	292
pLas + pR_H2B-BFP (1:1000)	20170608	T4	E12	pL43	87.20%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	3306
pLas + pR_H2B-BFP (1:1000)	20170608	T4	E12	sgRNA	88.00%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	176
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F05	pL43	94.40%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	2604
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F05	sgRNA	95.80%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	3619

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F06	pL43	97.10%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	3573
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F06	sgRNA	95.10%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	252
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F07	pL43	96.50%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA	3298
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F07	sgRNA	96.70%	CCAGTACAAAC CTACCTACG	FALSE	2	CCAGTACAAACC TACCTACG	177
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F08	pL43	97.10%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	3554
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F08	sgRNA	95.90%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	279
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F09	pL43	11.80%	TCCACCGGCGA AAGAGATCC	FALSE	8	CAATCGG	220
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F09	pL43	13.20%	AGAGCACTGCA CTCCTTCA	FALSE	8	CCAGTTA	245
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F09	pL43	16.50%	TCATATTACGAG TCAGTAGG	TRUE	8	AGAGAGA	306
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F09	pL43	18.00%	CCAGTACAAAC CTACCTACG	FALSE	8	AAGAGGA	334
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F09	pL43	23.90%	AGAGCACTGCA CTCCTTCA	FALSE	8	AGGCTCT	443
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F09	sgRNA	15.40%	TCCACCGGCGA AAGAGATCC	FALSE	8	TCCACCGGCGAA AGAGATCC	46
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F09	sgRNA	21.10%	AGAGCACTGCA CTCCTTCA	FALSE	8	AGAGCACTGCAC TCCTTCA	63
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F09	sgRNA	60.70%	CCAGTACAAAC CTACCTACG	FALSE	8	CCAGTACAAACC TACCTACG	181
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F11	pL43	93.80%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	3904
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F11	sgRNA	95.40%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	922
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F12	pL43	90.60%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA	3835
pLas + pR_H2B-BFP (1:1000)	20170608	T4	F12	sgRNA	95.80%	CCAGTACAAAC CTACCTACG	FALSE	2	CCAGTACAAACC TACCTACG	752

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pR_H2B-BFP (1:1000)	20170608	T4	G05	pL43	96.50%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	3920
pLas + pR_H2B-BFP (1:1000)	20170608	T4	G05	sgRNA	94.20%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	799
pLas + pR_H2B-BFP (1:1000)	20170608	T4	G06	pL43	96.80%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	4425
pLas + pR_H2B-BFP (1:1000)	20170608	T4	G06	sgRNA	95.30%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	1567
pLas + pR_H2B-BFP (1:1000)	20170608	T4	G07	pL43	95.20%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	3330
pLas + pR_H2B-BFP (1:1000)	20170608	T4	G07	sgRNA	93.40%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	2697
pLas + pR_H2B-BFP (1:1000)	20170608	T4	G08	pL43	95.90%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	3450
pLas + pR_H2B-BFP (1:1000)	20170608	T4	G08	sgRNA	95.50%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	191
pLas + pR_H2B-BFP (1:1000)	20170608	T4	G09	pL43	95.30%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	3053
pLas + pR_H2B-BFP (1:1000)	20170608	T4	G09	sgRNA	96.70%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	436
pLas + pR_H2B-BFP (1:1000)	20170608	T4	G10	pL43	92.40%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	3573
pLas + pR_H2B-BFP (1:1000)	20170608	T4	G10	sgRNA	93.90%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	371
pLas + pR_H2B-BFP (1:1000)	20170608	T4	G11	pL43	94.00%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA	3619
pLas + pR_H2B-BFP (1:1000)	20170608	T4	G11	sgRNA	96.00%	CCAGTACAAAC CTACCTACG	FALSE	2	CCAGTACAAACC TACCTACG	917
pLas + pR_H2B-BFP (1:1000)	20170608	T4	G12	pL43	94.80%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	4109
pLas + pR_H2B-BFP (1:1000)	20170608	T4	G12	sgRNA	95.60%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	562
pLas + pR_H2B-BFP (1:1000)	20170608	T4	H06	pL43	97.00%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	4164
pLas + pR_H2B-BFP (1:1000)	20170608	T4	H06	sgRNA	94.00%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	1025

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pR_H2B-BFP (1:1000)	20170608	T4	H07	pL43	97.10%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	4657
pLas + pR_H2B-BFP (1:1000)	20170608	T4	H07	sgRNA	95.50%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	1003
pLas + pR_H2B-BFP (1:1000)	20170608	T4	H08	pL43	97.80%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	4015
pLas + pR_H2B-BFP (1:1000)	20170608	T4	H08	sgRNA	95.20%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	460
pLas + pR_H2B-BFP (1:1000)	20170608	T4	H09	pL43	96.00%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	3802
pLas + pR_H2B-BFP (1:1000)	20170608	T4	H09	sgRNA	95.10%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	818
pLas + pR_H2B-BFP (1:1000)	20170608	T4	H11	pL43	95.90%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA	3996
pLas + pR_H2B-BFP (1:1000)	20170608	T4	H11	sgRNA	95.10%	CCAGTACAAAC CTACCTACG	FALSE	2	CCAGTACAAACC TACCTACG	855
pLas + pR_H2B-BFP (1:1000)	20170608	T4	H12	pL43	74.40%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	2767
pLas + pR_H2B-BFP (1:1000)	20170608	T4	H12	sgRNA	94.40%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	772
pLas + pUC19 (1:1000)	20170608	T3	A09	pL43	84.80%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	2367
pLas + pUC19 (1:1000)	20170608	T3	A09	sgRNA	95.00%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	2635
pLas + pUC19 (1:1000)	20170608	T3	A10	pL43	93.20%	AGTAGTCCGGG ATATCAGCG	TRUE	2	CCTCTTC	3551
pLas + pUC19 (1:1000)	20170608	T3	A10	sgRNA	95.30%	CCAGTACAAAC CTACCTACG	TRUE	2	CCAGTACAAACC TACCTACG	1346
pLas + pUC19 (1:1000)	20170608	T3	A11	pL43	95.10%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	3567
pLas + pUC19 (1:1000)	20170608	T3	A11	sgRNA	95.10%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	1483
pLas + pUC19 (1:1000)	20170608	T3	A12	pL43	96.50%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	4125
pLas + pUC19 (1:1000)	20170608	T3	A12	sgRNA	95.30%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	1775
pLas + pUC19 (1:1000)	20170608	T3	B09	pL43	74.90%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	2884
pLas + pUC19 (1:1000)	20170608	T3	B09	sgRNA	95.40%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	1102
pLas + pUC19 (1:1000)	20170608	T3	B10	pL43	13.90%	AGAGCACTGCA CTCCTTCA	TRUE	4	CCAGTTA	353

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pUC19 (1:1000)	20170608	T3	B10	pL43	20.20%	TCATATTACGAG TCAGTAGG	TRUE	4	AGAGAGA	512
pLas + pUC19 (1:1000)	20170608	T3	B10	pL43	30.80%	CCAGTACAAAC CTACCTACG	TRUE	4	AAGAGGA	781
pLas + pUC19 (1:1000)	20170608	T3	B10	sgRNA	89.30%	CGCCGCCCCCG GACGCGACC	TRUE	4	CGCCGCCCCCGG ACGCGACC	134
pLas + pUC19 (1:1000)	20170608	T3	B11	pL43	92.00%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	4607
pLas + pUC19 (1:1000)	20170608	T3	B11	sgRNA	94.90%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	632
pLas + pUC19 (1:1000)	20170608	T3	B12	pL43	10.30%	TCATATTACGAG TCAGTAGG	TRUE	4	AGAGAGA	343
pLas + pUC19 (1:1000)	20170608	T3	B12	pL43	16.50%	CCAGTACAAAC CTACCTACG	TRUE	4	AAGAGGA	549
pLas + pUC19 (1:1000)	20170608	T3	B12	pL43	45.00%	AGTAGTCCGGG ATATCAGCG	FALSE	4	CCTCTTC	1500
pLas + pUC19 (1:1000)	20170608	T3	B12	sgRNA	95.80%	AGTAGTCCGGG ATATCAGCG	FALSE	4	AGTAGTCCGGGA TATCAGCG	3532
pLas + pUC19 (1:1000)	20170608	T3	C09	pL43	93.70%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	3994
pLas + pUC19 (1:1000)	20170608	T3	C09	sgRNA	95.60%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	1916
pLas + pUC19 (1:1000)	20170608	T3	C10	pL43	15.70%	AGAGCACTGCA CTCCTTCA	TRUE	3	AGGCTCT	453
pLas + pUC19 (1:1000)	20170608	T3	C10	pL43	57.60%	TCCACCGGCGA AAGAGATCC	FALSE	3	CAATCGG	1658
pLas + pUC19 (1:1000)	20170608	T3	C10	sgRNA	94.60%	TCCACCGGCGA AAGAGATCC	FALSE	3	TCCACCGGCGAA AGAGATCC	1320
pLas + pUC19 (1:1000)	20170608	T3	C11	pL43	71.90%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	2500
pLas + pUC19 (1:1000)	20170608	T3	C11	sgRNA	95.30%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	61
pLas + pUC19 (1:1000)	20170608	T3	C12	pL43	10.80%	TCCACCGGCGA AAGAGATCC	TRUE	5	CAATCGG	302
pLas + pUC19 (1:1000)	20170608	T3	C12	pL43	16.20%	TCATATTACGAG TCAGTAGG	TRUE	5	AGAGAGA	456
pLas + pUC19 (1:1000)	20170608	T3	C12	pL43	17.10%	CCAGTACAAAC CTACCTACG	TRUE	5	AAGAGGA	480
pLas + pUC19 (1:1000)	20170608	T3	C12	pL43	40.00%	AGAGCACTGCA CTCCTTCA	FALSE	5	CCAGTTA	1123
pLas + pUC19 (1:1000)	20170608	T3	C12	sgRNA	94.90%	AGAGCACTGCA CTCCTTCA	FALSE	5	AGAGCACTGCAC TCCTTCA	1643
pLas + pUC19 (1:1000)	20170608	T3	D09	pL43	11.80%	CCAGTACAAAC CTACCTACG	TRUE	3	AAGAGGA	338
pLas + pUC19 (1:1000)	20170608	T3	D09	pL43	57.60%	TCATATTACGAG TCAGTAGG	FALSE	3	AGAGAGA	1647
pLas + pUC19 (1:1000)	20170608	T3	D09	sgRNA	91.00%	TCATATTACGAG TCAGTAGG	FALSE	3	TCATATTACGAGT CAGTAGG	783

TABLE 2-continued

condition	date	plate	well	pat-tern	frac-tion	pred sgRNA	soli-tary	matches per sample	match	count
pLas + pUC19 (1:1000)	20170608	T3	D10	pL43	94.70%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	4961
pLas + pUC19 (1:1000)	20170608	T3	D10	sgRNA	95.70%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	991
pLas + pUC19 (1:1000)	20170608	T3	D11	pL43	94.80%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	4155
pLas + pUC19 (1:1000)	20170608	T3	D11	sgRNA	95.70%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	933
pLas + pUC19 (1:1000)	20170608	T3	D12	pL43	76.80%	TCATATTACGAG TCAGTAGG	TRUE	2	AGAGAGA	2695
pLas + pUC19 (1:1000	20170608	T3	D12	sgRNA	94.90%	CCAGTACAAAC CTACCTACG	TRUE	2	CCAGTACAAACC TACCTACG	1313
pLas + pUC19 (1:1000)	20170608	T3	E09	pL43	91.10%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	3176
pLas + pUC19 (1:1000)	20170608	T3	E09	sgRNA	96.10%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	928
pLas + pUC19 (1:1000)	20170608	T3	E10	pL43	10.50%	AGAGCACTGCA CTCCTTCA	TRUE	7	AGGCTCT	288
pLas + pUC19 (1:1000)	20170608	T3	E10	pL43	12.50%	AGAGCACTGCA CTCCTTCA	TRUE	7	CCAGTTA	343
pLas + pUC19 (1:1000)	20170608	T3	E10	pL43	13.60%	TCCACCGGCGA AAGAGATCC	TRUE	7	ACTGGCT	371
pLas + pUC19 (1:1000)	20170608	T3	E10	pL43	13.70%	TCATATTACGAG TCAGTAGG	TRUE	7	AGAGAGA	375
pLas + pUC19 (1:1000)	20170608	T3	E10	pL43	13.80%	TCCACCGGCGA AAGAGATCC	TRUE	7	CAATCGG	376
pLas + pUC19 (1:1000)	20170608	T3	E10	pL43	19.30%	CCAGTACAAAC CTACCTACG	TRUE	7	AAGAGGA	529
pLas + pUC19 (1:1000)	20170608	T3	E10	sgRNA	85.30%	CCTGCAACGGG ACTAGTTGG	TRUE	7	CCTGCAACGGGA CTAGTTGG	320
pLas + pUC19 (1:1000)	20170608	T3	E11	pL43	94.90%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA	3540
pLas + pUC19 (1:1000)	20170608	T3	E11	sgRNA	95.40%	CCAGTACAAAC CTACCTACG	FALSE	2	CCAGTACAAACC TACCTACG	722
pLas + pUC19 (1:1000)	20170608	T3	E12	pL43	93.00%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	3594
pLas + pUC19 (1:1000)	20170608	T3	E12	sgRNA	93.80%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	61
pLas + pUC19 (1:1000)	20170608	T3	F09	pL43	95.60%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	3644
pLas + pUC19 (1:1000)	20170608	T3	F09	sgRNA	94.50%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	242
pLas + pUC19 (1:1000)	20170608	T3	F10	pL43	95.40%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	4252
pLas + pUC19 (1:1000)	20170608	T3	F10	sgRNA	94.30%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	644
pLas + pUC19 (1:1000)	20170608	T3	F11	pL43	12.20%	AGAGCACTGCA CTCCTTCA	TRUE	3	AGGCTCT	360

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pUC19 (1:1000)	20170608	T3	F11	pL43	72.70%	CCTGCAACGGG ACTAGTTGG	FALSE	3	CGTCATA	2141
pLas + pUC19 (1:1000)	20170608	T3	F11	sgRNA	94.50%	CCTGCAACGGG ACTAGTTGG	FALSE	3	CCTGCAACGGGA CTAGTTGG	2120
pLas + pUC19 (1:1000)	20170608	T3	F12	pL43	16.30%	AGAGCACTGCA CTCCTTCA	TRUE	3	AGGCTCT	460
pLas + pUC19 (1:1000)	20170608	T3	F12	pL43	67.60%	CCTGCAACGGG ACTAGTTGG	FALSE	3	CGTCATA	1906
pLas + pUC19 (1:1000)	20170608	T3	F12	sgRNA	95.50%	CCTGCAACGGG ACTAGTTGG	FALSE	3	CCTGCAACGGGA CTAGTTGG	708
pLas + pUC19 (1:1000)	20170608	T3	G09	pL43	13.20%	AGAGCACTGCA CTCCTTCA	FALSE	6	CCAGTTA	331
pLas + pUC19 (1:1000)	20170608	T3	G09	pL43	16.10%	CCAGTACAAAC CTACCTACG	TRUE	6	AAGAGGA	404
pLas + pUC19 (1:1000)	20170608	T3	G09	pL43	21.70%	TCCACCGGCGA AAGAGATCC	FALSE	6	CAATCGG	546
pLas + pUC19 (1:1000)	20170608	T3	G09	pL43	24.30%	TCATATTACGAG TCAGTAGG	TRUE	6	AGAGAGA	612
pLas + pUC19 (1:1000)	20170608	T3	G09	sgRNA	34.80%	AGAGCACTGCA CTCCTTCA	FALSE	6	AGAGCACTGCAC TCCTTCA	32
pLas + pUC19 (1:1000)	20170608	T3	G09	sgRNA	58.70%	TCCACCGGCGA AAGAGATCC	FALSE	6	TCCACCGGCGAA AGAGATCC	54
pLas + pUC19 (1:1000)	20170608	T3	G10	pL43	91.70%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	4180
pLas + pUC19 (1:1000)	20170608	T3	G10	sgRNA	93.80%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	1091
pLas + pUC19 (1:1000)	20170608	T3	G11	pL43	18.10%	TCCACCGGCGA AAGAGATCC	TRUE	4	CAATCGG	434
pLas + pUC19 (1:1000)	20170608	T3	G11	pL43	23.10%	CCAGTACAAAC CTACCTACG	TRUE	4	AAGAGGA	553
pLas + pUC19 (1:1000)	20170608	T3	G11	pL43	29.40%	AGAGCACTGCA CTCCTTCA	FALSE	4	CCAGTTA	703
pLas + pUC19 (1:1000)	20170608	T3	G11	sgRNA	93.70%	AGAGCACTGCA CTCCTTCA	FALSE	4	AGAGCACTGCAC TCCTTCA	6346
pLas + pUC19 (1:1000)	20170608	T3	G12	pL43	92.20%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	4422
pLas + pUC19 (1:1000)	20170608	T3	G12	sgRNA	95.40%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	1195
pLas + pUC19 (1:1000)	20170608	T3	H09	pL43	95.70%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	4388
pLas + pUC19 (1:1000)	20170608	T3	H09	sgRNA	95.90%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	845
pLas + pUC19 (1:1000)	20170608	T3	H10	pL43	94.30%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	3658
pLas + pUC19 (1:1000)	20170608	T3	H10	sgRNA	96.40%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	1427
pLas + pUC19 (1:1000)	20170608	T3	H11	pL43	95.10%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	4519

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pUC19 (1:1000)	20170608	T3	H11	sgRNA	95.80%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	364
pLas + pUC19 (1:1000)	20170608	T3	H12	pL43	93.60%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	4552
pLas + pUC19 (1:1000)	20170608	T3	H12	sgRNA	94.40%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	167
pLas + pUC19 (1:1000)	20170608	T4	A01	pL43	96.20%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	4068
pLas + pUC19 (1:1000)	20170608	T4	A01	sgRNA	95.00%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	1106
pLas + pUC19 (1:1000)	20170608	T4	A02	pL43	94.70%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	3081
pLas + pUC19 (1:1000)	20170608	T4	A02	sgRNA	94.80%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	311
pLas + pUC19 (1:1000)	20170608	T4	A03	pL43	91.20%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA	2564
pLas + pUC19 (1:1000)	20170608	T4	A03	sgRNA	96.10%	CCAGTACAAAC CTACCTACG	FALSE	2	CCAGTACAAACC TACCTACG	123
pLas + pUC19 (1:1000)	20170608	T4	A04	pL43	94.10%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	3348
pLas + pUC19 (1:1000)	20170608	T4	A04	sgRNA	94.70%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	1009
pLas + pUC19 (1:1000)	20170608	T4	B01	pL43	96.40%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	4085
pLas + pUC19 (1:1000)	20170608	T4	B01	sgRNA	95.30%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	946
pLas + pUC19 (1:1000)	20170608	T4	B02	pL43	93.10%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	3533
pLas + pUC19 (1:1000)	20170608	T4	B02	sgRNA	95.90%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	1965
pLas + pUC19 (1:1000)	20170608	T4	B03	pL43	93.90%	AGTAGTCCGGG ATATCAGCG	FALSE	2	CCTCTTC	3112
pLas + pUC19 (1:1000)	20170608	T4	B03	sgRNA	95.60%	AGTAGTCCGGG ATATCAGCG	FALSE	2	AGTAGTCCGGGA TATCAGCG	1585
pLas + pUC19 (1:1000)	20170608	T4	B04	pL43	95.10%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	3625
pLas + pUC19 (1:1000)	20170608	T4	B04	sgRNA	96.10%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	374
pLas + pUC19 (1:1000)	20170608	T4	C01	pL43	95.10%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	3670
pLas + pUC19 (1:1000)	20170608	T4	C01	sgRNA	93.70%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	848
pLas + pUC19 (1:1000)	20170608	T4	C02	pL43	85.10%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	2940
pLas + pUC19 (1:1000)	20170608	T4	C02	sgRNA	94.80%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	454
pLas + pUC19 (1:1000)	20170608	T4	C03	pL43	90.50%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	3055

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pUC19 (1:1000)	20170608	T4	C03	sgRNA	95.50%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	1330
pLas + pUC19 (1:1000)	20170608	T4	C04	pL43	92.00%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	2854
pLas + pUC19 (1:1000)	20170608	T4	C04	sgRNA	93.70%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	593
pLas + pUC19 (1:1000)	20170608	T4	D01	pL43	96.50%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	3679
pLas + pUC19 (1:1000)	20170608	T4	D01	sgRNA	95.80%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	692
pLas, 11 h packaging	20170608	T2	B05	pL43	96.80%	CCTGCAACGGG ACTAGTTGG	TRUE	2	CGTCATA	3770
pLas, 11 h packaging	20170608	T2	B05	sgRNA	95.30%	AGAGCACTGCA CTCCTTCA	TRUE	2	AGAGCACTGCAC TCCTTCA	1369
pLas, 11 h packaging	20170608	T2	B06	pL43	83.60%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	2362
pLas, 11 h packaging	20170608	T2	B06	sgRNA	95.70%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	1597
pLas, 11 h packaging	20170608	T2	B07	pL43	96.30%	TCATATTACGAG TCAGTAGG	TRUE	2	AGAGAGA	3817
pLas, 11 h packaging	20170608	T2	B07	sgRNA	94.40%	ATACAACTGCTT GCAACAGG	TRUE	2	ATACAACTGCTT GCAACAGG	1232
pLas, 11 h packaging	20170608	T2	B08	pL43	96.90%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	4509
pLas, 11 h packaging	20170608	T2	B08	sgRNA	95.90%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	649
pLas, 11 h packaging	20170608	T2	B09	pL43	87.80%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	3644
pLas, 11 h packaging	20170608	T2	B09	sgRNA	96.100	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	416
pLas, 11 h packaging	20170608	T2	B10	pL43	46.40%	CCAGTACAAAC CTACCTACG	FALSE	4	AAGAGGA	1539
pLas, 11 h packaging	20170608	T2	B10	pL43	47.30%	TCATATTACGAG TCAGTAGG	FALSE	4	AGAGAGA	1570
pLas, 11 h packaging	20170608	T2	B10	sgRNA	40.90%	TCATATTACGAG TCAGTAGG	FALSE	4	TCATATTACGAGT CAGTAGG	74
pLas, 11 h packaging	20170608	T2	B10	sgRNA	51.90%	CCAGTACAAAC CTACCTACG	FALSE	4	CCAGTACAAACC TACCTACG	94
pLas, 11 h packaging	20170608	T2	B11	pL43	75.30%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	3109
pLas, 11 h packaging	20170608	T2	B11	sgRNA	95.80%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	684
pLas, 11 h packaging	20170608	T2	B12	pL43	69.70%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	2542
pLas, 11 h packaging	20170608	T2	B12	sgRNA	95.00%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	1034
pLas, 11 h packaging	20170608	T2	C05	pL43	97.50%	TCCACCGGCGA AAGAGATCC	TRUE	2	CAATCGG	3989

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, 11 h packaging	20170608	T2	C05	sgRNA	94.70%	AGTAGTCCGGG ATATCAGCG	TRUE	2	AGTAGTCCGGGA TATCAGCG	1079
pLas, 11 h packaging	20170608	T2	C06	pL43	95.80%	ATACAACTGCTT GCAACAGG	TRUE	2	ATTCCGA	4057
pLas, 11 h packaging	20170608	T2	C06	sgRNA	94.40%	AGTAGTCCGGG ATATCAGCG	TRUE	2	AGTAGTCCGGGA TATCAGCG	725
pLas, 11 h packaging	20170608	T2	C07	pL43	94.70%	AGTAGTCCGGG ATATCAGCG	TRUE	2	CCTCTTC	3449
pLas, 11 h packaging	20170608	T2	C07	sgRNA	94.00%	ATACAACTGCTT GCAACAGG	TRUE	2	ATACAACTGCTT GCAACAGG	676
pLas, 11 h packaging	20170608	T2	C08	pL43	96.50%	TCCACCGGCGA AAGAGATCC	TRUE	2	CAATCGG	4264
pLas, 11 h packaging	20170608	T2	C08	sgRNA	95.70%	CCTGCAACGGG ACTAGTTGG	TRUE	2	CCTGCAACGGGA CTAGTTGG	737
pLas, 11 h packaging	20170608	T2	C09	pL43	96.00%	TCCACCGGCGA AAGAGATCC	FALSE	2	CAATCGG	4160
pLas, 11 h packaging	20170608	T2	C09	sgRNA	93.90%	TCCACCGGCGA AAGAGATCC	FALSE	2	TCCACCGGCGAA AGAGATCC	726
pLas, 11 h packaging	20170608	T2	C10	pL43	12.20%	AGTAGTCCGGG ATATCAGCG	TRUE	6	CCTCTTC	426
pLas, 11 h packaging	20170608	T2	C10	pL43	33.00%	AGAGCACTGCA CTCCTTCA	FALSE	6	AGGCTCT	1152
pLas, 11 h packaging	20170608	T2	C10	pL43	46.60%	TCCACCGGCGA AAGAGATCC	FALSE	6	CAATCGG	1625
pLas, 11 h packaging	20170608	T2	C10	sgRNA	22.00%	CGCCGCCCCCG GACGCGACC	TRUE	6	CGCCGCCCCCGG ACGCGACC	172
pLas, 11 h packaging	20170608	T2	C10	sgRNA	31.50%	AGAGCACTGCA CTCCTTCA	FALSE	6	AGAGCACTGCAC TCCTTCA	246
pLas, 11 h packaging	20170608	T2	C10	sgRNA	38.40%	TCCACCGGCGA AAGAGATCC	FALSE	6	TCCACCGGCGAA AGAGATCC	300
pLas, 11 h packaging	20170608	T2	C11	pL43	43.80%	AGTAGTCCGGG ATATCAGCG	TRUE	4	CCTCTTC	1695
pLas, 11 h packaging	20170608	T2	C11	pL43	52.20%	ATACAACTGCTT GCAACAGG	FALSE	4	ATTCCGA	2019
pLas, 11 h packaging	20170608	T2	C11	sgRNA	32.20% 0	ATACAACTGCTT GCAACAGG	FALSE	4	ATACAACTGCTT GCAACAGG	284
pLas, 11 h packaging	20170608	T2	C11	sgRNA	63.80%	CGCCGCCCCCG GACGCGACC	TRUE	4	CGCCGCCCCCGG ACGCGACC	563
pLas, 11 h packaging	20170608	T2	C12	pL43	11.10%	TCCACCGGCGA AAGAGATCC	TRUE	4	CAATCGG	322
pLas, 11 h packaging	20170608	T2	C12	pL43	17.90%	CCAGTACAAAC CTACCTACG	TRUE	4	AAGAGGA	518
pLas, 11 h packaging	20170608	T2	C12	pL43	38.60%	ATACAACTGCTT GCAACAGG	FALSE	4	ATTCCGA	1115
pLas, 11 h packaging	20170608	T2	C12	sgRNA	93.70%	ATACAACTGCTT GCAACAGG	FALSE	4	ATACAACTGCTT GCAACAGG	417
pLas, 11 h packaging	20170608	T2	D05	pL43	97.20%	AGAGCACTGCA CTCCTTCA	TRUE	2	CCAGTTA	4097

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, 11 h packaging	20170608	T2	D05	sgRNA	94.30%	ATACAACTGCTT GCAACAGG	TRUE	2	ATACAACTGCTT GCAACAGG	834
pLas, 11 h packaging	20170608	T2	D07	pL43	97.60%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	4546
pLas, 11 h packaging	20170608	T2	D07	sgRNA	93.20%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	205
pLas, 11 h packaging	20170608	T2	D08	pL43	92.00%	AGAGCACTGCA CTCCTTCA	TRUE	2	CCAGTTA	2574
pLas, 11 h packaging	20170608	T2	D08	sgRNA	93.80%	CCAGTACAAAC CTACCTACG	TRUE	2	CCAGTACAAACC TACCTACG	456
pLas, 11 h packaging	20170608	T2	D09	pL43	96.80%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	4523
pLas, 11 h packaging	20170608	T2	D09	sgRNA	94.70%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	304
pLas, 11 h packaging	20170608	T2	D10	pL43	95.60%	CGCCGCCCCCG GACGCGACC	TRUE	2	CATGCGT	4801
pLas, 11 h packaging	20170608	T2	D10	sgRNA	92.70%	ATACAACTGCTT GCAACAGG	TRUE	2	ATACAACTGCTT GCAACAGG	190
pLas, 11 h packaging	20170608	T2	D11	pL43	85.10%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA	3220
pLas, 11 h packaging	20170608	T2	D11	sgRNA	95.50%	CCAGTACAAAC CTACCTACG	FALSE	2	CCAGTACAAACC TACCTACG	778
pLas, 11 h packaging	20170608	T2	D12	pL43	94.90%	ATACAACTGCTT GCAACAGG	FALSE	2	ATTCCGA	4344
pLas, 11 h packaging	20170608	T2	D12	sgRNA	96.50%	ATACAACTGCTT GCAACAGG	FALSE	2	ATACAACTGCTT GCAACAGG	495
pLas, 11 h packaging	20170608	T2	E06	pL43	97.40%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	4683
pLas, 11 h packaging	20170608	T2	E06	sgRNA	96.70%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	468
pLas, 11 h packaging	20170608	T2	E07	pL43	95.50%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	3586
pLas, 11 h packaging	20170608	T2	E07	sgRNA	93.60%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	775
pLas, 11 h packaging	20170608	T2	E09	pL43	95.60%	ATACAACTGCTT GCAACAGG	TRUE	2	ATTCCGA	4076
pLas, 11 h packaging	20170608	T2	E09	sgRNA	96.30%	AGTAGTCCGGG ATATCAGCG	TRUE	2	AGTAGTCCGGGA TATCAGCG	441
pLas, 11 h packaging	20170608	T2	E10	pL43	94.00%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	4581
pLas, 11 h packaging	20170608	T2	E10	sgRNA	94.90%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	542
pLas, 11 h packaging	20170608	T2	E11	pL43	63.80%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	1983
pLas, 11 h packaging	20170608	T2	E11	sgRNA	94.60%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	913
pLas, 11 h packaging	20170608	T2	E12	pL43	91.40%	CGCCGCCCCCG GACGCGACC	TRUE	2	CATGCGT	3833

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, 11 h packaging	20170608	T2	E12	sgRNA	96.00%	TCATATTACGAG TCAGTAGG	TRUE	2	TCATATTACGAGT CAGTAGG	868
pLas, 11 h packaging	20170608	T2	F05	pL43	97.00%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	4286
pLas, 11 h packaging	20170608	T2	F05	sgRNA	96.30%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	209
pLas, 11 h packaging	20170608	T2	F06	pL43	96.60%	CGCCGCCCCCG GACGCGACC	TRUE	2	CATGCGT	3706
pLas, 11 h packaging	20170608	T2	F06	sgRNA	95.70%	CCTGCAACGGG ACTAGTTGG	TRUE	2	CCTGCAACGGGA CTAGTTGG	309
pLas, 11 h packaging	20170608	T2	F07	pL43	96.80%	AGAGCACTGCA CTCCTTCA	TRUE	2	CCAGTTA	4093
pLas, 11 h packaging	20170608	T2	F07	sgRNA	94.50%	AGTAGTCCGGG ATATCAGCG	TRUE	2	AGTAGTCCGGGA TATCAGCG	361
pLas, 11 h packaging	20170608	T2	F08	pL43	97.40%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	3440
pLas, 11 h packaging	20170608	T2	F08	sgRNA	94.20%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	98
pLas, 11 h packaging	20170608	T2	F10	pL43	94.60%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	4602
pLas, 11 h packaging	20170608	T2	F10	sgRNA	95.40%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	518
pLas, 11 h packaging	20170608	T2	F11	pL43	15.50%	AGAGCACTGCA CTCCTTCA	FALSE	4	AGGCTCT	626
pLas, 11 h packaging	20170608	T2	F11	pL43	80.40%	TCCACCGGCGA AAGAGATCC	TRUE	4	CAATCGG	3245
pLas, 11 h packaging	20170608	T2	F11	sgRNA	10.20%	AGAGCACTGCA CTCCTTCA	FALSE	4	AGAGCACTGCAC TCCTTCA	79
pLas, 11 h packaging	20170608	T2	F11	sgRNA	85.50%	TCATATTACGAG TCAGTAGG	TRUE	4	TCATATTACGAGT CAGTAGG	664
pLas, 11 h packaging	20170608	T2	F12	pL43	95.60%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	4146
pLas, 11 h packaging	20170608	T2	F12	sgRNA	95.30%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	486
pLas, 11 h packaging	20170608	T2	G05	pL43	97.20%	CGCCGCCCCCG GACGCGACC	FALSE	2	CATGCGT	3720
pLas, 11 h packaging	20170608	T2	G05	sgRNA	95.10%	CGCCGCCCCCG GACGCGACC	FALSE	2	CGCCGCCCCCGG ACGCGACC	509
pLas, 11 h packaging	20170608	T2	G06	pL43	97.30%	CCTGCAACGGG ACTAGTTGG	TRUE	2	CGTCATA	3869
pLas, 11 h packaging	20170608	T2	G06	sgRNA	95.80%	ATACAACTGCTT GCAACAGG	TRUE	2	ATACAACTGCTT GCAACAGG	159
pLas, 11 h packaging	20170608	T2	G07	pL43	85.90%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	1831
pLas, 11 h packaging	20170608	T2	G07	sgRNA	95.00%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	4525
pLas, 11 h packaging	20170608	T2	G08	pL43	95.30%	CCAGTACAAAC CTACCTACG	FALSE	2	AAGAGGA	3386

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, 11 h packaging	20170608	T2	G08	sgRNA	94.70%	CCAGTACAAAC CTACCTACG	FALSE	2	CCAGTACAAACC TACCTACG	160
pLas, 11 h packaging	20170608	T2	G09	pL43	95.20%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CGTCATA	4430
pLas, 11 h packaging	20170608	T2	G09	sgRNA	96.00%	CCTGCAACGGG ACTAGTTGG	FALSE	2	CCTGCAACGGGA CTAGTTGG	427
pLas, 11 h packaging	20170608	T2	G10	pL43	92.50%	AGAGCACTGCA CTCCTTCA	TRUE	2	CCAGTTA	4090
pLas, 11 h packaging	20170608	T2	G10	sgRNA	95.80%	AGTAGTCCGGG ATATCAGCG	TRUE	2	AGTAGTCCGGGA TATCAGCG	915
pLas, 11 h packaging	20170608	T2	G11	pL43	95.90%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	3667
pLas, 11 h packaging	20170608	T2	G11	sgRNA	94.80%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	307
pLas, 11 h packaging	20170608	T2	G12	pL43	92.40%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	4131
pLas, 11 h packaging	20170608	T2	G12	sgRNA	95.70%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	132
pLas, 11 h packaging	20170608	T2	H05	pL43	96.00%	AGTAGTCCGGG ATATCAGCG	TRUE	2	CCTCTTC	3216
pLas, 11 h packaging	20170608	T2	H05	sgRNA	95.40%	CCTGCAACGGG ACTAGTTGG	TRUE	2	CCTGCAACGGGA CTAGTTGG	1403
pLas, 11 h packaging	20170608	T2	H06	pL43	97.10%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	4069
pLas, 11 h packaging	20170608	T2	H06	sgRNA	95.00%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	892
pLas, 11 h packaging	20170608	T2	H07	pL43	97.10%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	4126
pLas, 11 h packaging	20170608	T2	H07	sgRNA	94.50%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	1827
pLas, 11 h packaging	20170608	T2	H08	pL43	97.00%	TCATATTACGAG TCAGTAGG	FALSE	2	AGAGAGA	4237
pLas, 11 h packaging	20170608	T2	H08	sgRNA	95.80%	TCATATTACGAG TCAGTAGG	FALSE	2	TCATATTACGAGT CAGTAGG	1067
pLas, 11 h packaging	20170608	T2	H09	pL43	19.00%	TCATATTACGAG TCAGTAGG	TRUE	3	AGAGAGA	337
pLas, 11 h packaging	20170608	T2	H09	pL43	35.90%	CCAGTACAAAC CTACCTACG	TRUE	3	AAGAGGA	636
pLas, 11 h packaging	20170608	T2	H09	sgRNA	94.10%	AGAGCACTGCA CTCCTTCA	TRUE	3	AGAGCACTGCAC TCCTTCA	9185
pLas, 11 h packaging	20170608	T2	H11	pL43	17.30%	AGAGCACTGCA CTCCTTCA	TRUE	5	CCAGTTA	426
pLas, 11 h packaging	20170608	T2	H11	pL43	18.50%	TCATATTACGAG TCAGTAGG	TRUE	5	AGAGAGA	456
pLas, 11 h packaging	20170608	T2	H11	pL43	20.30%	TCCACCGGCGA AAGAGATCC	TRUE	5	CAATCGG	502
pLas, 11 h packaging	20170608	T2	H11	pL43	21.10%	CCAGTACAAAC CTACCTACG	TRUE	5	AAGAGGA	522

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, 11 h packaging	20170608	T2	H11	sgRNA	95.40%	CGCCGCCCCCG GACGCGACC	TRUE	5	CGCCGCCCCCGG ACGCGACC	3088
pLas, 11 h packaging	20170608	T2	H12	pL43	90.50%	AGAGCACTGCA CTCCTTCA	FALSE	2	CCAGTTA	3677
pLas, 11 h packaging	20170608	T2	H12	sgRNA	95.20%	AGAGCACTGCA CTCCTTCA	FALSE	2	AGAGCACTGCAC TCCTTCA	598
pLas + pR_LG (1:10)	20170924	T1	A01	pL42_ pool1	97.00%	CAAGGAGGACG GCAACATCC	FALSE	2	CTATATATGACC	4947
pLas + pR_LG (1:10)	20170924	T1	A01	sgRNA	89.50%	CAAGGAGGACG GCAACATCC	FALSE	2	CAAGGAGGACGG CAACATCC	3492
pLas + pR_LG (1:10)	20170924	T1	A02	pL42_ pool1	97.20%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GACATGCGTAGC	5560
pLas + pR_LG (1:10)	20170924	T1	A02	sgRNA	89.80%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GCCGTGCCGTAG CTATCCGG	3437
pLas + pR_LG (1:10)	20170924	T1	A03	pL42_ pool1	96.20%	TGTACTCCAGCT TGTGCCCC	FALSE	2	AGCTCTGACACA	5246
pLas + pR_LG (1:10)	20170924	T1	A03	sgRNA	89.70%	TGTACTCCAGCT TGTGCCCC	FALSE	2	TGTACTCCAGCTT GTGCCCC	4470
pLas + pR_LG (1:10)	20170924	T1	A04	pL42_ pool1	96.30% 0	AAGGAGGACGG CAACATCCT	FALSE	2	TCCAAAGAGACA	5671
pLas + pR_LG (1:10)	20170924	T1	A04	sgRNA	90.00%	AAGGAGGACGG CAACATCCT	FALSE	2	AAGGAGGACGGC AACATCCT	4800
pLas + pR_LG (1:10)	20170924	T1	A05	pL42_ pool1	97.20%	CAAGGAGGACG GCAACATCC	FALSE	2	CTATATATGACC	5430
pLas + pR_LG (1:10)	20170924	T1	A05	sgRNA	91.50%	CAAGGAGGACG GCAACATCC	FALSE	2	CAAGGAGGACGG CAACATCC	5875
pLas + pR_LG (1:10)	20170924	T1	A06	pL42_ pool1	96.90%	GCCGTGCCGTA GCTATCCGG	FALSE	2	AGATGATAACGG	5589
pLas + pR_LG (1:10)	20170924	T1	A06	sgRNA	89.20%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GCCGTGCCGTAG CTATCCGG	5212
pLas + pR_LG (1:10)	20170924	T1	A07	pL42_ pool1	96.50% 0	AAGGAGGACGG CAACATCCT	FALSE	2	TCCAAAGAGACA	5717
pLas + pR_LG (1:10)	20170924	T1	A07	sgRNA	89.70%	AAGGAGGACGG CAACATCCT	FALSE	2	AAGGAGGACGGC AACATCCT	5701
pLas + pR_LG (1:10)	20170924	T1	A08	pL42_ pool1	96.40%	GTCCGTTCGACA ATTTCACA	FALSE	2	AGATGGGTTCCG	5163
pLas + pR_LG (1:10)	20170924	T1	A08	sgRNA	86.70%	GTCCGTTCGACA ATTTCACA	FALSE	2	GTCCGTTCGACA ATTTCACA	4141
pLas + pR_LG (1:10)	20170924	T1	A09	pL42_ pool1	96.40%	GTACAGCTAAG TTAAACTCG	FALSE	2	AGCACGGAGACA	5313
pLas + pR_LG (1:10)	20170924	T1	A09	sgRNA	88.80%	GTACAGCTAAG TTAAACTCG	FALSE	2	GTACAGCTAAGT TAAACTCG	3082
pLas + pR_LG (1:10)	20170924	T1	A10	pL42_ pool1	96.80%	AAGGAGGACGG CAACATCCT	FALSE	2	GAATCCGCTCGC	5743
pLas + pR_LG (1:10)	20170924	T1	A10	sgRNA	90.60%	AAGGAGGACGG CAACATCCT	FALSE	2	AAGGAGGACGGC AACATCCT	4341
pLas + pR_LG (1:10)	20170924	T1	A11	pL42_ pool1	96.30%	GTCCGTTCGACA ATTTCACA	FALSE	2	GACAAGTACACT	5168

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pR_LG (1:10)	20170924	T1	A11	sgRNA	88.20%	GTCCGTTCGACA ATTTCACA	FALSE	2	GTCCGTTCGACA ATTTCACA	4120
pLas + pR_LG (1:10)	20170924	T1	B01	pL42_ pool1	97.10%	GTCCGTTCGACA ATTTCACA	FALSE	2	CTCAATTTACAG	5092
pLas + pR_LG (1:10)	20170924	T1	B01	sgRNA	87.20%	GTCCGTTCGACA ATTTCACA	FALSE	2	GTCCGTTCGACA ATTTCACA	2546
pLas + pR_LG (1:10)	20170924	T1	B02	pL42_ pool1	96.90%	AAGGAGGACGG CAACATCCT	FALSE	2	CTAGTGTCCACA	5442
pLas + pR_LG (1:10)	20170924	T1	B02	sgRNA	91.80%	AAGGAGGACGG CAACATCCT	FALSE	2	AAGGAGGACGGC AACATCCT	3877
pLas + pR_LG (1:10	20170924	T1	B03	pL42_ pool1	97.00%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GACAACGAGAAC	5605
pLas + pR_LG (1:10)	20170924	T1	B03	sgRNA	90.70%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GCCGTGCCGTAG CTATCCGG	4741
pLas + pR_LG (1:10)	20170924	T1	B04	pL42_ pool1	96.90%	GGACGCTAAAC CAACGGTGC	FALSE	2	AGAGACTTCACA	5232
pLas + pR_LG (1:10)	20170924	T1	B04	sgRNA	90.00%	GGACGCTAAAC CAACGGTGC	FALSE	2	GGACGCTAAACC AACGGTGC	4847
pLas + pR_LG (1:10)	20170924	T1	B05	pL42_ pool1	96.90%	GTCCGTTCGACA ATTTCACA	FALSE	2	AGATGGGTTCCG	5302
pLas + pR_LG (1:10)	20170924	T1	B05	sgRNA	88.00%	GTCCGTTCGACA ATTTCACA	FALSE	2	GTCCGTTCGACA ATTTCACA	3966
pLas + pR_LG (1:10)	20170924	T1	B06	pL42_ pool1	97.40%	GGACGCTAAAC CAACGGTGC	FALSE	2	GACAGGCTACCT	5500
pLas + pR_LG (1:10)	20170924	T1	B06	sgRNA	91.60%	GGACGCTAAAC CAACGGTGC	FALSE	2	GGACGCTAAACC AACGGTGC	4698
pLas + pR_LG (1:10)	20170924	T1	B07	pL42_ pool1	96.30%	AAGGAGGACGG CAACATCCT	FALSE	2	GAATGAACCACG	6121
pLas + pR_LG (1:10)	20170924	T1	B07	sgRNA	91.90%	AAGGAGGACGG CAACATCCT	FALSE	2	AAGGAGGACGGC AACATCCT	5193
pLas + pR_LG (1:10)	20170924	T1	B08	pL42_ pool1	97.40%	CAACATCCTGG GGCACAAGC	FALSE	2	GAACGCGAAAGC	5179
pLas + pR_LG (1:10)	20170924	T1	B08	sgRNA	90.70%	CAACATCCTGG GGCACAAGC	FALSE	2	CAACATCCTGGG GCACAAGC	4939
pLas + pR_LG (1:10)	20170924	T1	B09	pL42_ pool1	97.00%	GTCCGTTCGACA ATTTCACA	FALSE	2	GACAAGTACACT	5307
pLas + pR_LG (1:10)	20170924	T1	B09	sgRNA	88.30%	GTCCGTTCGACA ATTTCACA	FALSE	2	GTCCGTTCGACA ATTTCACA	4370
pLas + pR_LG (1:10)	20170924	T1	B10	pL42_ pool1	95.90%	GCCGTGCCGTA GCTATCCGG	FALSE	2	CTCACTGACACT	5921
pLas + pR_LG (1:10)	20170924	T1	B10	sgRNA	90.20%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GCCGTGCCGTAG CTATCCGG	4136
pLas + pR_LG (1:10)	20170924	T1	B11	pL42_ pool1	97.20%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GACATGCGTAGC	5359
pLas + pR_LG (1:10)	20170924	T1	B11	sgRNA	89.30%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GCCGTGCCGTAG CTATCCGG	3745
pLas + pR_LG (1:10)	20170924	T1	C01	pL42_ pool1	97.00%	AAGGAGGACGG CAACATCCT	FALSE	2	TCCAAAGAGACA	5345

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pR_LG (1:10)	20170924	T1	C01	sgRNA	89.30%	AAGGAGGACGG CAACATCCT	FALSE	2	AAGGAGGACGGC AACATCCT	5246
pLas + pR_LG (1:10)	20170924	T1	C02	pL42_ pool1	97.80%	GCTGCTTGCGAT ACCAATAG	FALSE	2	AGCAGCCCTAGC	5419
pLas + pR_LG (1:10)	20170924	T1	C02	sgRNA	89.90%	GCTGCTTGCGAT ACCAATAG	FALSE	2	GCTGCTTGCGAT ACCAATAG	4883
pLas + pR_LG (1:10)	20170924	T1	C03	pL42_ pool1	96.20%	GCCGTGCCGTA GCTATCCGG	FALSE	2	CTCACTGACACT	5307
pLas + pR_LG (1:10)	20170924	T1	C03	sgRNA	89.60%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GCCGTGCCGTAG CTATCCGG	5020
pLas + pR_LG (1:10)	20170924	T1	C04	pL42_ pool1	96.90%	CAACATCCTGG GGCACAAGC	FALSE	2	AGAGCAGAAAGG CAACATCCTGGG	5495
pLas + pR_LG (1:10)	20170924	T1	C04	sgRNA	88.30%	CAACATCCTGG GGCACAAGC	FALSE	2	GCACAAGC	4555
pLas + pR_LG (1:10)	20170924	T1	C05	pL42_ pool1	97.10%	GCCGTGCCGTA GCTATCCGG	FALSE	2	AGATGATAACGG GCCGTGCCGTAG	5613
pLas + pR_LG (1:10)	20170924	T1	C05	sgRNA	88.20%	GCCGTGCCGTA GCTATCCGG	FALSE	2	CTATCCGG	4590
pLas + pR_LG (1:10)	20170924	T1	C06	pL42_ pool1	97.10%	GGACGCTAAAC CAACGGTGC	FALSE	2	TCCAGAGCACCT GGACGCTAAACC	6229
pLas + pR_LG (1:10)	20170924	T1	C06	sgRNA	89.80%	GGACGCTAAAC CAACGGTGC	FALSE	2	AACGGTGC	4789
pLas + pR_LG (1:10)	20170924	T1	C07	pL42_ pool1	96.50%	AGGAGGACGGC AACATCCTG	FALSE	2	AGCGACCTTACA AGGAGGACGGCA	5522
pLas + pR_LG (1:10)	20170924	T1	C07	sgRNA	90.50%	AGGAGGACGGC AACATCCTG	FALSE	2	ACATCCTG	5621
pLas + pR_LG (1:10)	20170924	T1	C08	pL42_ pool1	96.70%	GCTGCTTGCGAT ACCAATAG	FALSE	2	AGCAGTGTACCT GCTGCTTGCGAT	5399
pLas + pR_LG (1:10)	20170924	T1	C08	sgRNA	87.90%	GCTGCTTGCGAT ACCAATAG	FALSE	2	ACCAATAG	3869
pLas + pR_LG (1:10)	20170924	T1	C09	pL42_ pool1	96.60%	GCCGTGCCGTA GCTATCCGG	FALSE	2	AGATGATAACGG GCCGTGCCGTAG	5137
pLas + pR_LG (1:10)	20170924	T1	C09	sgRNA	89.50%	GCCGTGCCGTA GCTATCCGG	FALSE	2	CTATCCGG	3866
pLas + pR_LG (1:10)	20170924	T1	C10	pL42_ pool1	97.30%	TGTACTCCAGCT TGTGCCCC	FALSE	2	AGCTAGCCTAGG TGTACTCCAGCTT	6254
pLas + pR_LG (1:10)	20170924	T1	C10	sgRNA	89.90%	TGTACTCCAGCT TGTGCCCC	FALSE	2	GTGCCCC	4656
pLas + pR_LG (1:10)	20170924	T1	C11	pL42_ pool1	97.20%	TGTACTCCAGCT TGTGCCCC	FALSE	2	AGCTAGCCTAGG TGTACTCCAGCTT	5845
pLas + pR_LG (1:10)	20170924	T1	C11	sgRNA	89.60%	TGTACTCCAGCT TGTGCCCC	FALSE	2	GTGCCCC	4302
pLas + pR_LG (1:10)	20170924	T1	C12	pL42_ pool1	96.80%	GTCCGTTCGACA ATTTCACA	FALSE	2	AGATGGGTTCCG GTCCGTTCGACA	5299
pLas + pR_LG (1:10)	20170924	T1	C12	sgRNA	86.90%	GTCCGTTCGACA ATTTCACA	FALSE	2	ATTTCACA	3506
pLas + pR_LG (1:10)	20170924	T1	D01	pL42_ pool1	96.30%	GGACGCTAAAC CAACGGTGC	FALSE	2	AGATCGACCACC GGACGCTAAACC	5164

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pR_LG (1:10)	20170924	T1	D01	sgRNA	90.90%	GGACGCTAAAC CAACGGTGC	FALSE	2	AACGGTGC	4652
pLas + pR_LG (1:10)	20170924	T1	D02	pL42_ pool1	95.90%	CAAGGAGGACG GCAACATCC	FALSE	2	CTATATATGACC CAAGGAGGACGG	519
pLas + pR_LG (1:10)	20170924	T1	D02	sgRNA	94.10%	CAAGGAGGACG GCAACATCC	FALSE	2	CAACATCC	5149
pLas + pR_LG (1:10)	20170924	T1	D03	pL42_ pool1	97.10%	GTCCGTTCGACA ATTTCACA	FALSE	2	CTCAATTTACAG	5103
pLas + pR_LG (1:10)	20170924	T1	D03	sgRNA	88.70%	GTCCGTTCGACA ATTTCACA	FALSE	2	GTCCGTTCGACA ATTTCACA	4837
pLas + pR_LG (1:10)	20170924	T1	D04	pL42_ pool1	97.30%	TGTACTCCAGCT TGTGCCCC	FALSE	2	AGCGCCGTCATT	5431
pLas + pR_LG (1:10)	20170924	T1	D04	sgRNA	90.80%	TGTACTCCAGCT TGTGCCCC	FALSE	2	TGTACTCCAGCTT GTGCCCC	5191
pLas + pR_LG (1:10)	20170924	T1	D05	pL42_ pool1	96.90%	GCTGCTTGCGAT ACCAATAG	FALSE	2	GAAGTGGGCAAC	5282
pLas + pR_LG (1:10)	20170924	T1	D05	sgRNA	90.70%	GCTGCTTGCGAT ACCAATAG	FALSE	2	GCTGCTTGCGAT ACCAATAG	4882
pLas + pR_LG (1:10)	20170924	T1	D06	pL42_ pool1	97.40%	TGTACTCCAGCT TGTGCCCC	FALSE	2	GAACTAGCCACT	6051
pLas + pR_LG (1:10)	20170924	T1	D06	sgRNA	90.70%	TGTACTCCAGCT TGTGCCCC	FALSE	2	TGTACTCCAGCTT GTGCCCC	4812
pLas + pR_LG (1:10)	20170924	T1	D07	pL42_ pool1	97.90%	TGTACTCCAGCT TGTGCCCC	FALSE	2	AGCTAGCCTAGG	6191
pLas + pR_LG (1:10)	20170924	T1	D07	sgRNA	90.60%	TGTACTCCAGCT TGTGCCCC	FALSE	2	TGTACTCCAGCTT GTGCCCC	4713
pLas + pR_LG (1:10)	20170924	T1	D08	pL42_ pool1	95.60%	GGACGCTAAAC CAACGGTGC	FALSE	2	AGATCGACCACC	5062
pLas + pR_LG (1:10)	20170924	T1	D08	sgRNA	91.10%	GGACGCTAAAC CAACGGTGC	FALSE	2	GGACGCTAAACC AACGGTGC	4437
pLas + pR_LG (1:10)	20170924	T1	D10	pL42_ pool1	97.00%	GTACAGCTAAG TTAAACTCG	FALSE	2	AGCACGGAGACA	4601
pLas + pR_LG (1:10)	20170924	T1	D10	sgRNA	91.70%	GTACAGCTAAG TTAAACTCG	FALSE	2	GTACAGCTAAGT TAAACTCG	4341
pLas + pR_LG (1:10)	20170924	T1	D11	pL42_ pool1	97.40%	GTCCGTTCGACA ATTTCACA	FALSE	2	GACAAGTACACT	5112
pLas + pR_LG (1:10)	20170924	T1	D11	sgRNA	88.80%	GTCCGTTCGACA ATTTCACA	FALSE	2	GTCCGTTCGACA ATTTCACA	3948
pLas + pR_LG (1:10)	20170924	T1	D12	pL42_ pool1	97.40%	GCCGTGCCGTA GCTATCCGG	FALSE	2	AGATGATAACGG	5286
pLas + pR_LG (1:10)	20170924	T1	D12	sgRNA	91.20%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GCCGTGCCGTAG CTATCCGG	3873
pLas + pR_LG (1:10)	20170924	T1	E01	pL42_ pool1	97.50%	GCCGTGCCGTA GCTATCCGG	FALSE	2	AGATGATAACGG	5806
pLas + pR_LG (1:10)	20170924	T1	E01	sgRNA	88.40%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GCCGTGCCGTAG CTATCCGG	4418
pLas + pR_LG (1:10)	20170924	T1	E02	pL42_ pool1	96.70%	CAAGGAGGACG GCAACATCC	FALSE	2	CTATATATGACC	4937

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pR_LG (1:10)	20170924	T1	E02	sgRNA	92.60%	CAAGGAGGACG GCAACATCC	FALSE	2	CAAGGAGGACGG CAACATCC	4515
pLas + pR_LG (1:10)	20170924	T1	E03	pL42_ pool1	96.30%	GCCGTGCCGTA GCTATCCGG	FALSE	2	CTCACTGACACT	5638
pLas + pR_LG (1:10)	20170924	T1	E03	sgRNA	90.40%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GCCGTGCCGTAG CTATCCGG	4364
pLas + pR_LG (1:10)	20170924	T1	E04	pL42_ pool1	96.90%	GTCCGTTCGACA ATTTCACA	FALSE	2	CTCAATTTACAG GTCCGTTCGACA	5383
pLas + pR_LG (1:10)	20170924	T1	E04	sgRNA	87.50%	GTCCGTTCGACA ATTTCACA	FALSE	2	ATTTCACA	4141
pLas + pR_LG (1:10)	20170924	T1	E05	pL42_ pool1	97.30%	GGACGCTAAAC CAACGGTGC	FALSE	2	GACAGGCTACCT GGACGCTAAACC	5329
pLas + pR_LG (1:10)	20170924	T1	E05	sgRNA	88.30%	GGACGCTAAAC CAACGGTGC	FALSE	2	AACGGTGC	4383
pLas + pR_LG 1:10)	20170924	T1	E06	pL42_ pool1	97.40%	GTCCGTTCGACA ATTTCACA	FALSE	2	AGATGGGTTCCG GTCCGTTCGACA	5458
pLas + pR_LG (1:10)	20170924	T1	E06	sgRNA	88.70%	GTCCGTTCGACA ATTTCACA	FALSE	2	ATTTCACA	4981
pLas + pR_LG (1:10)	20170924	T1	E07	pL42_ pool1	97.00%	GTCCGTTCGACA ATTTCACA	FALSE	2	GACAAGTACACT GTCCGTTCGACA	5252
pLas + pR_LG (1:10)	20170924	T1	E07	sgRNA	88.20%	GTCCGTTCGACA ATTTCACA	FALSE	2	ATTTCACA	4925
pLas + pR_LG (1:10)	20170924	T1	E08	pL42_ pool1	96.60%	GTACAGCTAAG TTAAACTCG	FALSE	2	AGCACGGAGACA	5176
pLas + pR_LG (1:10)	20170924	T1	E08	sgRNA pL42_	91.50%	GTACAGCTAAG TTAAACTCG	FALSE	2	GTACAGCTAAGT TAAACTCG	4568
pLas + pR_LG (1:10)	20170924	T1	E09	pool1	97.00%	GTCCGTTCGACA ATTTCACA	FALSE	2	AGATGGGTTCCG	5147
pLas + pR_LG (1:10)	20170924	T1	E09	sgRNA pL42_	87.80%	GTCCGTTCGACA ATTTCACA	FALSE	2	GTCCGTTCGACA ATTTCACA	3963
pLas + pR_LG (1:10)	20170924	T1	E10	pool1	97.10%	GTCCGTTCGACA ATTTCACA	FALSE	2	AGATGGGTTCCG	4793
pLas + pR_LG (1:10)	20170924	T1	E10	sgRNA	88.00%	GTCCGTTCGACA ATTTCACA	FALSE	2	GTCCGTTCGACA ATTTCACA	4321
pLas + pR_LG (1:10)	20170924	T1	E11	pL42_ pool1	97.50%	CAAGGAGGACG GCAACATCC	FALSE	2	GAACTCAGGACA	4387
pLas + pR_LG (1:10)	20170924	T1	E11	sgRNA	91.10%	CAAGGAGGACG GCAACATCC	FALSE	2	CAAGGAGGACGG CAACATCC	4034
pLas + pR_LG (1:10)	20170924	T1	F01	pL42_ pool1	97.20%	CAAGGAGGACG GCAACATCC	FALSE	2	CTATATATGACC	5619
pLas + pR_LG (1:10)	20170924	T1	F01	sgRNA	89.10%	CAAGGAGGACG GCAACATCC	FALSE	2	CAAGGAGGACGG CAACATCC	2595
pLas + pR_LG (1:10)	20170924	T1	F02	pL42_ pool1	96.80%	CAAGGAGGACG GCAACATCC	FALSE	2	GAACTCAGGACA	5330
pLas + pR_LG (1:10)	20170924	T1	F02	sgRNA	92.50%	CAAGGAGGACG GCAACATCC	FALSE	2	CAAGGAGGACGG CAACATCC	3447
pLas + pR_LG (1:10)	20170924	T1	F03	pL42_ pool1	97.00%	CAACATCCTGG GGCACAAGC	FALSE	2	AGATTCATGACG	5301

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pR_LG (1:10)	20170924	T1	F03	sgRNA	89.20%	CAACATCCTGG GGCACAAGC	FALSE	2	CAACATCCTGGG GCACAAGC	4453
pLas + pR_LG (1:10)	20170924	T1	F04	pL42_ pool1	97.60%	TGTACTCCAGCT TGTGCCCC	FALSE	2	AGCGCCGTCATT	5303
pLas + pR_LG (1:10)	20170924	T1	F04	sgRNA	89.70%	TGTACTCCAGCT TGTGCCCC	FALSE	2	TGTACTCCAGCTT GTGCCCC	4379
pLas + pR_LG (1:10)	20170924	T1	F05	pL42_ pool1	96.70%	GTCCGTTCGACA ATTTCACA	FALSE	2	AGCAACTTCACT	5379
pLas + pR_LG (1:10)	20170924	T1	F05	sgRNA	86.80%	GTCCGTTCGACA ATTTCACA	FALSE	2	GTCCGTTCGACA ATTTCACA	4602
pLas + pR_LG (1:10)	20170924	T1	F06	pL42_ pool1	97.10%	GTCCGTTCGACA ATTTCACA	FALSE	2	AGATGGGTTCCG	5479
pLas + pR_LG (1:10)	20170924	T1	F06	sgRNA	88.40%	GTCCGTTCGACA ATTTCACA	FALSE	2	GTCCGTTCGACA ATTTCACA	4357
pLas + pR_LG (1:10)	20170924	T1	F07	pL42_ pool1	97.20%	GCTGCTTGCGAT ACCAATAG	TRUE	2	AGAGCTGCTACG	5788
pLas + pR_LG (1:10)	20170924	T1	F07	sgRNA	88.60%	GCCGTGCCGTA GCTATCCGG	TRUE	2	GCCGTGCCGTAG CTATCCGG	4696
pLas + pR_LG (1:10)	20170924	T1	F08	pL42_ pool1	96.70%	AAGGAGGACGG CAACATCCT	FALSE	2	TCCAAAGAGACA	5231
pLas + pR_LG (1:10)	20170924	T1	F08	sgRNA	90.40%	AAGGAGGACGG CAACATCCT	FALSE	2	AAGGAGGACGGC AACATCCT	4692
pLas + pR_LG (1:10)	20170924	T1	F09	pL42_ pool1	97.00%	CAAGGAGGACG GCAACATCC	FALSE	2	AGCCACCAGTAT	5024
pLas + pR_LG (1:10)	20170924	T1	F09	sgRNA	91.50%	CAAGGAGGACG GCAACATCC	FALSE	2	CAAGGAGGACGG CAACATCC	3869
pLas + pR_LG (1:10)	20170924	T1	F10	pL42_ pool1	95.90%	GGACGCTAAAC CAACGGTGC	FALSE	2	TCCAGAGCACCT	5167
pLas + pR_LG (1:10)	20170924	T1	F10	sgRNA	89.70%	GGACGCTAAAC CAACGGTGC	FALSE	2	GGACGCTAAACC AACGGTGC	4575
pLas + pR_LG (1:10)	20170924	T1	F11	pL42_ pool1	97.00%	GCTGCTTGCGAT ACCAATAG	FALSE	2	AGCAGTGTACCT	5144
pLas + pR_LG (1:10)	20170924	T1	F11	sgRNA	89.10%	GCTGCTTGCGAT ACCAATAG	FALSE	2	GCTGCTTGCGAT ACCAATAG	4141
pLas + pR_LG (1:10)	20170924	T1	F12	pL42_ pool1	96.40%	GTACAGCTAAG TTAAACTCG	FALSE	2	GAATTAGTGACC	5578
pLas + pR_LG (1:10)	20170924	T1	F12	sgRNA	88.80%	GTACAGCTAAG TTAAACTCG	FALSE	2	GTACAGCTAAGT TAAACTCG	3825
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A01	pL42_ pool1	97.40%	TGTACTCCAGCT TGTGCCCC	FALSE	2	AGCGCCGTCATT	5888
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A01	sgRNA	90.00%	TGTACTCCAGCT TGTGCCCC	FALSE	2	TGTACTCCAGCTT GTGCCCC	4612
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A02	pL42_ pool1	98.10%	TGTACTCCAGCT TGTGCCCC	FALSE	2	AGCTAGCCTAGG	6329
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A02	sgRNA	91.60%	TGTACTCCAGCT TGTGCCCC	FALSE	2	TGTACTCCAGCTT GTGCCCC	3870

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A05	pL42_ pool1	96.60%	TGTACTCCAGCT TGTGCCCC	FALSE	2	AGCTCTGACACA	6816
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A05	sgRNA	90.10%	TGTACTCCAGCT TGTGCCCC	FALSE	2	TGTACTCCAGCTT GTGCCCC	3081
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A06	pL42_ pool1	96.70%	TGTACTCCAGCT TGTGCCCC	FALSE	2	CATGATCCCACA	5634
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A06	sgRNA	91.10%	TGTACTCCAGCT TGTGCCCC	FALSE	2	TGTACTCCAGCTT GTGCCCC	3763
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A07	pL42_ pool1	96.10%	GCCGTGCCGTA GCTATCCGG	FALSE	2	CTCACTGACACT	5778
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A07	sgRNA	89.40%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GCCGTGCCGTAG CTATCCGG	3233
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A08	pL42_ pool1	96.40%	AAGGAGGACGG CAACATCCT	FALSE	2	GAATGAACCACG	5705
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A08	sgRNA	91.70%	AAGGAGGACGG CAACATCCT	FALSE	2	AAGGAGGACGGC AACATCCT	2902
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A09	pL42_ pool1	97.40%	CAAGGAGGACG GCAACATCC	FALSE	2	CTATATATGACC	4537
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A09	sgRNA	92.00%	CAAGGAGGACG GCAACATCC	FALSE	2	CAAGGAGGACGG CAACATCC	2869
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A10	pL42_ pool1	97.00%	TGTACTCCAGCT TGTGCCCC	FALSE	2	GAACTAGCCACT	6008
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A10	sgRNA	90.70%	TGTACTCCAGCT TGTGCCCC	FALSE	2	TGTACTCCAGCTT GTGCCCC	3110
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A11	pL42_ pool1	97.10%	GTCCGTTCGACA ATTTCACA	FALSE	2	GACAAGTACACT	5570
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A11	sgRNA	86.90%	GTCCGTTCGACA ATTTCACA	FALSE	2	GTCCGTTCGACA ATTTCACA	3042
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A12	pL42_ pool1	97.70%	GCTGCTTGCGAT ACCAATAG	FALSE	2	AGCAGCCCTAGC	5860
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	A12	sgRNA	89.60%	GCTGCTTGCGAT ACCAATAG	FALSE	2	GCTGCTTGCGAT ACCAATAG	2508
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B01	pL42_ pool1	96.20%	AGGAGGACGGC AACATCCTG	FALSE	2	AGCGACCTTACA	5516
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B01	sgRNA	91.00%	AGGAGGACGGC AACATCCTG	FALSE	2	AGGAGGACGGCA ACATCCTG	3684

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B02	pL42_ pool1	96.20%	CAAGGAGGACG GCAACATCC	FALSE	2	GAACTCAGGACA	6017
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B02	sgRNA	92.90%	CAAGGAGGACG GCAACATCC	FALSE	2	CAAGGAGGACGG CAACATCC	3527
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B03	pL42_ pool1	97.30%	GTCCGTTCGACA ATTTCACA	FALSE	2	GACAAGTACACT	5069
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B03	sgRNA	88.00%	GTCCGTTCGACA ATTTCACA	FALSE	2	GTCCGTTCGACA ATTTCACA	3034
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B04	pL42_ pool1	96.60%	AGGAGGACGGC AACATCCTG	FALSE	2	AGCGACCTTACA	5231
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B04	sgRNA	90.20%	AGGAGGACGGC AACATCCTG	FALSE	2	AGGAGGACGGCA ACATCCTG	3211
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B05	pL42_ pool1	97.30%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GACATGCGTAGC	5816
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B05	sgRNA	89.70%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GCCGTGCCGTAG CTATCCGG	3329
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B06	pL42_ pool1	95.70%	GGACGCTAAAC CAACGGTGC	FALSE	2	AGATCGACCACC	5445
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B06	sgRNA	90.40%	GGACGCTAAAC CAACGGTGC	FALSE	2	GGACGCTAAACC AACGGTGC	2914
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B07	pL42_ pool1	96.30%	AAGGAGGACGG CAACATCCT	FALSE	2	GAATGAACCACG	5476
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B07	sgRNA	90.40%	AAGGAGGACGG CAACATCCT	FALSE	2	AAGGAGGACGGC AACATCCT	3405
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B08	pL42_ pool1	96.70%	TGTACTCCAGCT TGTGCCCC	FALSE	2	AGCTCTGACACA	5351
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B08	sgRNA	90.90%	TGTACTCCAGCT TGTGCCCC	FALSE	2	TGTACTCCAGCTT GTGCCCC	3306
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B09	pL42_ pool1	97.40%	GTACAGCTAAG TTAAACTCG	FALSE	2	TCCATCAATACG	5332
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B09	sgRNA	90.30%	GTACAGCTAAG TTAAACTCG	FALSE	2	GTACAGCTAAGT TAAACTCG	3539
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B10	pL42_ pool1	96.80%	GGACGCTAAAC CAACGGTGC	FALSE	2	GACAGGCTACCT	5495
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B10	sgRNA	90.90%	GGACGCTAAAC CAACGGTGC	FALSE	2	GGACGCTAAACC AACGGTGC	3426

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B11	pL42_ pool1	96.20%	GCCGTGCCGTA GCTATCCGG	FALSE	2	CTCACTGACACT	5434
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B11	sgRNA	90.00%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GCCGTGCCGTAG CTATCCGG	2941
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B12	pL42_ pool1	96.30%	AGGAGGACGGC AACATCCTG	FALSE	2	AGCGACCTTACA	5569
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	B12	sgRNA	91.10%	AGGAGGACGGC AACATCCTG	FALSE	2	AGGAGGACGGCA ACATCCTG	2966
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	C01	pL42_ pool1	97.70%	GTACAGCTAAG TTAAACTCG	FALSE	2	CTAGATGTTAGC	6135
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	C01	sgRNA	88.80%	GTACAGCTAAG TTAAACTCG	FALSE	2	GTACAGCTAAGT TAAACTCG	3119
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	C02	pL42_ pool1	97.10%	TGTACTCCAGCT TGTGCCCC	FALSE	2	AGCGCCGTCATT	5592
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	C02	sgRNA	90.60%	TGTACTCCAGCT TGTGCCCC	FALSE	2	TGTACTCCAGCTT GTGCCCC	3382
pLas + LX_TRC313_ LacZ (1:1000)	20170924	T2	C03	pL42_ pool1	96.90%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GACAACGAGAAC	5672
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	C03	sgRNA	90.70%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GCCGTGCCGTAG CTATCCGG	3822
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	C04	pL42_ pool1	97.20%	AGGAGGACGGC AACATCCTG	FALSE	2	GAATGGACAGCG	5859
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	C04	sgRNA	91.00%	AGGAGGACGGC AACATCCTG	FALSE	2	AGGAGGACGGCA ACATCCTG	3447
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	C05	pL42_ pool1	97.30%	CAACATCCTGG GGCACAAGC	FALSE	2	GAACGCGAAAGC	5788
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	C05	sgRNA	89.70%	CAACATCCTGG GGCACAAGC	FALSE	2	CAACATCCTGGG GCACAAGC	3877
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	C06	pL42_ pool1	96.90%	GTCCGTTCGACA ATTTCACA	FALSE	2	GACAAGTACACT	6389
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	C06	sgRNA	87.60%	GTCCGTTCGACA ATTTCACA	FALSE	2	GTCCGTTCGACA ATTTCACA	3539
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	C09	pL42_ pool1	96.10%	GCCGTGCCGTA GCTATCCGG	FALSE	2	CTCACTGACACT	5733
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	C09	sgRNA	90.70%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GCCGTGCCGTAG CTATCCGG	3107

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	C11	pL42_ pool1	96.50%	AAGGAGGACGG CAACATCCT	FALSE	2	TCCAAAGAGACA	5408
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	C11	sgRNA	91.40%	AAGGAGGACGG CAACATCCT	FALSE	2	AAGGAGGACGGC AACATCCT	3554
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	C12	pL42_ pool1	96.40%	GGACGCTAAAC CAACGGTGC	FALSE	2	TCCAGAGCACCT	6109
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	C12	sgRNA	89.80%	GGACGCTAAAC CAACGGTGC	FALSE	2	GGACGCTAAACC AACGGTGC	3255
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D01	pL42_ pool1	96.90%	GGACGCTAAAC CAACGGTGC	FALSE	2	AGAGACTTCACA	5626
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D01	sgRNA	88.60%	GGACGCTAAAC CAACGGTGC	FALSE	2	GGACGCTAAACC AACGGTGC	2686
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D02	pL42_ pool1	96.80%	GGACGCTAAAC CAACGGTGC	FALSE	2	TCCAGAGCACCT	6040
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D02	sgRNA	91.20%	GGACGCTAAAC CAACGGTGC	FALSE	2	GGACGCTAAACC AACGGTGC	3286
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D03	pL42_ pool1	97.10%	GCTGCTTGCGAT ACCAATAG	TRUE	2	GAAGTGGGCAAC	5323
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D03	sgRNA	90.30%	TGTACTCCAGCT TGTGCCCC	TRUE	2	TGTACTCCAGCTT GTGCCCC	3042
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D04	pL42_ pool1	96.30%	TGTACTCCAGCT TGTGCCCC	FALSE	2	AGCTCTGACACA	5512
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D04	sgRNA	89.40%	TGTACTCCAGCT TGTGCCCC	FALSE	2	TGTACTCCAGCTT GTGCCCC	2991
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D05	pL42_ pool1	96.20%	GCCGTGCCGTA GCTATCCGG	FALSE	2	CTCACTGACACT GCCGTGCCGTAG	5837
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D05	sgRNA	89.70%	GCCGTGCCGTA GCTATCCGG	FALSE	2	CTATCCGG	3416
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D06	pL42_ pool1	98.00%	TGTACTCCAGCT TGTGCCCC	FALSE	2	AGCTAGCCTAGG	6296
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D06	sgRNA	90.50%	TGTACTCCAGCT TGTGCCCC	FALSE	2	TGTACTCCAGCTT GTGCCCC	3879
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D07	pL42_ pool1	96.80%	AAGGAGGACGG CAACATCCT	FALSE	2	CTAGTGTCCACA	5837
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D07	sgRNA	91.60%	AAGGAGGACGG CAACATCCT	FALSE	2	AAGGAGGACGGC AACATCCT	3677

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D08	pL42_ pool1	97.10%	CAAGGAGGACG GCAACATCC	FALSE	2	AGCCAGTCAATC	6163
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D08	sgRNA	90.60%	CAAGGAGGACG GCAACATCC	FALSE	2	CAAGGAGGACGG CAACATCC	3415
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D09	pL42_ pool1	97.50%	GCCGTGCCGTA GCTATCCGG	TRUE	2	GACATGCGTAGC	5736
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D09	sgRNA	88.00%	GTCCGTTCGACA ATTTCACA	TRUE	2	GTCCGTTCGACA ATTTCACA	3192
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D10	pL42_ pool1	45.70%	GCCGTGCCGTA GCTATCCGG	FALSE	4	AGATGATAACGG	2661
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D10	pL42_ pool1	51.10%	GTCCGTTCGACA ATTTCACA	FALSE	4	AGCAACTTCACT	2976
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D10	sgRNA	43.30%	GCCGTGCCGTA GCTATCCGG	FALSE	4	GCCGTGCCGTAG CTATCCGG	1374
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D10	sgRNA	44.70%	GTCCGTTCGACA ATTTCACA	FALSE	4	GTCCGTTCGACA ATTTCACA	1416
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D11	pL42_ pool1	96.60%	GTCCGTTCGACA ATTTCACA	FALSE	2	AGCAACTTCACT	5158
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D11	sgRNA	86.80%	GTCCGTTCGACA ATTTCACA	FALSE	2	GTCCGTTCGACA ATTTCACA	2929
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D12	pL42_ pool1	97.30%	GCTGCTTGCGAT ACCAATAG	FALSE	2	AGCAGCCCTAGC	5908
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	D12	sgRNA	89.00%	GCTGCTTGCGAT ACCAATAG	FALSE	2	GCTGCTTGCGAT ACCAATAG	3297
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E01	pool1	97.50%	CAAGGAGGACG GCAACATCC	FALSE	2	GAACTCAGGACA	6341
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E01	sgRNA	90.10%	CAAGGAGGACG GCAACATCC	FALSE	2	CAAGGAGGACGG CAACATCC	3297
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E02	pL42_ pool1	96.60%	CAAGGAGGACG GCAACATCC	FALSE	2	CTATATATGACC	5665
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E02	sgRNA	92.20%	CAAGGAGGACG GCAACATCC	FALSE	2	CAAGGAGGACGG CAACATCC	3177
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E03	pL42_ pool1	96.00%	GTCCGTTCGACA ATTTCACA	FALSE	2	CTCAATTTACAG	5694
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E03	sgRNA	86.90%	GTCCGTTCGACA ATTTCACA	FALSE	2	GTCCGTTCGACA ATTTCACA	2666

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E04	pL42_ pool1	96.20%	GGACGCTAAAC CAACGGTGC	FALSE	2	TCCAGAGCACCT	5711
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E04	sgRNA	88.20%	GGACGCTAAAC CAACGGTGC	FALSE	2	GGACGCTAAACC AACGGTGC	3074
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E05	pL42_ pool1	96.10%	GGACGCTAAAC CAACGGTGC	FALSE	2	AGAGACTTCACA	6920
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E05	sgRNA	88.80%	GGACGCTAAAC CAACGGTGC	FALSE	2	GGACGCTAAACC AACGGTGC	3316
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E06	pL42_ pool1	96.50%	CAAGGAGGACG GCAACATCC	FALSE	2	AGCCACCAGTAT	5948
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E06	sgRNA	90.70%	CAAGGAGGACG GCAACATCC	FALSE	2	CAAGGAGGACGG CAACATCC	3701
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E07	pL42_ pool1	96.90%	CAACATCCTGG GGCACAAGC	FALSE	2	GAACGCGAAAGC	6218
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E07	sgRNA	88.20%	CAACATCCTGG GGCACAAGC	FALSE	2	CAACATCCTGGG GCACAAGC	3216
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E09	pL42_ pool1	97.30%	TGTACTCCAGCT TGTGCCCC	FALSE	2	AGCTAGCCTAGG	6260
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E09	sgRNA	89.40%	TGTACTCCAGCT TGTGCCCC	FALSE	2	TGTACTCCAGCTT GTGCCCC	2857
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E10	pL42_ pool1	95.60%	AGGAGGACGGC AACATCCTG	FALSE	2	AGCGACCTTACA	5526
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E10	sgRNA	90.80%	AGGAGGACGGC AACATCCTG	FALSE	2	AGGAGGACGGCA ACATCCTG	3033
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E11	pL42_ pool1	97.20%	AAGGAGGACGG CAACATCCT	FALSE	2	GAATCCGCTCGC	5387
pLas + pLX_TRC313_ LacZ (1:1000)	20170924	T2	E11	sgRNA	91.20%	AAGGAGGACGG CAACATCCT	FALSE	2	AAGGAGGACGGC AACATCCT	2772
pLas, standard_400	20170924	T2	F01	pL42_ pool1	97.50%	GCCGTGCCGTA GCTATCCGG	FALSE	2	AGATGATAACGG	6077
pLas, standard_400	20170924	T2	F01	sgRNA	88.50%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GCCGTGCCGTAG CTATCCGG	3723
pLas, standard_400	20170924	T2	F02	pL42_ pool1	97.50%	CAAGGAGGACG GCAACATCC	FALSE	2	AGCCACCAGTAT	5535
pLas, standard_400	20170924	T2	F02	sgRNA	91.70%	CAAGGAGGACG GCAACATCC	FALSE	2	CAAGGAGGACGG CAACATCC	3850
pLas, standard_400	20170924	T2	F04	pL42_ pool1	96.80%	GTACAGCTAAG TTAAACTCG	TRUE	2	TCCATCAATACG	5844
pLas, standard_400	20170924	T2	F04	sgRNA	90.30%	CAAGGAGGACG GCAACATCC	TRUE	2	CAAGGAGGACGG CAACATCC	3878

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, standard_400	20170924	T2	F05	pL42_pool1	96.90%	GTCCGTTCGACAATTTCACA	FALSE	2	AGATGGGTTCCG	5399
pLas, standard_400	20170924	T2	F05	sgRNA	86.50%	GTCCGTTCGACAATTTCACA	FALSE	2	GTCCGTTCGACAATTTCACA	3780
pLas, standard_400	20170924	T2	F06	pL42_pool1	96.20%	GCCGTGCCGTAGCTATCCGG	FALSE	2	CTCACTGACACTGCCGTGCCGTAG	6156
pLas, standard_400	20170924	T2	F06	sgRNA	90.90%	GCCGTGCCGTAGCTATCCGG	FALSE	2	CTATCCGG	3688
pLas, standard_400	20170924	T2	F07	pL42_pool1	97.00%	GTCCGTTCGACAATTTCACA	FALSE	2	AGATGGGTTCCG	6019
pLas, standard_400	20170924	T2	F07	sgRNA	88.60%	GTCCGTTCGACAATTTCACA	FALSE	2	GTCCGTTCGACAATTTCACA	3235
pLas, standard_400	20170924	T2	G01	pL42_pool1	46.40%	GTCCGTTCGACAATTTCACA	FALSE	4	AGCAACTTCACT	2689
pLas, standard_400	20170924	T2	G01	pL42_pool1	50.90%	TGTACTCCAGCTTGTGCCCC	TRUE	4	AGCTAGCCTAGG	2953
pLas, standard_400	20170924	T2	G01	sgRNA	40.80%	GTCCGTTCGACAATTTCACA	FALSE	4	GTCCGTTCGACAATTTCACA	1683
pLas, standard_400	20170924	T2	G01	sgRNA	41.40%	CAAGGAGGACGGCAACATCC	TRUE	4	CAAGGAGGACGGCAACATCC	1711
pLas, standard_400	20170924	T2	G02	pL42_pool1	97.00%	GTCCGTTCGACAATTTCACA	FALSE	2	GACAAGTACACT	5757
pLas, standard_400	20170924	T2	G02	sgRNA	87.80%	GTCCGTTCGACAATTTCACA	FALSE	2	GTCCGTTCGACAATTTCACA	3507
pLas, standard_400	20170924	T2	G03	pL42_pool1	96.80%	GTCCGTTCGACAATTTCACA	TRUE	2	AGATGGGTTCCG	5176
pLas, standard_400	20170924	T2	G03	sgRNA	90.90%	AAGGAGGACGGCAACATCCT	TRUE	2	AAGGAGGACGGCAACATCCT	3746
pLas, standard_400	20170924	T2	G04	pL42_pool1	97.00%	CAAGGAGGACGGCAACATCC	TRUE	2	AGCCAGTCAATC	8030
pLas, standard_400	20170924	T2	G04	sgRNA	86.70%	GTCCGTTCGACAATTTCACA	TRUE	2	GTCCGTTCGACAATTTCACA	3434
pLas, standard_400	20170924	T2	G05	pL42_pool1	96.80%	GTCCGTTCGACAATTTCACA	TRUE	2	AGCAACTTCACT	5624
pLas, standard_400	20170924	T2	G05	sgRNA	90.20%	CAACATCCTGGGGCACAAGC	TRUE	2	CAACATCCTGGGGCACAAGC	4140
pLas, standard_400	20170924	T2	G06	pL42_pool1	44.90%	GGACGCTAAACCAACGGTGC	FALSE	4	GACAGGCTACCT	2487
pLas, standard_400	20170924	T2	G06	pL42_pool1	52.20%	AGGAGGACGGCAACATCCTG	FALSE	4	GAATGGACAGCG	2895
pLas, standard_400	20170924	T2	G06	sgRNA	44.80%	GGACGCTAAACCAACGGTGC	FALSE	4	GGACGCTAAACCAACGGTGC	1766
pLas, standard_400	20170924	T2	G06	sgRNA	46.10%	AGGAGGACGGCAACATCCTG	FALSE	4	AGGAGGACGGCAACATCCTG	1817
pLas, standard_400	20170924	T2	G07	pL42_pool1	97.30%	TGTACTCCAGCTTGTGCCCC	TRUE	2	AGCGCCGTCATT	5570
pLas, standard_400	20170924	T2	G07	sgRNA	89.90%	AAGGAGGACGGCAACATCCT	TRUE	2	AAGGAGGACGGCAACATCCT	3693

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, standard_400	20170924	T2	G08	pL42_pool1	96.60%	TGTACTCCAGCTTGTGCCCC	TRUE	2	AGCGCCGTCATT	5248
pLas, standard_400	20170924	T2	G08	sgRNA	91.60%	AAGGAGGACGGCAACATCCT	TRUE	2	AAGGAGGACGGCAACATCCT	3721
pLas, standard_400	20170924	T2	G09	pL42_pool1	47.40%	AAGGAGGACGGCAACATCCT	TRUE	4	GAATGAACCACG	2772
pLas, standard_400	20170924	T2	G09	pL42_pool1	49.50%	CAACATCCTGGGGCACAAGC	FALSE	4	GAACGCGAAAGC	2895
pLas, standard_400	20170924	T2	G09	sgRNA	43.30%	CAACATCCTGGGGCACAAGC	FALSE	4	CAACATCCTGGGGCACAAGC	1706
pLas, standard_400	20170924	T2	G09	sgRNA	44.60%	GCCGTGCCGTAGCTATCCGG	TRUE	4	GCCGTGCCGTAGCTATCCGG	1760
pLas, standard_400	20170924	T2	G10	pL42_pool1	96.50%	CAAGGAGGACGGCAACATCC	FALSE	2	AGCCAGTCAATC	6342
pLas, standard_400	20170924	T2	G10	sgRNA	91.60%	CAAGGAGGACGGCAACATCC	FALSE	2	CAAGGAGGACGGCAACATCC	3814
pLas, standard_400	20170924	T2	G11	pL42_pool1	97.20%	AGGAGGACGGCAACATCCTG	FALSE	2	AGCGGTATAACT	5601
pLas, standard_400	20170924	T2	G11	sgRNA	90.60%	AGGAGGACGGCAACATCCTG	FALSE	2	AGGAGGACGGCAACATCCTG	3625
pLas, standard_400	20170924	T2	G12	pL42_pool1	97.00%	GTACAGCTAAGTTAAACTCG	FALSE	2	TCCATCAATACG	6172
pLas, standard_400	20170924	T2	G12	sgRNA	90.50%	GTACAGCTAAGTTAAACTCG	FALSE	2	GTACAGCTAAGTTAAACTCG	4107
pLas, standard_400	20170924	T2	H02	pL42_pool1	96.60%	CAACATCCTGGGGCACAAGC	FALSE	2	AGCTTTCTGACT	6904
pLas, standard_400	20170924	T2	H02	sgRNA	89.70%	CAACATCCTGGGGCACAAGC	FALSE	2	CAACATCCTGGGGCACAAGC	4167
pLas, standard_400	20170924	T2	H04	pL42_pool1	97.10%	CAACATCCTGGGGCACAAGC	FALSE	2	GAACGCGAAAGC	6597
pLas, standard_400	20170924	T2	H04	sgRNA	88.90%	CAACATCCTGGGGCACAAGC	FALSE	2	CAACATCCTGGGGCACAAGC	4441
pLas, standard_400	20170924	T2	H05	pL42_pool1	96.90%	AGGAGGACGGCAACATCCTG	FALSE	2	AGCGGTATAACT	5605
pLas, standard_400	20170924	T2	H05	sgRNA	91.70%	AGGAGGACGGCAACATCCTG	FALSE	2	AGGAGGACGGCAACATCCTG	5041
pLas, standard_400	20170924	T2	H06	pL42_pool1	97.20%	GCTGCTTGCGATACCAATAG	TRUE	2	AGAGCTGCTACG	6005
pLas, standard_400	20170924	T2	H06	sgRNA	90.60%	AAGGAGGACGGCAACATCCT	TRUE	2	AAGGAGGACGGCAACATCCT	4160
pLas, standard_400	20170924	T2	H07	pL42_pool1	97.00%	CAAGGAGGACGGCAACATCC	TRUE	2	AGCCAGTCAATC	6670
pLas, standard_400	20170924	T2	H07	sgRNA	91.40%	TGTACTCCAGCTTGTGCCCC	TRUE	2	TGTACTCCAGCTTGTGCCCC	3692
pLas, standard_400	20170924	T2	H08	pL42_pool1	47.30%	AAGGAGGACGGCAACATCCT	TRUE	4	GAATGAACCACG	2843
pLas, standard_400	20170924	T2	H08	pL42_pool1	49.30%	CAACATCCTGGGGCACAAGC	FALSE	4	GAACGCGAAAGC	2960

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas, standard_400	20170924	T2	H08	sgRNA	42.30%	CAACATCCTGG GGCACAAGC	FALSE	4	CAACATCCTGGG GCACAAGC	1458
pLas, standard_400	20170924	T2	H08	sgRNA	46.70%	GCCGTGCCGTA GCTATCCGG	TRUE	4	GCCGTGCCGTAG CTATCCGG	1607
pLas, standard_400	20170924	T2	H09	pL42_ pool1	97.10%	AGGAGGACGGC AACATCCTG	FALSE	2	AGCGGTATAACT	6040
pLas, standard_400	20170924	T2	H09	sgRNA	91.30%	AGGAGGACGGC AACATCCTG	FALSE	2	AGGAGGACGGCA ACATCCTG	4335
pLas, standard_400	20170924	T2	H10	pL42_ pool1	96.40%	GTACAGCTAAG TTAAACTCG	FALSE	2	TCCATCAATACG	6012
pLas, standard_400	20170924	T2	H10	sgRNA	91.80%	GTACAGCTAAG TTAAACTCG	FALSE	2	GTACAGCTAAGT TAAACTCG	4678
pLas, standard_400	20170924	T2	H11	pL42_ pool1	97.20%	GGACGCTAAAC CAACGGTGC	FALSE	2	GACAGGCTACCT	2525
pLas, standard_400	20170924	T2	H11	sgRNA	90.50%	GGACGCTAAAC CAACGGTGC	FALSE	2	GGACGCTAAACC AACGGTGC	4621
pLas, standard_400	20170924	T2	H12	pL42_ pool1	96.60%	GGACGCTAAAC CAACGGTGC	FALSE	2	AGAGACTTCACA	6601
pLas, standard_400	20170924	T2	H12	sgRNA	90.60%	GGACGCTAAAC CAACGGTGC	FALSE	2	GGACGCTAAACC AACGGTGC	5162
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G01	pL42_ pool1	96.40%	AGGAGGACGGC AACATCCTG	FALSE	2	GATATCGTGACC	5913
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G01	sgRNA	89.90%	AGGAGGACGGC AACATCCTG	FALSE	2	AGGAGGACGGCA ACATCCTG	1376
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G02	pL42_ pool1	97.00%	CAACATCCTGG GGCACAAGC	FALSE	2	CAACGCCCAAGG	5458
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G02	sgRNA	91.20%	CAACATCCTGG GGCACAAGC	FALSE	2	CAACATCCTGGG GCACAAGC	4271
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G03	pL42_ pool1	46.10%	AAGGAGGACGG CAACATCCT	FALSE	4	TAGGAAGTTAGG	2373
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G03	pL42_ pool1	50.90%	TGTACTCCAGCT TGTGCCCC	FALSE	4	TTCGCCGAAAGC	2622
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G03	sgRNA	43.60%	TGTACTCCAGCT TGTGCCCC	FALSE	4	TGTACTCCAGCTT GTGCCCC	2285
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G03	sgRNA	47.10%	AAGGAGGACGG CAACATCCT	FALSE	4	AAGGAGGACGGC AACATCCT	2470
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G04	pL42_ pool1	97.80%	CAAGGAGGACG GCAACATCC	FALSE	2	AGGCTATTAATG	5677
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G04	sgRNA	90.80%	CAAGGAGGACG GCAACATCC	FALSE	2	CAAGGAGGACGG CAACATCC	4803
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G05	pL42_ pool1	97.20%	GCTGCTTGCGAT ACCAATAG	FALSE	2	ATCAGTGGCAGC	5807

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G05	sgRNA	89.20%	GCTGCTTGCGAT ACCAATAG	FALSE	2	GCTGCTTGCGAT ACCAATAG	4589
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G06	pL42_ pool1	96.90%	CAACATCCTGG GGCACAAGC	TRUE	2	TGTTAATGCAGG	7332
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G06	sgRNA	90.50%	GGACGCTAAAC CAACGGTGC	TRUE	2	GGACGCTAAACC AACGGTGC	4568
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G07	pL42_ pool1	96.80%	CAACATCCTGG GGCACAAGC	FALSE	2	TCTATTTGACGG	5698
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G07	sgRNA	89.70%	CAACATCCTGG GGCACAAGC	FALSE	2	CAACATCCTGGG GCACAAGC	3855
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G08	pL42_ pool1	95.60%	CAACATCCTGG GGCACAAGC	FALSE	2	CCGTAACGAACA	5272
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G08	sgRNA	89.80%	CAACATCCTGG GGCACAAGC	FALSE	2	CAACATCCTGGG GCACAAGC	3373
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G09	pL42_ pool1	97.20%	GGACGCTAAAC CAACGGTGC	FALSE	2	AGTTTGCAGCCA	5286
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G09	sgRNA	90.80%	GGACGCTAAAC CAACGGTGC	FALSE	2	GGACGCTAAACC AACGGTGC	3837
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G10	pL42_ pool1	95.30%	GGACGCTAAAC CAACGGTGC	FALSE	2	TCGAAATGACAC	5229
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G10	sgRNA	90.70%	GGACGCTAAAC CAACGGTGC	FALSE	2	GGACGCTAAACC AACGGTGC	4325
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G11	pL42_ pool1	96.80%	AGGAGGACGGC AACATCCTG	FALSE	2	TCAGTGAATACG	4733
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G11	sgRNA	90.90%	AGGAGGACGGC AACATCCTG	FALSE	2	AGGAGGACGGCA ACATCCTG	3508
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G12	pL42_ pool1	96.50%	GCCGTGCCGTA GCTATCCGG	FALSE	2	CGCAAAAGGATT	5455
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	G12	sgRNA	89.20%	GCCGTGCCGTA GCTATCCGG	FALSE	2	GCCGTGCCGTAG CTATCCGG	2269
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	H01	pL42_ pool1	97.10%	GCTGCTTGCGAT ACCAATAG	FALSE	2	ATCAGTGGCAGC	5905
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	H01	sgRNA	88.90%	GCTGCTTGCGAT ACCAATAG	FALSE	2	GCTGCTTGCGAT ACCAATAG	1305
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	H02	pL42_ pool1	47.60%	GCTGCTTGCGAT ACCAATAG	TRUE	4	AACGATGGGACT	2653

TABLE 2-continued

condition	date	plate	well	pattern	fraction	pred sgRNA	solitary	matches per sample	match	count
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	H02	pL42_ pool1	49.00%	AGGAGGACGGC AACATCCTG	FALSE	4	TCATTCAGAGCG	2735
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	H02	sgRNA	44.80%	AAGGAGGACGG CAACATCCT	TRUE	4	AAGGAGGACGGC AACATCCT	1222
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	H02	sgRNA	44.90%	AGGAGGACGGC AACATCCTG	FALSE	4	AGGAGGACGGCA ACATCCTG	1224
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	H03	pL42_ pool1	95.50%	CAACATCCTGG GGCACAAGC	FALSE	2	TCTTCACAACCG	5074
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	H03	sgRNA	90.00%	CAACATCCTGG GGCACAAGC	FALSE	2	CAACATCCTGGG GCACAAGC	4002
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	H04	pL42_ pool1	48.50%	GTACAGCTAAG TTAAACTCG	TRUE	3	CGTGTGATGATA	3104
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	H04	pL42_ pool1	48.60%	AAGGAGGACGG CAACATCCT	FALSE	3	ATTGCTATTCGG	3108
pLas + pLX_TRC313_ LacZ (1:100)	20170924	T1	H04	sgRNA	90.60%	AAGGAGGACGG CAACATCCT	FALSE	3	AAGGAGGACGGC AACATCCT	3883

SEQ ID NO: 1574

LOCUS pLas 7963 bp ds-DNA circular

01-FEB-2018

DEFINITION.

FEATURES

Location/Qualifiers		
feature	3591..4166	/label = "WPRE"
feature	292..336	/label = "HIV-1_psi_pack"
feature	1..181	/label = "HIV-1_5_LTR"
promoter	1854..3111	/label = "EF-1a"
misc_feature	1756..1841	/label = "scaffold_Dang_2015"
misc_feature	3118..3492	/label = "ZeoR"
regulatory	846..1079	/ label = "RRE"
primer	1657..1676	/label = "LKO1_5_primer"
feature	4302..4482	/label = "HIV-1_5_LTR"
feature	4249..4301	/label = "delta_U3"
variation	2242..2242	/label = "C in all sequences"
feature	4232..4253	/label = "U3PPT"
misc_feature	3516..3527	/label = "barcode"

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misc_feature 1736..1755 /label = "sgRNA"

feature 4232..4247 /label = "cPPT"

misc_feature 241..280 /label = "DIS_1"

promoter 1495..1734 /label = "hU6_promoter"

ORIGIN

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   121  tgtgactctg gtaactagag atccctcaga ccctttttagt cagtgtggaa aatctctagc
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2281 ggaagtgggt gggagagttc gaggccttgc gcttaaggag ccccttcgcc tcgtgcttga

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2581 cggggcctgc gagcgcggcc accgagaatc ggacgggggt agtctcaagc tggccggcct

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3241 GTCCGGGACG ACGTGACCCT GTTCATCAGC GCGGTCCAGG ACCAGGTGGT GCCGGACAAC

3301 ACCCTGGCCT GGGTGTGGGT GCGCGGCCTG GACGAGCTGT ACGCCGAGTG GTCGGAGGTC

3361 GTGTCCACGA ACTTCCGGGA CGCCTCCGGG CCGGCCATGA CCGAGATCGG CGAGCAGCCG

3421 TGGGGGCGGG AGTTCGCCCT GCGCGACCCG GCCGGCAACT GCGTGCACTT CGTGGCCGAG

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3661 tgtggatacg ctgctttaat gcctttgtat catgctattg cttcccgtat ggctttcatt

3721 ttctcctcct tgtataaatc ctggttgctg tctctttatg aggagttgtg gcccgttgtc

3781 aggcaacgtg gcgtggtgtg cactgtgttt gctgacgcaa cccccactgg ttggggcatt

3841 gccaccacct gtcagctcct ttccgggact ttcgctttcc ccctccctat tgccacggcg

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4021 acctggattc tgcgcgggac gtccttctgc tacgtccctt cggccctcaa tccagcggac

4081 cttccttccc gcggcctgct gccggctctg cggcctcttc cgcgtcttcg ccttcgccct

4141 cagacgagtc ggatctccct ttgggccgcc tccccgcgtc gactttaaga ccaatgactt

4201 acaaggcagc tgtagatctt agccactttt taaaagaaaa ggggggactg gaagggctaa

4261 ttcactccca acgaagacaa gatctgcttt ttgcttgtac tgggtctctc tggttagacc

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4441 gatccctcag acccttttag tcagtgtgga aaatctctag cagtacgtat agtagttcat

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4801 ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggctttttg gaggcctagg

4861 gacgtaccca attcgcccta tagtgagtcg tattacgcgc gctcactggc cgtcgtttta

4921 caacgtcgtg actgggaaaa ccctggcgtt acccaactta atcgccttgc agcacatccc

4981 cctttcgcca gctggcgtaa tagcgaagag gcccgcaccg atcgcccttc ccaacagttg

5041 cgcagcctga atggcgaatg ggacgcgccc tgtagcggcg cattaagcgc ggcgggtgtg

5101 gtggttacgc gcagcgtgac cgctacactt gccagcgccc tagcgcccgc tcctttcgct

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6001 gagaattatg cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga

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6121 ctcgccttga tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca

6181 ccacgatgcc tgtagcaatg gcaacaacgt tgcgcaaact attaactggc gaactactta

6241 ctctagcttc ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac

6301 ttctgcgctc ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc

6361 gtgggtctcg cggtatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag

6421 ttatctacac gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga

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6721  caaaaaaacc accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt
6781  ttccgaaggt aactggcttc agcagagcgc agataccaaa tactgttctt ctagtgtagc
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6901  tcctgttacc agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa
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7261  tatggaaaaa cgccagcaac gcggcctttt tacggttcct ggccttttgc tggccttttg
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7441  aagcggaaga gcgcccaata cgcaaaccgc ctctccccgc gcgttggccg attcattaat
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7861  cttattagga aggcaacaga cgggtctgac atggattgga cgaaccactg aattgccgca
7921  ttgcagagat attgtattta agtgcctagc tcgatacata aac
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Example 2

[0236] An example method of constructing libraries of genetic elements. Provide A provides an example method of libraries comprising two engineered associations. The lentiviral vector shown under "mRNA contains barcode" (panel A) is an example of a vector with two elements (sgRNA and barcode) that will normally undergo swapping unless the co-packaging protocol is used. The associations did not undergo swapping because the libraries were constructed using the co-packaging methods described herein. The scatter plot (panel B) shows the accuracy of mapping over 1000 barcodes to two categories. The mapped barcodes did not have recombination, indicating the accuracy was improved by the co-packaging protocol disclosed herein.

[0237] Various modifications and variations of the described methods, pharmaceutical compositions, and kits of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific embodiments, it will be understood that it is capable of further modifications and that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention that are obvious to those skilled in the art are intended to be within the scope of the invention. This application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the present disclosure come within known customary practice within the art to which the invention pertains and may be applied to the essential features herein before set forth.

1-37. (canceled)

38. A non-naturally occurring engineered lentiviral or retroviral system comprising:

a) a plurality of payload vectors, each encoding a lentiviral or retroviral genome comprising at least one genetic perturbation and a barcode sequence that identifies each genetic perturbation, wherein each genome sequence is modified to reduce dimerization of the genomes; and

b) one or more packaging vectors encoding lentiviral or retroviral packaging proteins for generating packaging cells or a packaging cell line encoding the lentiviral or retroviral packaging proteins,

whereby transfection of the plurality of payload vectors into packaging cells produces a viral expression library comprising viral particles biased to a single genome per virion.

39. The engineered system of claim **38**, wherein the reduced dimerization comprises deletion, introduction, and/or relocation of a dimer initiation site/dimer linkage sequence (DIS/DLS) region in the genome sequence.

40. The engineered system of claim **38**, wherein the reduced dimerization comprises reduced hairpin formation.

41. The engineered system of claim **40**, wherein stem-loop 1 (SL1) in the DIS/DLS is modified or knocked out.

42. The engineered system of any of claim **38**, wherein the genome sequence is modified to reduce or knock out U5:AUG pairing.

43. A non-naturally occurring engineered lentiviral or retroviral system comprising:

a) a plurality of payload vectors, each encoding a lentiviral or retroviral genome comprising at least one genetic perturbation and a barcode sequence that identifies each genetic perturbation; and

b) one or more packaging vectors encoding lentiviral or retroviral packaging proteins for generating packaging cells or a packaging cell line encoding the lentiviral or retroviral packaging proteins, wherein the packaging proteins comprise one or more modified packaging proteins capable of reducing recombination, template switching, and/or multiple integration of the lentiviral or retroviral genomes in transduced viral particles, optionally, further comprising an inhibitor of template switching,

whereby transfection of the plurality of payload vectors in the packaging cells produces a viral expression library comprising viral particles, such that target cells transduced with the viral expression library have reduced recombination, template switching, and/or multiple integration of the lentiviral or retroviral genomes.

44. The engineered system of claim **43**, wherein a packaging protein involved in dimerization is modified, knocked down, or knocked out.

45. The engineered system of claim **44**, wherein a nucleocapsid (NC) protein is modified, knocked down, or knocked out.

46. The engineered system of claim **45**, wherein the nucleocapsid (NC) protein is modified by a mutation in the zinc-finger region of the NC.

47. The engineered system of claim **43**, wherein template-switching activity of the reverse transcriptase is knocked down or knocked out.

48. The engineered system of claim **43**, wherein gag polyprotein cleavage is inhibited by a mutation in a protease.

49. A non-naturally occurring engineered lentiviral or retroviral system comprising:

a) a plurality of payload vectors, each encoding a lentiviral or retroviral genome comprising at least one genetic perturbation and a barcode sequence that identifies each genetic perturbation;

b) a carrier vector encoding for a polynucleotide designed to hybridize with all or part of the 5' UTR of the lentiviral or retroviral genome; and

c) one or more vectors encoding lentiviral or retroviral packaging proteins for obtaining packaging cells or a packaging cell line encoding lentiviral or retroviral packaging proteins,

whereby co-transfection of the plurality of payload vectors and the carrier vector into packaging cells produces a viral expression library comprising viral particles biased to a single genome per virion.

50. The engineered system of claim **49**, wherein the polynucleotide is designed to hybridize with the U5-PBS complex.

51. The engineered system of claim **49**, wherein the polynucleotide is designed to hybridize with the dimer initiation site (DIS).

52. A non-naturally occurring engineered lentiviral or retroviral system comprising:

a) a plurality of payload vectors, each encoding a lentiviral or retroviral genome comprising at least one genetic perturbation and a barcode sequence that identifies each genetic perturbation;

b) a plurality of carrier vectors, wherein the plurality of carrier vectors:

i. encode for a non-recombinogenic lentiviral or retroviral genome capable of being packaged into a viral particle as a dimer with a lentiviral or retroviral genome encoded for by the payload vector and not capable of recombination with the lentiviral or retroviral genome encoded for by the payload vector; or

ii. does not encode for a lentiviral or retroviral genome and is not capable of being packaged into a viral particle; and

c) one or more vectors encoding lentiviral or retroviral packaging proteins for obtaining packaging cells or a packaging cell line encoding lentiviral or retroviral packaging proteins,

whereby co-transfection of the plurality of payload vectors and the carrier vectors into packaging cells produces a viral expression library comprising viral particles, such that target cells transduced with the viral expression library have reduced recombination, template switching, and/or multiple integration of the lentiviral or retroviral genomes as compared to packaging cells transfected with only the plurality of payload vectors.

53. The engineered system of claim **52**, wherein the non-recombinogenic lentiviral or retroviral genome is a non-integrating lentivirus genome.

54. The engineered system of claim **52**, wherein the ratio of carrier vector to payload vector is greater than 5:1.

55. The engineered system of any of claim **38**, further comprising an inhibitor of template switching.

56. The engineered system of any of claim **38**, wherein the genetic perturbation comprises an over expressed gene, RNAi based system, a zinc finger nuclease, a transcription activator-like effector nuclease (TALEN), a meganuclease, a CRISPR-Cas system, or a component thereof.

57. The engineered system of claim **56**, wherein the genetic perturbation comprises a CRISPR-Cas system or a component thereof.

58. The engineered system of claim **57**, wherein the CRISPR-Cas system is a CRISPR-Cas9 system.

59. The engineered system of claim **58**, wherein the genetic perturbation is one or more guide sequences.

60. A method of screening cells for at least one genetic perturbation comprising:

providing a population of cells;

introducing a viral expression library obtained using the system of claim **38** to the population of cells, such that each cell receives a lentiviral or retroviral genome encoded for by a payload vector;

detecting genomic, genetic, proteomic, epigenetic and/or phenotypic differences in single cells receiving a lentiviral or retroviral genome; and

identifying the genetic perturbation in each cell based on the barcode sequence.

61. A viral expression library comprising viral particles obtained using the system of claim **38**.

62. A packaging cell line for producing lentiviral or retroviral viral particles comprising:

a) polynucleotide sequences encoding lentiviral or retroviral packaging proteins, wherein the packaging proteins comprise one or more modified packaging proteins capable of reducing recombination, template switching, and/or multiple integration of the lentiviral or retroviral genomes in transduced viral particles, optionally, further comprising an inhibitor of template switching; or

b) polynucleotide sequences encoding lentiviral or retroviral packaging proteins, wherein the packaging proteins comprise an inhibitor of template switching.

63. The packaging cell line of claim **62**, wherein a packaging protein involved in dimerization is modified, knocked down, or knocked out.

64. The packaging cell line of claim **63**, wherein a nucleocapsid (NC) protein is modified, knocked down, or knocked out.

65. The packaging cell line of claim **64**, wherein the nucleocapsid (NC) protein is modified by a mutation in the zinc-finger region of the NC.

66. The packaging cell line of claim **62**, wherein template-switching activity of the reverse transcriptase is knocked down or knocked out.

67. The packaging cell line of claim **62**, wherein gag polyprotein cleavage is inhibited by a mutation in a protease.

68. A method of reducing intermolecular recombination between lentiviral genomes in a transduced library comprising packaging viral particles for transduction using the system of claim **38**.

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