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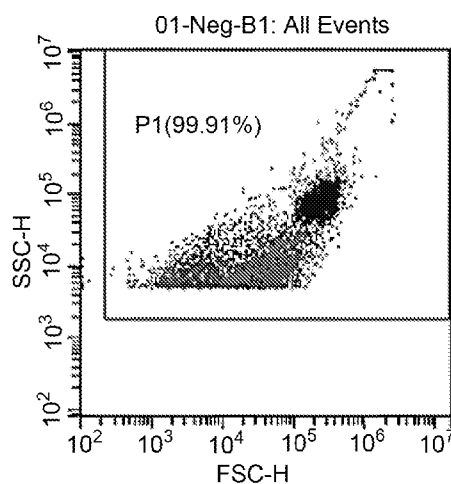


Figure 1A

(57) Abstract: The present disclosure provides for non-viral compositions and methods for delivering nucleic acids into eukaryotic cells (e.g., stem cells) with high efficiency and low genotoxicity.

GENE TRANSFER SYSTEMS FOR STEM CELL ENGINEERING

Cross-Reference to Related Application

The present application claims priority to U.S. Provisional Patent Application No. 62/534,300 filed on July 19, 2018, which is incorporated herein by reference in its entirety.

Sequence Listing

The instant application contains a Sequence Listing which has been filed electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on July 11, 2018, is named 10491_006017-WO0_SL.txt and is 25,173 bytes in size.

Field of the Invention

The present invention relates to compositions and methods for delivering a nucleic acid such as a gene into mammalian cells.

Background of the Invention

Stem cells have the ability to self-renew and transform into various cell types in an organism. Due to this unique characteristic, they have been used as a source of donor cells to replace damaged organs. In addition, current evidence indicates that systemically administered mesenchymal stem cells (MSCs) can migrate to primary and metastatic solid tumors and deliver therapeutic molecules to tumor foci ^{1, 2, 3, 4}. It is envisioned that stem cell-mediated gene delivery could emerge as a strategy to improve the efficacy and minimize the toxicity of various cancer gene therapy approaches ^{4, 5}. For such purposes, MSCs are first harvested from donors and then genetically modified *ex vivo* to express a variety of bioactive agents. For example, MSCs can be engineered to express prodrug converting enzymes or antiproliferative, pro-apoptotic, anti-angiogenic agents ^{6, 7}. The vector that is used for stem cell transfection needs to be highly efficient because the methods to rapidly produce unlimited quantities of undifferentiated stem cells have not yet been perfected.

Moreover, stem cells in cell culture change/mutate over time (usually after eight to ten passages), thereby providing a limited window of opportunity for processing.

Vectors that are currently used for stem cell engineering can be categorized into viral (adenovirus, lentivirus, AAV) and non-viral (polymer and lipid based). Adenoviral (Ad) vectors can be used to mediate transient and high-level transgene expression. However, for adenoviral vectors to achieve transduction efficiency beyond 50% in MSCs, the multiplicity of infection (MOI) needs to be increased to >5000. Unfortunately, presence of such large amounts of viral proteins in transfected cells could elicit immune response after implantation into the human body, resulting in rapid clearance of transfected MSCs ⁸. Integrating vectors such as lentivirus and AAVs can transfect stem cells efficiently but are marred by the potential for insertional mutagenesis ⁹. Consequently, the transfected stem cells require an extensive screening process to ensure safety, which in turn, raises the concern of cost-effectiveness in clinical trials. Electroporation is another method for MSC transfection, but it leads to excessive cell death ¹⁰.

Commercially available non-viral vectors based on polymers and lipids bear a positive surface charge and have the ability to condense plasmid DNA (pDNA) into nanosize particles suitable for cellular uptake. While such nanoparticles may not show significant toxicity in terms of impact on metabolic activity, as evaluated by MTT or similar assays, recent studies show that these nanoparticles may cause genotoxicity ^{11, 12}. This could become notably problematic when dealing with stem cells because such vectors could theoretically turn a normal mesenchymal stem cell into a cancer initiating cell.

As high levels of safety are expected, there is a need for efficient and non-genotoxic systems for engineering stem cells.

Brief Description of the Drawings

Figures 1A-1G show flow cytometry plots for quantification of micronuclei formation in transfected stem cells.

Figures 2A-2F show fusion polypeptide schematics and characterization of nanoparticles in terms of size, charge and shape. Figure 2A: Schematics of the fusion

polypeptide composed of a fusogenic peptide GALA (G) to disrupt endosomal membranes, a DNA condensing motif with inherent nuclear localization signal (H4) and a HER2 targeting peptide (TP). Figure 2B: By removing the HER2 targeting peptide and replacing it with VEGFR targeting or cell penetrating peptides, the fusion polypeptide is tailor-made for carrying genes into MSCs. The 3-D structure of each motif was simulated independently by I-TASSER server for protein structure and function prediction ³⁷. Figure 2C: The size of the DBV/pEGFP nanocomplexes as determined by dynamic light scattering. Figure 2D: The surface charge of the DBV/pEGFP nanocomplexes as determined by laser doppler velocimetry. Figure 2E: The shape of the DBV/pEGFP nanocomplexes captured by TEM. The scale bar is 100nm (Magnification: 75000x). Figure 2F: The surface charge analysis of the commercial vectors in complex with pEGFP.

Figure 3A-3C show characterization of adipose-derived stem cells (ADSCs) in terms of cell cycle and expression of VEGFR-1. Figure 3A: Flow cytometry histograms showing the percentage of cells in each phase at different time points (i.e., 16-28 hours). Figure 3B: Bar chart summarizing the percentage of cell population in each cell cycle phase at different time points. Since the percentages of cells in Sub G1 phase is very low, they are not observable in the bar chart. Figure 3C: Flow cytometry histogram/dotplots showing the overexpression of VEGFR-1 on the surface of ADSCs, A431 cells and in comparison.

Figures 4A-4G are bar graphs showing evaluation of the transfection efficiency and impact on cell proliferation rate of DBVs and commercial vectors. Figures 4A-C: Bar charts that quantitatively demonstrate the percentage of transfected cells using DBVs and commercial non-viral and viral vectors. The arrows point at the most efficient vectors. Figures 4D-F: Bar charts that demonstrate the impact of DBVs and commercial vectors on the proliferation rate of ADSCs. The arrows highlight the vectors which had high efficiencies (>25%) with acceptable impacts on cell proliferation rate. Figure 4G: LDH release assay demonstrating the impact of vectors on cell membrane integrity.

Figures 5A-5B: Figure 5A: Evaluation of the impact of the gene delivery systems on the formation of micronuclei in transfected ADSCs. The percentage of

micronuclei in untransfected cells is normalized to a one-fold increase and is considered as the negative control. Figure 5B: The PCR microarray analysis of the dysregulated genes in cells transfected with H4G (0.3 and 0.4 μ g pEGFP), Vanta-H4G (0.4 μ g pEGFP) and Ad-GFP (MOI: 5K and 50K). Only the upregulated (ur) and downregulated (dr) genes are mentioned in each panel.

Figures 6A-6B: ADSC differentiation into adipocyte. Figure 6A: Fluorescent microscopy images of the differentiated ADSCs. Figure 6B: Bar chart showing the percentages of differentiated cells in each treated and untreated group using flow cytometry.

Figure 7: SDS-PAGE analysis of the purified designer biomimetic vectors (DBVs). Lanes 1 to 5: H4G (19.75 kDa), Pep1-H4G (22.58 kDa), MPG-H4G (22.54 kDa), Vago-H4G (22.33 kDa), Vanta-H4G (22.45 kDa), respectively.

Figures 8A and 8B show fluorescent microscopy images of the transfected cells with commercial vectors. Figure 8A: Transfected ADSCs by commercial non-viral vectors using different amounts of pEGFP. Figure 8B: Transfected ADSCs by Ad-GFP at different MOIs ranging from 100 to 50,000.

Figure 9 shows fluorescent microscopy images of the transfected cells with DBVs using different amounts of pEGFP.

Figures 10A-10B show flow cytometry histogram (Figure 10A) and fluorescent microscope image (Figure 10B) of HEK293 cells transfected with H4G/pEGFP nanocomplexes. The percentage of transfected cells is determined by flow cytometry (mean $\pm$ s.d., n=3).

Figures 11A-11C show the transfection efficiency of ADSC cells (VEGFR-1 positive) and U87 (VEGFR-1 negative) cells transfected with Vanta-H4G. Figure 11A: Flow cytometry histogram of transfected ADSCs (n=3). Figure 11B: Flow cytometry histogram of transfected U87 cells (n=3). Figure 11C: Bar chart showing the percentage of transfected cells in each cell line as determined by flow cytometry.

Figures 12A-12B show flow cytometry histogram (Figure 12A) and fluorescent microscope image (Figure 12B) of SKOV-3 cells transfected with Pepl-H4G carrying 0.5 μ g of pEGFP. The percentage of transfected cells is determined by flow cytometry.

Figure 13 shows light microscopy images of the transfected cells with commercial vectors carrying different amounts of pEGFP (μ g) showing different levels of toxicities.

Figure 14 shows light microscopy images of the transfected cells with DBVs carrying different amounts of pEGFP (μ g) showing different levels of toxicities.

Figure 15 shows a bar chart that quantitatively demonstrates the percentage of transfected cells using Vanta-H4G. Transfection of ADSCs, bone marrow-derived stem cells (BMSCs) and neural stem cells (NSCs) by using Vanta-H4G with 0.4 μ g of pEGFP. The results show that Vanta-H4G can transfect all three cell lines with high efficiency. The data are presented as mean $\pm$ s.d. (n=3).

Figures 16A-16B show the transfection efficiency and cell viability of ADSC cells transfected with 100 ng pEGFP using Lipofectamine 3000. Figure 16A: Bar chart showing the percentage of transfected cells as determined by flow cytometry. Figure 16B: Bar chart showing the percentage of viable cells as determined by flow cytometry. The data are presented as mean $\pm$ s.d. (n=3).

DBV: designer biomimetic vector. As used herein, DBVs are embodiments of the present systems.

Summary

The present disclosure provides for a fusion polypeptide, comprising (or consisting essentially of, or consisting of): (i) a cell surface receptor-binding peptide; (ii) a nucleic acid-binding polypeptide; and (iii) an endosomolytic peptide.

The cell surface receptor-binding peptide may be a vascular endothelial growth factor receptor (VEGFR)-binding peptide, an insulin-like growth factor receptor (IGFR)-binding peptide, a fibroblast growth factor receptor (FGFR)-binding peptide, an epidermal growth factor receptor (EGFR)-binding peptide, a platelet-derived growth factor receptor (PDGFR)-binding peptide, or an integrin-binding peptide.

In certain embodiments, the fusion polypeptide comprises (or consists essentially of, or consists of) an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90% identical to the amino acid sequence set forth in SEQ ID NO: 10 or SEQ ID NO: 11.

In certain embodiments, the fusion polypeptide comprises (or consists essentially of, or consists of) an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, or SEQ ID NO: 26.

In certain embodiments, the fusion polypeptide comprises (or consists essentially of, or consists of) an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 7.

In certain embodiments, the cell surface receptor-binding peptide is located at the N-terminus of the fusion polypeptide. In certain embodiments, the endosomolytic peptide is located at the C-terminus of the fusion polypeptide.

The present disclosure provides for a fusion polypeptide, comprising (or consisting essentially of, or consisting of): (i) a cell-penetrating peptide; (ii) a nucleic acid-binding polypeptide; and (iii) an endosomolytic peptide.

In certain embodiments, the cell-penetrating peptide is Pep1. In certain embodiments, the cell-penetrating peptide is MPG.

In certain embodiments, the cell-penetrating peptide comprises (or consists essentially of, or consists of) an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90% identical to the amino acid sequence set forth in SEQ ID NO: 3.

In certain embodiments, the cell-penetrating peptide comprises (or consists essentially of, or consists of) an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90% identical to the amino acid sequence set forth in SEQ ID NO: 4.

In certain embodiments, the cell-penetrating peptide is located at the N-terminus of the fusion polypeptide. In certain embodiments, the endosomolytic peptide is located at the C-terminus of the fusion polypeptide.

In certain embodiments, the fusion polypeptide comprises (or consists essentially of, or consists of) an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90% identical to the amino acid sequence set forth in SEQ ID NO: 8 or SEQ ID NO: 9.

In certain embodiments, the VEGFR-binding peptide is an antagonist of VEGFR. In certain embodiments, the VEGFR-binding peptide is an agonist of VEGFR.

In certain embodiments, the VEGFR-binding peptide comprises (or consists essentially of, or consists of) an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90% identical to the amino acid sequence set forth in SEQ ID NO: 1.

In certain embodiments, the VEGFR-binding peptide comprises (or consists essentially of, or consists of) an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90% identical to the amino acid sequence set forth in SEQ ID NO: 2.

In certain embodiments, the nucleic acid-binding polypeptide comprises repeats of a histone, a histone variant, or a fragment thereof. In certain embodiments, the nucleic acid-binding polypeptide comprises repeats of a fragment of histone H2A. In certain embodiments, the nucleic acid-binding polypeptide comprises 1 to 10 repeats of a N-terminal fragment of histone H2A, and wherein the fragment has 15-50 amino acid residues in length. In one embodiment, the nucleic acid-binding polypeptide comprises 4 repeats of a N-terminal fragment of histone H2A, and wherein the fragment has about 37 amino acid residues in length. In one embodiment, the nucleic acid-binding polypeptide comprises a nuclear localization sequence.

In certain embodiments, the nucleic acid-binding polypeptide comprises (or consists essentially of, or consists of) an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90% identical to the amino acid sequence set forth in SEQ ID NO: 5.

In certain embodiments, the endosomolytic peptide is GALA, INF-7, KALA, RALA, or H5WYG.

In certain embodiments, the endosomolytic peptide comprises (or consists essentially of, or consists of) an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90% identical to the amino acid sequence set forth in SEQ ID NO: 6.

In certain embodiments, the VEGFR-binding peptide is located at the N-terminus of the fusion polypeptide. In certain embodiments, the endosomolytic peptide is located at the C-terminus of the fusion polypeptide.

Also encompassed by the present disclosure is a system for transfection of a nucleic acid into a cell, comprising: (a) the present fusion polypeptide; and (b) a nucleic acid.

In certain embodiments, the fusion polypeptide and the nucleic acid are suspended in an aqueous medium with a conductivity no greater than 10 mS/cm, or no greater than 2 mS/cm. In one embodiment, the fusion polypeptide and the nucleic acid are suspended in an aqueous medium with a conductivity of about 0.45 mS/cm.

In certain embodiments, the system further comprises dexamethasone, insulin (or its fragment), transferrin (or its fragment), a selenite, or combinations thereof. In one embodiment, the system further comprises about 0.1 µg/ml to about 0.6 µg/ml dexamethasone, about 5 µg/ml to about 20 µg/ml insulin (or its fragment), about 3 µg/ml to about 10 µg/ml transferrin (or its fragment), and about 0.003 µg/ml to about 0.010 µg/ml selenite.

In certain embodiments, the N:P ratio of the system ranges from about 1:1 to about 12:1. In one embodiment, the N:P ratio is about 5:1.

The present disclosure provides for a method of transfecting a nucleic acid into a cell, the method comprising contacting the cell with the present system. The contacting step of the method may be *in vitro*, *ex vivo* and/or *in vivo*.

The cell may be a eukaryotic cell, including mammalian cell. In one embodiment, the cell is a stem cell.

The present disclosure also provides for a kit comprising the present fusion polypeptide, or comprising the present system.

Detailed Description

The present disclosure provides for non-viral compositions and methods for delivering nucleic acids into eukaryotic cells (e.g., stem cells) with high efficiency and low genotoxicity and/or cytotoxicity. The present fusion polypeptide may facilitate entry of nucleic acids into a cell, and release of nucleic acids from compartments or organelles (e.g., endosomes) within the transfected cells.

The present system and method achieve transfection efficiency of at least about 20%, at least about 30%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, or at least about 90%. The transfection efficiency of the present system and method may be at least 1.2 fold, at least 1.5 fold, at least 2 fold, at least 2.5 fold, or at least 3 fold, of the transfection efficiency of the lipid-based or polymer-based transfection system of the prior art.

The present system and method has low cytotoxicity, killing less than about 40%, less than about 30%, less than about 25%, less than about 20%, less than about 15%, less than about 10%, or less than about 5%, of the cells which have been in contact with the present system or which have been transfected. In certain embodiments, the present system and method do not show any (or show minimal) genotoxicity and/or cytotoxicity, or negative impact on gene function or ability of the cell to differentiate.

The present disclosure provides for a fusion polypeptide, comprising (or consisting essentially of, or consisting of): (i) a cell surface receptor-binding peptide; (ii) a nucleic acid-binding polypeptide; and (iii) an endosomolytic peptide.

The cell surface receptor-binding peptide may be a vascular endothelial growth factor receptor (VEGFR)-binding peptide, an insulin-like growth factor receptor (IGFR)-binding peptide, a fibroblast growth factor receptor (FGFR)-binding peptide, an epidermal growth factor receptor (EGFR)-binding peptide, a platelet-derived growth factor receptor (PDGFR)-binding peptide, or an integrin-binding peptide.

The present disclosure provides for a fusion polypeptide, comprising: (i) a vascular endothelial growth factor receptor (VEGFR)-binding peptide; (ii) a nucleic acid-binding polypeptide; and (iii) an endosomolytic peptide.

In certain embodiments, the fusion polypeptide comprises (or consists essentially of, or consists of) an amino acid sequence at least about 50%, at least about 55%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 99%, about 70%, about 75%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequence set forth in SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, or SEQ ID NO: 26 (Table 2).

In certain embodiments, the cell surface receptor-binding peptide is located at the N-terminus or C-terminus of the fusion polypeptide. In certain embodiments, the endosomolytic peptide is located at the C-terminus or N-terminus of the fusion polypeptide.

In certain embodiments, the VEGFR-binding peptide is located at the N-terminus or C-terminus of the fusion polypeptide. In certain embodiments, the endosomolytic peptide is located at the C-terminus or N-terminus of the fusion polypeptide.

The present disclosure also provides for a fusion polypeptide, comprising: (i) a cell-penetrating peptide; (ii) a nucleic acid-binding polypeptide; and (iii) an endosomolytic peptide.

In certain embodiments, the fusion polypeptide comprises (or consists essentially of, or consists of) an amino acid sequence at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 99%, about 70%, about 75%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequence set forth in SEQ ID NO: 8 or SEQ ID NO: 9 (Table 2).

In certain embodiments, the fusion polypeptide further comprises the Arg-Gly-Asp (RGD) peptide.

In certain embodiments, the cell-penetrating peptide is located at the N-terminus or C-terminus of the fusion polypeptide. In certain embodiments, the

endosomolytic peptide is located at the C-terminus or N-terminus of the fusion polypeptide.

The fusion polypeptide can be designed to place the various functional moieties (a nucleic acid-binding polypeptide, an endosomolytic peptide, a cell surface receptor-binding peptide, and/or a cell-penetrating peptide) in any order. In the fusion polypeptide, these functional moieties may be covalently ligated continuously or non-continuously (e.g., they may be separated by linkers (e.g., linker amino acid residues)). The linker may have up to 30, up to 20, up to 18, up to 15, up to 12, up to 11, or up to 10, amino acid residues in length. In certain embodiments, the linker has about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10-20, 8-10, 8-12, 8-15, 8-20, or 8-30 amino acid residues in length. In certain embodiments, the linker has about 7-10, 7-12, 7-15, 7-20, or 7-30 amino acid residues in length.

The present polypeptides or peptides may include variants, analogs, orthologs, homologs and derivatives of amino acids or peptides. The present polypeptides or peptides may contain one or more analogs of amino acids (including, for example, non-naturally occurring amino acids, amino acids which only occur naturally in an unrelated biological system, modified amino acids etc.), peptides with substituted linkages, as well as other modifications known in the art. The present polypeptides or peptides may comprise a peptidomimetic, such as a peptoid. The present polypeptides or peptides may contain one or more amino acid residues modified by, e.g., glycosylation, acylation (e.g., acetylation, formylation, myristoylation, palmitoylation, lipoylation), alkylation (e.g., methylation), isoprenylation or prenylation (e.g., farnesylation, geranylgeranylation), sulfation, amidation, hydroxylation, succinylation, etc.

In certain embodiments, the present fusion polypeptide includes a nuclear localization sequence (NLS) to direct the nucleic acid to the nucleus.

The present disclosure provides for a system (e.g., a nucleic acid delivery system, such as a gene delivery system) for delivering a nucleic acid into a cell, or a system for transfecting a cell. In certain embodiments, the system comprises: (a) the fusion polypeptide as described herein; and (b) a nucleic acid.

In certain embodiments, the present system further comprises one or more steroids (e.g., dexamethasone, prednisolone, methylprednisolone, etc.) insulin (or its

fragment), transferrin (or its fragment), selenious acid, selenite, or combinations thereof. The steroids may be a corticosteroid (including glucocorticoids and mineralocorticoids) or a sex steroid.

In one embodiment, the present system comprises (a) the fusion polypeptide as described herein; (b) a nucleic acid, and (c) dexamethasone, insulin (or its fragment), transferrin (or its fragment), and/or selenious acid (and/or selenite).

The concentration of the steroid (e.g., dexamethasone, prednisolone, methylprednisolone, etc.) in the present system may range from about 0.01 $\mu\text{g/ml}$ to about 1.00 $\mu\text{g/ml}$, from about 0.05 $\mu\text{g/ml}$ to about 0.8 $\mu\text{g/ml}$, or from about 0.1 $\mu\text{g/ml}$ to about 0.6 $\mu\text{g/ml}$. In one embodiment, the steroid (e.g., dexamethasone, prednisolone, methylprednisolone, etc.) is in the present system at a concentration of about 0.40 $\mu\text{g/ml}$.

The concentration of insulin (or its fragment) in the present system may range from about 1 $\mu\text{g/ml}$ to about 40 $\mu\text{g/ml}$, from about 3 $\mu\text{g/ml}$ to about 30 $\mu\text{g/ml}$, or from about 5 $\mu\text{g/ml}$ to about 20 $\mu\text{g/ml}$. In one embodiment, insulin (or its fragment) is in the present system at a concentration of about 10 $\mu\text{g/ml}$. In certain embodiments, the insulin is human insulin. In certain embodiments, the insulin is from other non-human species as described herein.

The concentration of transferrin (or its fragment) in the present system may range from about 1 $\mu\text{g/ml}$ to about 20 $\mu\text{g/ml}$, from about 2 $\mu\text{g/ml}$ to about 15 $\mu\text{g/ml}$, or from about 3 $\mu\text{g/ml}$ to about 10 $\mu\text{g/ml}$. In one embodiment, transferrin (or its fragment) is in the present system at a concentration of about 6 $\mu\text{g/ml}$. In another embodiment, transferrin (or its fragment) is present in the present system at a concentration of about 5.5 $\mu\text{g/ml}$. In certain embodiments, the transferrin is human transferrin. In certain embodiments, the transferrin is from other non-human species as described herein.

The concentration of selenious acid or selenite in the present system may range from about 0.001 $\mu\text{g/ml}$ to about 0.015 $\mu\text{g/ml}$, from about 0.002 $\mu\text{g/ml}$ to about 0.012 $\mu\text{g/ml}$, or from about 0.003 $\mu\text{g/ml}$ to about 0.010 $\mu\text{g/ml}$. In one embodiment, selenious acid or selenite is in the present system at a concentration of about 0.007 $\mu\text{g/ml}$. In another embodiment, selenious acid or selenite is in the present system at a concentration of about 0.0067 $\mu\text{g/ml}$. In one embodiment, the selenite is sodium selenite.

In certain embodiments, a solution of the fusion polypeptide is desalted before mixing with the nucleic acids. In certain embodiments, the salt concentration of the solution of the fusion polypeptide is lowered before mixing with the nucleic acids.

The desalting step (or the step to lower the salt concentration) may be by using gel filtration chromatography (e.g., a desalting column), dialysis, ultrafiltration, and/or other methods known in the art.

In certain embodiments, before mixing with the nucleic acid, the fusion polypeptide is in an aqueous medium with a conductivity no greater than 10 mS/cm (milliSiemens per centimeter), no greater than 9 mS/cm, no greater than 8 mS/cm, no greater than 7 mS/cm, no greater than 6 mS/cm, no greater than 5 mS/cm, no greater than 4 mS/cm, no greater than 3 mS/cm, no greater than 2 mS/cm, no greater than 1 mS/cm, or no greater than 0.5 mS/cm. In one embodiment, the aqueous medium has a conductivity of about 0.45 mS/cm. In another embodiment, the aqueous medium has a conductivity of about 0.5 mS/cm.

The present disclosure also provides for a method of delivering a nucleic acid into a cell, or a method for transfecting a cell. The method may comprise contacting the cell with the present system. The contacting step may occur *in vitro*, *ex vivo* and/or *in vivo* (e.g., to treat a subject in need of treatment by the present system or method).

In certain embodiments, the present fusion polypeptide is used in an effective amount. An "effective amount" of the fusion polypeptide is an amount that will allow transfection to occur.

In certain embodiments, the present fusion polypeptides and nucleic acids form a complex in an aqueous solution. Such complexes may be formed spontaneously by mixing the fusion polypeptides with nucleic acids at the desired ratio.

The ratio of fusion polypeptides to nucleic acids may be balanced to maximize transfection efficiency and minimize genotoxicity and/or cytotoxicity.

In certain embodiments, the nucleic acids/fusion polypeptides complexes (e.g., nanoparticles) may have a N:P ratio ranging from about 1:1 to about 15:1, from about 1:1 to about 12:1, from about 1:1 to about 10:1, from about 1:1 to about 9:1, from about 1:1 to about 8:1, from about 1:1 to about 7:1, from about 1:1 to about 6:1, from about 1:1 to about 5:1, from about 1:1 to about 4:1, from about 4:1 to about 5:1, from about 4:1 to about 12:1, from about 5:1 to about 12:1, from about 4:1 to about 10:1,

from about 5:1 to about 10:1, greater than 2:1, greater than 3:1, greater than 4:1, greater than 5:1, about 4:1, or about 5:1.

As used herein, the term “N:P ratio” refers to the molar ratio of positively charged nitrogen atoms in the nucleic acid-binding peptide to negatively charged phosphates in the nucleic acid (e.g., DNA, RNA, or any other nucleic acid as described herein). As the number of positive side-groups in a peptide side chain depends upon the sequence, different peptides will have differing numbers of positive charges per unit mass. In order to calculate this, the following equation may be used:

$$\text{N:P ratio} = M_{\text{peptide}} / M_{\text{nucleic acid}} \cdot C_{\text{NP}}$$

M_{peptide} is the mass of the peptide (e.g., the nucleic acid-binding peptide). $M_{\text{nucleic acid}}$ is the mass of the nucleic acid (e.g., DNA, RNA, or any other nucleic acid as described herein). C_{NP} is the N:P constant. The N:P constant is the ratio of the peptide's side chain positive charge density to the nucleic acid's backbone density, with the charge density being the charge of a substance divided by its molecular mass. In certain embodiments, for the peptide, lysine, arginine and histidine side groups are counted. In certain embodiments, for the nucleic acid, the average mass of one single base pair, and the charge of the phosphate group are used.

In certain embodiments, the fusion polypeptide and the nucleic acid are in an aqueous medium with a conductivity no greater than 10 mS/cm (milliSiemens per centimeter), no greater than 9 mS/cm, no greater than 8 mS/cm, no greater than 7 mS/cm, no greater than 6 mS/cm, no greater than 5 mS/cm, no greater than 4 mS/cm, no greater than 3 mS/cm, no greater than 2 mS/cm, no greater than 1 mS/cm, or no greater than 0.5 mS/cm. In one embodiment, the aqueous medium has a conductivity of about 0.45 mS/cm. In another embodiment, the aqueous medium has a conductivity of about 0.5 mS/cm.

In certain embodiments, the fusion polypeptides and nucleic acids form nanoparticles. In certain embodiments, the nanoparticles have sizes ranging from about 10 nm to about 600 nm, from about 10 nm to about 500 nm, from about 10 nm to about 400 nm, from about 50 nm to about 400 nm, from about 20 nm to about 150 nm, from about 10 nm to about 100 nm, from about 20 nm to about 100 nm, from about 10 nm to about 150 nm, from about 20 nm to about 150 nm, or from about 50 nm to about 150 nm.

In certain embodiments, the nucleic acids/fusion polypeptides nanoparticles are formed by the Flash Mixing method¹⁹. In brief, the fusion polypeptide solution is added to the nucleic acid (e.g., DNA, RNA, or other nucleic acid described herein) solution rapidly and flash mixed. The mixture is incubated, and then added/administered to the cells.

In certain embodiments, the nucleic acids/fusion polypeptides nanoparticles are formed by adding the nucleic acid solution to the fusion polypeptide solution dropwise while stirring. In certain embodiments, the nucleic acids/fusion polypeptides nanoparticles are formed by adding the fusion polypeptide solution to the nucleic acid solution dropwise while stirring. In certain embodiments, the nucleic acids/fusion polypeptides nanoparticles are formed by simultaneous mixing of the nucleic acid and fusion polypeptide solution using a microfluidic chamber.

The present fusion polypeptide may further include a fragment (e.g., tag) useful for polypeptide production and/or detection, including, but not limited to, poly-histidine (e.g., six histidine residues) a maltose binding protein, GST, green fluorescent protein (GFP), hemagglutinin, or alkaline phosphatase, secretion signal peptides (e.g., preprotrypsin signal sequence), c-myc, and/or FLAG.

The present fusion polypeptide can be derivatized or linked to another functional molecule. For example, present fusion polypeptide can be functionally linked (by chemical coupling, genetic fusion, noncovalent interaction, etc.) to one or more other molecular entities, such as an antibody or antibody fragment, a detectable agent, an immunosuppressant, a cytotoxic agent, a pharmaceutical agent, a protein or peptide that can mediate association with another molecule (such as a streptavidin core region or a polyhistidine tag), amino acid linkers, signal sequences, immunogenic carriers, or ligands useful in protein purification, such as glutathione-S-transferase, histidine tag, and staphylococcal protein A. Cytotoxic agents may include radioactive isotopes, chemotherapeutic agents, and toxins such as enzymatically active toxins of bacterial, fungal, plant, or animal origin, and fragments thereof.

One type of derivatized protein is produced by crosslinking two or more polypeptides (of the same type or of different types). Suitable crosslinkers include those that are heterobifunctional, having two distinct reactive groups separated by an appropriate spacer (e.g., m-maleimidobenzoyl-N-hydroxysuccinimide ester) or homobifunctional (e.g., disuccinimidyl suberate). Useful detectable agents with which a protein can be derivatized (or labeled) include fluorescent agents, various enzymes,

prosthetic groups, luminescent materials, bioluminescent materials, and radioactive materials. Non-limiting, exemplary fluorescent detectable agents include fluorescein, fluorescein isothiocyanate, rhodamine, and, phycoerythrin. A polypeptide can also be derivatized with detectable enzymes, such as alkaline phosphatase, horseradish peroxidase, beta-galactosidase, acetylcholinesterase, glucose oxidase and the like. A polypeptide can also be derivatized with a prosthetic group (e.g., streptavidin/biotin and avidin/biotin).

In certain embodiments, the present system does not contain lipids. In certain embodiments, the present system comprises lipids.

The term "transfection" is used herein generally to mean the delivery and introduction of biologically functional nucleic acid (or polynucleotide) into a cell, e.g., a eukaryotic cell, in such a way that the nucleic acid retains its function within the cell. Transfection encompasses delivery and introduction of expressible nucleic acid into a cell such that the cell is rendered capable of expressing that nucleic acid. The term "transfecting" also means that a polynucleotide becomes associated with a selected cell. The polynucleotide can be on the membrane of the cell or inside the cytoplasm, nucleus, or other organelle of the cell. Other terms sometimes used interchangeably with transfecting include "delivering" or "transferring" to a cell.

The term "contacting" or "contact" as used herein in connection with contacting a cell includes subjecting the cell to an appropriate solution, buffer, or culture medium which comprises the present system. Where the cell is *in vivo*, "contacting" or "contact" includes administering the present system in a pharmaceutical composition to a subject via an appropriate administration route so that the nucleic acids contacts the cell *in vivo*.

As used herein, the term "genotoxicity" refers to the destructive effect of a nucleic acid delivery system (e.g., a gene delivery system) on a cell's genetic material (DNA and/or RNA) affecting its integrity. In certain embodiments, genotoxicity is reflected by micronuclei formation.

As used herein, the term "cytotoxicity" refers to the loss of cell viability after cell exposure to a nucleic acid delivery system (e.g., a gene delivery system), or a component or a solution of a nucleic acid delivery system.

Transfection activity or efficiency may be measured by detecting the presence of the transfected nucleic acid in a cell. In certain embodiments, a transfected nucleic

acid is detected by measuring the biological function of the peptide/protein encoded by the nucleic acid in the cell. In certain embodiments, a transfected nucleic acid is assessed by measuring the level of transient or stable expression of a reporter gene contained in the transfected nucleic acid. The level of reporter gene expression may depend on, among other things, the amount of nucleic acid transfected. Generally, there are two classes of reporter gene detection systems used for reporter gene assays to determine gene transfer efficiency: quantitation and visualization. Quantitative methods use the appropriate substrates to measure a reporter gene product's activity. For example, the bioluminescent enzyme luciferase catalyzes the oxidative carboxylation of beet luciferin, emitting photons that may be measured using a luminometer. The amount of luciferase activity is usually proportional to the overall efficiency of transfection for a cell sample. In one common approach to measuring luciferase activity in a sample of transfected cells, cell extracts are prepared and the amount of luciferase activity in the extract is determined. Measurements of the activities of reporter gene products may be used in turn to determine the gene transfection efficiency. In certain embodiments, transfection activity or efficiency is assessed by determining the percent of cells in a sample that have been transfected. With these techniques, individual cells are visualized under a microscope and the number of cells exhibiting characteristics of the transfected reporter gene are counted. For example, cells transfected with the reporter gene beta-galactosidase undergo X-gal staining, during which the beta-galactosidase present in a cell will hydrolyze X-gal (5-bromo-4-chloro-3-indoyl-beta-D-galactopyranoside) and yield a blue precipitate. Other detection and quantitative methods which may be used are well known in the art.

In certain embodiments, medium employed in transfection is similar to the medium used to culture cells for transfection. The medium may contain serum or may be serum-free medium.

It will also be apparent to those of ordinary skill in the art that methods, reagents, procedures and techniques other than those specifically detailed herein may be employed or readily adapted to produce the systems of the present disclosure and practice the present transfection methods. Such alternative methods, reagents, procedures and techniques are within the spirit and scope of this disclosure.

Cell surface receptor-binding peptides

In certain embodiments, the present fusion polypeptide comprises a peptide (e.g., a receptor-binding peptide) that binds to a cell surface receptor. Non-limiting examples of the cell surface receptors include growth factor receptors (e.g., vascular endothelial growth factor (VEGF) receptor, fibroblast growth factor receptor (FGFR), epidermal growth factor receptor (EGFR), etc.) or hormone receptors. Non-limiting examples of the cell surface receptors also include insulin-like growth factor receptor (IGFR), platelet-derived growth factor receptor (PDGFR), and integrin.

In certain embodiments, the present fusion polypeptide comprises a peptide (e.g., a cell surface antigen-binding peptide) that binds to a cell surface antigen.

The VEGF receptors (VEGFRs) may be VEGFR-1 (Flt-1), VEGFR-2 (KDR/Flk-1), or VEGFR-3 (Flt-4). A VEGFR may be membrane-bound (mbVEGFR) or soluble (sVEGFR). The VEGFR-binding peptide may be VEGFR-1-binding peptide, VEGFR-2-binding peptide, or VEGFR-3-binding peptide.

In certain embodiments, the VEGFR-binding peptide is an antagonist of VEGFR (e.g., VEGFR-1, VEGFR-2, and/or VEGFR-3). In certain embodiments, the VEGFR-binding peptide is an agonist of VEGFR (e.g., VEGFR-1, VEGFR-2, and/or VEGFR-3). In certain embodiments, the VEGFR-binding peptide is neither an antagonist nor an agonist of VEGFR (e.g., VEGFR-1, VEGFR-2, and/or VEGFR-3).

In certain embodiments, the VEGFR-binding peptide is an antibody (or a fragment thereof) that is specific for VEGFR (e.g., VEGFR-1, VEGFR-2, and/or VEGFR-3). For example, antibodies directed to VEGF, VEGFR1, VEGFR2, or the VEGF-VEGFR1 or VEGF-VEGFR2 complex are described in U.S. Patent Publication No. 20020032313, which is incorporated by reference in its entirety. Such antibodies can be monoclonal or polyclonal antibodies. Antibodies can also be variant antibodies, such as chimeric antibodies and humanized antibodies, and hybrid antibodies comprising immunoglobulin chains capable of binding VEGFR or the VEGF-VEGFR complex. The antibodies include all immunoglobulin classes (e.g., IgA, IgD, IgE, IgG, and IgM) and subclasses, as well as antibody fragments, so long as they are capable of binding VEGFR, or the VEGF-VEGFR complex. In certain embodiments, the antibody fragment has an antigen-binding portion. In certain embodiments, antibody fragments include, but are not limited to, Fab, F(ab')₂, Fab', F(ab)', Fv, a disulfide linked Fv, single chain Fv (scFv), bivalent scFv (bi-scFv),

trivalent scFv (tri-scFv), Fd, dAb fragment (e.g., Ward et al., *Nature*, 341:544-546 (1989)), an isolated CDR, diabodies, affibodies, triabodies, tetrabodies, linear antibodies, single-chain antibody molecules. Single chain antibodies produced by joining antibody fragments using recombinant methods, or a synthetic linker, are also encompassed by the present disclosure. Bird et al. *Science*, 1988, 242:423-426. Huston et al., *Proc. Natl. Acad. Sci. USA*, 1988, 85:5879-5883. Antibody fragments comprise only a portion of an intact antibody, generally including an antigen binding site of the intact antibody and thus retaining the ability to bind antigen. Examples of antibody fragments encompassed by the present invention include: the Fab fragment, having a light chain variable domain (V_L), light chain constant domain (C_L), heavy chain variable domain (V_H), and heavy chain constant domain (C_H); the Fab' fragment, which is a Fab fragment having one or more cysteine residues at the C-terminus of the C_H domain; the Fd fragment having V_H and C_H domains; the Fd' fragment having V_H and C_H domains and one or more cysteine residues at the C-terminus of the C_H domain; the Fv fragment having the V_L and V_H domains of a single arm of an antibody; the dAb fragment (Ward et al., "Binding Activities of a Repertoire of Single Immunoglobulin Variable Domains Secreted from *Escherichia coli*," *Nature* 341:544-546 (1989), which is hereby incorporated by reference in its entirety) which consists of a V_H domain; isolated CDR regions; F(ab')₂ fragments, a bivalent fragment including two Fab' fragments linked by a disulphide bridge at the hinge region; single chain antibody molecules (Bird et al., "Single-Chain Antigen Binding Proteins," *Science* 242:423-426 (1988); and Huston et al., "Protein Engineering of Antibody Binding Sites: Recovery of Specific Activity in an Anti-Digoxin Single-Chain Fv Analogue Produced in *Escherichia coli*," *PNAS* 85:5879-5883 (1988), which are hereby incorporated by reference in their entirety); diabodies with two antigen binding sites, comprising a V_H domain connected to a V_L domain in the same polypeptide chain (see, e.g., WO 93/11161 to Whitlow et al. and Hollinger et al., "Diabodies: Small Bivalent and Bispecific Antibody Fragments," *PNAS* 90:6444-6448 (1993), which are hereby incorporated by reference in their entirety); affibodies which are triple helix high affinity peptides (see, e.g., Nygren P., Alternative binding proteins: Affibody binding proteins developed from a small three-helix bundle scaffold, *FEBS Journal* 275 (2008) 2668-2676, which is hereby incorporated by reference in its entirety), and linear antibodies comprising a pair of tandem Fd segments (V_H-CH1-V_H-CH1) which, together with complementary light

chain polypeptides, form a pair of antigen binding regions (Zapata et al., "Engineering Linear F(ab')₂ Fragments for Efficient Production in *Escherichia coli* and Enhanced Antiproliferative Activity," *Protein Eng.* 8(10): 1057-1062 (1995); and U.S. Pat. No. 5,641,870, which are hereby incorporated by reference in their entirety). See U.S. Patent No. 8,580,755.

In certain embodiments, the VEGFR-binding peptide has up to 100, up to 90, up to 80, up to 70, up to 60, up to 50, up to 40, up to 30, up to 20, up to 18, up to 15, up to 12, up to 11, or up to 10, amino acid residues in length. In certain embodiments, the VEGFR-binding peptide has about 10-20, 8-10, 8-12, 8-15, 8-20, 8-30, 8-40, 8-50, or 8-60 amino acid residues in length. In certain embodiments, the VEGFR-binding peptide has about 7-10, 7-12, 7-15, 7-20, 7-30, 7-40, 7-50, or 7-60 amino acid residues in length.

In certain embodiments, the VEGFR-binding peptide comprises (or consists essentially of, or consists of) an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 99%, about 70%, about 75%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequence set forth in SEQ ID NO: 1 or SEQ ID NO: 2 (Table 1).

In certain embodiments, the VEGFR-binding peptide is an antagonist of VEGFR-1 as described in U.S. Patent No. 7,250,395, incorporated herein by reference in its entirety.

In certain embodiments, the VEGFR-binding peptide is a fragment of VEGF (vascular endothelial growth factor) including, e.g., VEGF-A, placenta growth factor (PGF), VEGF-B, VEGF-C and VEGF-D. In certain embodiments, the VEGFR-binding peptide is a derivative, or a modified form of a fragment of VEGF. In certain embodiments, the VEGFR-binding peptide is a VEGF biomimetic peptide. In certain embodiments, the VEGFR-binding peptide is a fragment of a VEGF variant. Exemplary VEGF variant proteins are described in U.S. Patent Publication No. 20060286636 and 20070253952, which are hereby incorporated by reference in their entirety.

In certain embodiments, the VEGFR is human VEGFR. In certain embodiments, the VEGF is human VEGF.

The FGF receptors (FGFRs) may be FGFR1, FGFR2, FGFR3, FGFR4, FGFR1, or FGFR6. The FGFR-binding peptide may be FGFR1-binding peptide, FGFR2-binding peptide, FGFR3-binding peptide, FGFR4-binding peptide, FGFR1-binding peptide, or FGFR6-binding peptide.

The EGF receptors (EGFRs) may be EGFR (ErbB-1), HER2/neu (ErbB-2), Her 3 (ErbB-3), or Her 4 (ErbB-4). The EGFR-binding peptide may be ErbB-1-binding peptide, ErbB-2-binding peptide, ErbB-3-binding peptide, or ErbB-4-binding peptide.

The IGF receptors (IGFRs) may be IGFR-1. The IGFR-binding peptide may be IGFR-1-binding peptide.

In certain embodiments, the cell surface receptor-binding peptide is an antagonist of the cell surface receptor. In certain embodiments, the cell surface receptor-binding peptide is an agonist of the cell surface receptor. In certain embodiments, the cell surface receptor-binding peptide is neither an antagonist nor an agonist of the cell surface receptor.

In certain embodiments, the cell surface receptor-binding peptide is an antibody (or a fragment thereof) that is specific for the cell surface receptor. Such antibodies can be monoclonal or polyclonal antibodies. Antibodies can also be variant antibodies, such as chimeric antibodies and humanized antibodies, and hybrid antibodies comprising immunoglobulin chains capable of binding the cell surface receptor or the cell surface receptor-ligand complex. The antibodies include all immunoglobulin classes (e.g., IgA, IgD, IgE, IgG, and IgM) and subclasses, as well as antibody fragments, so long as they are capable of binding the cell surface receptor, or the cell surface receptor-ligand complex. In certain embodiments, the antibody fragment has an antigen-binding portion. In certain embodiments, antibody fragments include, but are not limited to, Fab, F(ab')₂, Fab', F(ab)', Fv, a disulfide linked Fv, single chain Fv (scFv), bivalent scFv (bi-scFv), trivalent scFv (tri-scFv), Fd, dAb fragment (e.g., Ward et al., *Nature*, 341:544-546 (1989)), an isolated CDR, diabodies, triabodies, tetrabodies, linear antibodies, single-chain antibody molecules. Single chain antibodies produced by joining antibody fragments using recombinant methods, or a synthetic linker, are also encompassed by the present disclosure. Bird et al. *Science*, 1988, 242:423-426. Huston et al., *Proc. Natl. Acad. Sci. USA*, 1988, 85:5879-5883. Antibody fragments comprise only a portion of an intact antibody,

generally including an antigen binding site of the intact antibody and thus retaining the ability to bind antigen. Examples of antibody fragments encompassed by the present invention include: the Fab fragment, having a light chain variable domain (V_L), light chain constant domain (C_L), heavy chain variable domain (V_H), and heavy chain constant domain (C_H); the Fab' fragment, which is a Fab fragment having one or more cysteine residues at the C-terminus of the C_H domain; the Fd fragment having V_H and C_H domains; the Fd' fragment having V_H and C_H domains and one or more cysteine residues at the C-terminus of the C_H domain; the Fv fragment having the V_L and V_H domains of a single arm of an antibody; the dAb fragment (Ward et al., "Binding Activities of a Repertoire of Single Immunoglobulin Variable Domains Secreted from *Escherichia coli*," *Nature* 341:544-546 (1989), which is hereby incorporated by reference in its entirety) which consists of a V_H domain; isolated CDR regions; F(ab')₂ fragments, a bivalent fragment including two Fab' fragments linked by a disulphide bridge at the hinge region; single chain antibody molecules (Bird et al., "Single-Chain Antigen Binding Proteins," *Science* 242:423-426 (1988); and Huston et al., "Protein Engineering of Antibody Binding Sites: Recovery of Specific Activity in an Anti-Digoxin Single-Chain Fv Analogue Produced in *Escherichia coli*," *PNAS* 85:5879-5883 (1988), which are hereby incorporated by reference in their entirety); diabodies with two antigen binding sites, comprising a V_H domain connected to a V_L domain in the same polypeptide chain (see, e.g., WO 93/11161 to Whitlow et al. and Hollinger et al., "Diabodies: Small Bivalent and Bispecific Antibody Fragments," *PNAS* 90:6444-6448 (1993), which are hereby incorporated by reference in their entirety); and linear antibodies comprising a pair of tandem Fd segments ($VH-CH1-VH-CH1$) which, together with complementary light chain polypeptides, form a pair of antigen binding regions (Zapata et al., "Engineering Linear F(ab')₂ Fragments for Efficient Production in *Escherichia coli* and Enhanced Antiproliferative Activity," *Protein Eng.* 8(10): 1057-1062 (1995); and U.S. Pat. No. 5,641,870, which are hereby incorporated by reference in their entirety). See U.S. Patent No. 8,580,755.

In certain embodiments, the cell surface receptor-binding peptide has up to 100, up to 90, up to 80, up to 70, up to 60, up to 50, up to 40, up to 30, up to 20, up to 18, up to 15, up to 12, up to 11, or up to 10, amino acid residues in length. In certain embodiments, the cell surface receptor-binding peptide has about 10-20, 8-10, 8-12, 8-15, 8-20, 8-30, 8-40, 8-50, or 8-60 amino acid residues in length. In certain

embodiments, the the cell surface receptor-binding peptide has about 7-10, 7-12, 7-15, 7-20, 7-30, 7-40, 7-50, or 7-60 amino acid residues in length.

In certain embodiments, the cell surface receptor-binding peptide comprises (or consists essentially of, or consists of) an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 99%, about 70%, about 75%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequence set forth in SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, or SEQ ID NO: 21 (Table 1).

In certain embodiments, the FGFR is human FGFR. In certain embodiments, the FGF is human FGF.

In certain embodiments, the EGFR is human EGFR. In certain embodiments, the EGF is human EGF.

In certain embodiments, the IGFR is human IGFR. In certain embodiments, the IGF is human IGF.

In certain embodiments, the PDGFR is human PDGFR. In certain embodiments, the PDGF is human PDGF.

In certain embodiments, the integrin is human integrin.

Non-limiting examples of cell surface receptor-binding peptides also include the cell surface receptor-binding peptides in Tables 10-11. Liu et al., Tumor-targeting peptides from combinatorial libraries, *Advanced Drug Delivery Reviews* 110-111 (2017) 13-37, the content of which is incorporated herein by reference in its entirety.

Table 10

Receptor	Sequence	SEQ ID NO
GPC3	DHLASLWWGTEL (TJ12P1)	SEQ ID NO: 127
PD-L1	NYSKPTDRQYHF (APP1)	SEQ ID NO: 128
β -Catenin	ACAQKLDGCSYISWSCG (BC1),	SEQ ID NO: 129
	ACSGWWPKCQGYIPGCG (BC2)	SEQ ID NO: 130
	ACAPGVYRCNQNFITWCG (BC3)	SEQ ID NO: 131
PDGFR β	IPLPPSRPFFK	SEQ ID NO: 132

Receptor	Sequence	SEQ ID NO
PKC δ	LMNPNNHPRTPR (PKC-bp)	SEQ ID NO: 133
PTPRJ	CHHNLTHAC (PTPRJ-pep19),	SEQ ID NO: 134
	CLHHYHGSC (PTPRJ-pep24)	SEQ ID NO: 135
	CHHALTHAC (PTPRJ-pep19.4)	SEQ ID NO: 136
TIR 1	SPRPRHTLRLSL (B18)	SEQ ID NO: 137
Tie 2	TMGFTAPRIPHY	SEQ ID NO: 138
CD-21	RMWPSSTVNLSAGRR (P1)	SEQ ID NO: 139
VEGFR1 (Flt-1)	NGYEIEWYSWVTHGMY (SP5.2)	SEQ ID NO: 140
IL-10 RA	FRSFESCLAKSH	SEQ ID NO: 141
EGFR	YHWYGYTPQNV (GE11)	SEQ ID NO: 142
	QHYNIVNTQSRV	SEQ ID NO: 143
	QRHKPRE	SEQ ID NO: 144
FGF8b	HSQAAVP (P12)	SEQ ID NO: 145
aFGF	AGNWTPI (AP8)	SEQ ID NO: 146
bFGF	PLLQATL (P7)	SEQ ID NO: 147
IL-6R α	LSLITRL (S7)	SEQ ID NO: 148
$\alpha 5\beta 1$	CRGDCL	SEQ ID NO: 149
	GACRGDCLGA (synthetic peptide)	SEQ ID NO: 150
	CRRETAWAC	SEQ ID NO: 151
	GACRRETAWACGA (synthetic peptide)	SEQ ID NO: 152
$\alpha 6\beta 1$	VSWFSRHRYSPPFAVS (P3)	SEQ ID NO: 153
$\alpha v\beta 3/\alpha v\beta 5$	CDCRGDCFC (RGD-4C)	SEQ ID NO: 154
$\alpha v\beta 6$	RTDLDSLRTYTL	SEQ ID NO: 155
MMP-9	CTTHWGFTLC (CTT)	SEQ ID NO: 156
CD133	APSPMIW, LQNAPRS	SEQ ID NO: 157
N-cadherin	SWTLYTPSGQSK	SEQ ID NO: 158
E-cadherin	SWELYYPRLANL	SEQ ID NO: 159
PSMA	WQPDTAHHWATL	SEQ ID NO: 160
VEGFR-3	CSDSWHYWC (P1)	SEQ ID NO: 161
	WHWLPNLRHYAS (peptide III)	SEQ ID NO: 162
EGFRvIII/EGFR	WTEILKSYPEb, LPAFFVTNQTQD	SEQ ID NO: 163

Receptor	Sequence	SEQ ID NO
Carbonic anhydrase IX	YNTNHVPLSPKY (CAIX-P1)	SEQ ID NO: 164
EphA2	YSAYPDSVPMMS (YSA)	SEQ ID NO: 165
EphB4	TNYLFSPNGPIA (TNYL)	SEQ ID NO: 166
PS	CLSYYPSTYC	SEQ ID NO: 167
HER2	ACSLQDPNC#DWWGHYCG (H8)	SEQ ID NO: 168
	ACGLQGYGCWGMYGKCG (H30)	SEQ ID NO: 169
	CVGVLP SQDAIGIC (L-26-19)	SEQ ID NO: 170
	CGPLPVDWYWC (L-26-24)	SEQ ID NO: 171
	CEWKFDPLGLGQARC (N-12-1)	SEQ ID NO: 172
	CDYMTDGRAASKIC (N-12-2)	SEQ ID NO: 173
	KCCYSL (p6.1)	SEQ ID NO: 174
	MARSGL, MARAKE, MSRTMS	SEQ ID NO: 175
	WTGWCLNPEESTWGFCTGSF (EC-1)	SEQ ID NO: 176
	MCGVCLSAQRWT, SGLWWLGVDILG	SEQ ID NO: 177 SEQ ID NO: 178
TGA-72	NPGTCKDKWIECLLNG (A3-10)	SEQ ID NO: 179
	DPRHCQKRVLPCPAWL,	SEQ ID NO: 180
	FRERC DKHPQKCTKFL	SEQ ID NO: 181
	GGVSCMQTSPVCENNL (A2-6)	SEQ ID NO: 182
Galectin-3	ANTPCGPYTHDCPVKR (G3-C12),	SEQ ID NO: 183
	PQNSKIPGPTFLDPH (G3-A9)	SEQ ID NO: 184
T antigen	IVWHRWYAWSPASRI (P30-1)	SEQ ID NO: 185
	HGRFILPWWYAFSPS (P-30)	SEQ ID NO: 186
Fibrin-fibronectin complexes	CGLIIQKNEC (CTL1)	SEQ ID NO: 187
	CNAGESSKNC (CTL2)	SEQ ID NO: 188
FGFR	AESGDDYCVLVFTDSA WTKICDWS HFRN (C19)	SEQ ID NO: 189
	MQPLAT	SEQ ID NO: 190
	CRALLRGAPFLAEC	SEQ ID NO: 191
E-selectin	IELLQAR	SEQ ID NO: 192
MMP2-processed collagen IV	TLTYTWS	SEQ ID NO: 193
PSA	CVAYCIEHHCWTC (C-4)	SEQ ID NO: 194

Receptor	Sequence	SEQ ID NO
Notch1 NRR	ACERYQGCFSVGGYCG (NRR17)	SEQ ID NO: 195
CD44	THENWPA (CV-1)	SEQ ID NO: 196
	WHPWSYLWTQQA (RP-1)	SEQ ID NO: 197
FGF3	VLWLKNR (FP16)	SEQ ID NO: 198
Extracellular domain-B fibronectin	CTVRTSADC (ZD2)	SEQ ID NO: 199
APRIL	AAAPLAQPHMWA (sAPRIL-BP1)	SEQ ID NO: 200
p16	SHSLSS	SEQ ID NO: 201
pre-miR-21	ALWPPNLHAWVP	SEQ ID NO: 202

GPC3: Glypican-3; T antigen: Thomsen–Friedenreich glycoantigen; PS: Phosphatidyl serine; IL-10 RA: human interleukin-10 receptor alpha; TfR 1: human transferrin receptor 1; IL-6R α : Interleukin 6 receptor chain α ; Notch1 NRR, negative regulatory region in Notch 1; p16: Protein p (16INK4a).

Table 11

Receptor	Sequence	SEQ ID NO
HER2	LTVSPWY	SEQ ID NO: 203
α -Enolase	SSMDIVLRAPLM (pHCT74)	SEQ ID NO: 204
EGFR	FPMFNHWEQWPP	SEQ ID NO: 205
	SYPIPDT (P1)	SEQ ID NO: 206
	HTSDQTN (P2)	SEQ ID NO: 207
MUC18	CLFMRLAWC	SEQ ID NO: 208
Nucleolin	DMPGTVLP	SEQ ID NO: 209
	DWRGDSMDS	SEQ ID NO: 210
	VPTDTDYS	SEQ ID NO: 211
	VEEGGYIAA	SEQ ID NO: 212
GP130	VTWTPQAWFQWV (VTW)	SEQ ID NO: 213
Nestin	AQYLNPS	SEQ ID NO: 214
Cadherins	CSSRTMHHC	SEQ ID NO: 215
$\alpha 4\beta 1$	CPLDIDFYC	SEQ ID NO: 216
$\alpha 5\beta 1$	CPIEDRPMC (RPMrel)	SEQ ID NO: 217

Receptor	Sequence	SEQ ID NO
$\alpha v \beta 6$	RGDLATLRQLAQEDGVVG- VR (H2009.1)	SEQ ID NO: 218
	SPRGDLAVLGHK (HBP)	SEQ ID NO: 219
	SPRGDLAVLGHKY (HBP-1)	SEQ ID NO: 220
$\alpha v \beta 3$ (RMS-I)	CQQSNRGDRKRC (RMS-I)	SEQ ID NO: 221
	CMGNKCRSAKRP (RMS-II)	SEQ ID NO: 222
IL-13R $\alpha 2$	CGEMGWVRC	SEQ ID NO: 223
VPAC1	GFRFGALHEYNS (VP2)	SEQ ID NO: 224
IGHC	CTLPHLKMC	SEQ ID NO: 225
HSPG	ASGALSPSRLDT (OSP-1)	SEQ ID NO: 226
Adenoviral receptor	SWDIAWPPLKVP	SEQ ID NO: 227
GRP78	CTVALPGGYVRVC (Pep42)	SEQ ID NO: 228
GRP78	ETAPLSTMLSPY (GMBP1)	SEQ ID NO: 229
GRP78	GIRLRG	SEQ ID NO: 230
APP	CPCPEGAGC	SEQ ID NO: 231
IL-11R α	CGRRAGGSC	SEQ ID NO: 232
PDGFR β	CRGRRST (RGR)	SEQ ID NO: 233
APN (CD13)	CNGRCVSGCAGRC (NGR)	SEQ ID NO: 234
p32/gC1qR	CGNKRTRGC (LyP-1)	SEQ ID NO: 235
TIP-1	HVGGSSV	SEQ ID NO: 236
$\alpha 2 b \beta 3$	RGDGSSV	SEQ ID NO: 237
$\alpha 3 \beta 1$	SWKLPPS	SEQ ID NO: 238
$\alpha v \beta 3$ $\alpha v \beta 5$	CRGDKRGPDC (iRGD)	SEQ ID NO: 239
NRP-1	GGKRPAR (P4)	SEQ ID NO: 240
	RIGRPLR (P7)	SEQ ID NO: 241
	CGFYWLRSC	SEQ ID NO: 242
	RPARPAR	SEQ ID NO: 243
MMP2-processed collagen IV	TLTYTWS	SEQ ID NO: 244
VAV3	SSQPFWS	SEQ ID NO: 245
CRKL	YRCTLNSPFFWEDMTHEC-	SEQ ID NO: 246

Receptor	Sequence	SEQ ID NO
	HA	
Plectin-1	KTLLPTP (PTP)	SEQ ID NO: 247

IGHC: immuno-globulin heavy chain; HSPG: heparin sulfate proteoglycans; IL-13R α 2: Interleukin 13 receptor α 2; GRP78: glucose-regulated protein 78; APP: aminopeptidase P; NRP-1: neuropilin-1; APN: aminopeptidase N.

Nucleic acid-binding polypeptides

Nucleic acid-binding polypeptides may complex with a nucleic acid and compact the nucleic acid. Nucleic acid-binding polypeptides may bind to nucleic acids through electrostatic, hydrophobic, and/or steric interactions.

In certain embodiments, the nucleic acid-binding polypeptide is a cationic polypeptide.

In certain embodiments, the nucleic acid-binding polypeptide is wild-type, mutated, or modified.

In certain embodiments, the nucleic acid-binding polypeptide comprises one, or two or more repeats, of a nucleic acid-binding peptide (monomer). In the nucleic acid-binding polypeptide, these monomers may be repeated continuously or non-continuously. Thus, they may be separated by linkers (e.g., linker amino acid residues).

In some embodiments, the nucleic acid-binding peptide (monomer) has one or more lysine, arginine, and/or histidine residues. In some embodiments, the nucleic acid-binding peptide (monomer) further contains one or more cysteine residues.

In certain embodiments, the nucleic acid-binding polypeptide comprises one, or two or more repeats, of a nucleic acid-binding peptide (monomer), including, but not limited to, histones, nucleolin, protamines (e.g., PRM1 and PRM2), helix-loop-helix (HLH) proteins, zinc finger proteins, polylysines, transcription factors, polyhistidines, polyarginines, spermine, spermidine, DNA-binding peptides (such as the DNA-binding peptide μ from adenovirus), and fragments or variants thereof. In certain embodiments, the nucleic acid-binding peptide may comprise a N-terminal fragment of a C-terminal fragment of histones, nucleolin, protamines (e.g., PRM1 and PRM2), helix-loop-helix (HLH) proteins, zinc finger proteins, polylysines, transcription factors, polyhistidines, polyarginines, spermine, spermidine, DNA-

binding peptides (such as the DNA-binding peptide mu from adenovirus). Nishikawa et al., Targeted delivery of plasmid DNA to hepatocytes in vivo: optimization of the pharmacokinetics of plasmid DNA/galactosylated poly(L-lysine) complexes by controlling their physicochemical properties. *J Pharmacol Exp Ther* 1998;287(1):408-15. Strydom et al., Studies on the transfer of DNA into cells through use of avidin-polylysine conjugates complexed to biotinylated transferrin and DNA. *J Drug Target* 1993; 1(2): 165-74.

In certain embodiments, the nucleic acid-binding polypeptide comprises one, or two or more repeats, of a histone (wildtype or mutated), a histone variant, or fragments thereof. Histones are basic proteins with high a content of lysine or arginine and function in the packaging of DNA. Histones are highly conserved and can be grouped into five major classes: H1/H5, H2A, H2B, H3, and H4.

As described herein, a histone may be a full-length histone, a histone variant, or a fragment of a histone.

A histone variant may be a histone modified by, for example, the deletion, addition and/or substitution of one or more amino acid residues (10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, amino acid residues or 1 amino acid residue). Alternatively, a histone may be modified by acetylation and/or methylation. In certain embodiments, the modifications do not substantially compromise the polycationic nature of the histone.

Suitable amino acid substitutions include, but are not necessarily limited to, amino acid substitutions known in the art as "conservative". A "conservative" substitution is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the biological activity, secondary structure and/or hydrophobic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine, histidine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) Ala, Pro, Gly, Glu, Asp, Gln, Asn, Ser, Thr; (2)

Cys, Ser, Tyr, Thr; (3) Val, Ile, Leu, Met, Ala, Phe; (4) Lys, Arg, His; And (5) Phe, Tyr, Trp, His. A histone variant may also, or alternatively, contain non-conservative amino acid changes.

As used herein, the term variant also denotes any peptide, pseudopeptide (peptide incorporating non-biochemical elements) or protein differing from the wildtype protein or peptide, obtained by one or more genetic and/or chemical modifications. Genetic and/or chemical modification may be understood to mean any mutation, substitution, deletion, addition and/or modification of one or more residues of the protein or peptide considered. Chemical modification may refer to any modification of the peptide or protein generated by chemical reaction or by chemical grafting of biological or non-biological molecule(s) onto any number of residues of the protein.

The nucleic acid-binding polypeptide may be glycosylated, sulfonated and/or phosphorylated and/or grafted to complex sugars or to a lipophilic compound such as, for example, a polycarbon chain or a cholesterol derivative.

The sequence of a variant of a histone (histone variant) may be at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 83%, at least about 85%, at least about 88%, at least about 90%, at least about 93%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical to the sequence of a wildtype histone or a reference histone.

Also included within the meaning of the term "histone variant" are homologues of histones. A histone homologue is typically from a different species but sharing substantially the same biological function or activity as the corresponding histone from another species. For example, homologues of histones include but are not limited to, those from different species of mammals or microorganisms.

The histone fragment may be greater than 50 amino acids in length, between about 5 and about 50 amino acid residues in length, between about 5 and about 45 amino acid residues in length, between about 5 and about 40 amino acid residues in length, between about 5 and about 35 amino acid residues in length, between about 5 and about 30 amino acid residues in length, between about 5 and about 25 amino acid residues in length, between about 5 and about 20 amino acid residues in length, between about 5 and about 15 amino acid residues in length, or between about 5 and

about 10 amino acid residues in length. In certain embodiments, a fragment of a polypeptide (e.g., histone) is 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, or more than 40 amino acid residues in length.

In certain embodiments, the nucleic acid-binding polypeptide comprises about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, about 1-10, about 2-10, about 3-10, about 4-10, about 5-10, about 2-100, about 2-50, about 2-20, or about 3-15, repeating units, of a nucleic acid-binding peptide (monomer).

In certain embodiments, the nucleic acid-binding polypeptide comprises two or more tandem repeats of a nucleic acid-binding peptide (monomer). The term "tandem repeat" means at least one identical nucleic acid-binding peptide (monomer) after another in tandem within the nucleic acid-binding polypeptide, also identified as (monomer) n , where n is about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, about 1-10, about 2-10, about 3-10, about 4-10, about 5-10, about 2-100, about 2-50, about 2-20, or about 3-15.

In certain embodiments, the nucleic acid-binding polypeptide has from about 10% to about 80%, from about 15% to about 70%, from about 20% to about 70%, from about 30% to about 70%, from about 30% to about 60%, or from about 30% to about 50%, lysine and/or arginine residues.

In certain embodiments, the nucleic acid-binding polypeptide comprises about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, about 1-10, about 2-10, about 3-10, about 4-10, about 5-10, about 2-100, about 2-50, about 2-20, or about 3-15 repeats of H2A, H2A variant, or a fragment of H2A.

In certain embodiments, the nucleic acid-binding polypeptide comprises 2 to 10 repeats of a N-terminal fragment of histone H2A, and where the fragment has 15-50 amino acid residues in length.

In certain embodiments, the nucleic acid-binding polypeptide comprises 4 repeats of a N-terminal fragment of histone H2A, and wherein the fragment has about 37 amino acid residues in length.

In certain embodiments, the nucleic acid-binding polypeptide comprises (or consists essentially of, or consists of) about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, about 1-10, about 2-10, about 3-10, about 4-10, about 5-10, about 2-100, about 2-50, about 2-20, or about 3-15 repeating units of an amino acid sequence at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about

90%, at least about 95%, at least about 99%, about 70%, about 75%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequence set forth in SEQ ID NO: 5 (Table 1).

In certain embodiments, the nucleic acid-binding polypeptide comprises one or more repeats of one or more types of the nucleic acid-binding peptide (monomer) as described herein.

Endosomolytic peptides

The endosomolytic peptide is capable of (or promotes) disrupting or lysing the endosome membrane facilitating/resulting in the release of the endosomal content into the cytoplasm of the cell. In certain embodiments, the endosomolytic peptide promotes the lysis of, and/or transport of the present fusion polypeptides and/or nucleic acids from, the cellular compartments such as the endosome, lysosome, endoplasmic reticulum (ER), golgi apparatus, microtubule, peroxisome, or other vesicular bodies within the cell, to the cytoplasm of the cell. In certain embodiments, the endosomolytic peptides include pH-sensitive peptides, natural or synthetic fusogenic lipids, and natural or synthetic cationic lipids.

In certain embodiments, the endosomolytic peptide is rich in histidine. The percentage of histidine in the endosomolytic peptide may range from about 10% to about 70%, or from about 20% to about 40%. In one embodiment, the endosomolytic peptide contains histidine, lysine, and/or arginine. In certain embodiments, the endosomolytic peptide includes one or more amino acids with imidazole side chains.

In certain embodiments, the endosomolytic peptide has up to 60, up to 50, up to 40, up to 30, up to 20, up to 18, up to 15, up to 12, up to 11, or up to 10, amino acid residues in length. In certain embodiments, the endosomolytic peptide has about 10-20, 8-10, 8-12, 8-15, 8-20, 8-30, 8-40, 8-50, or 8-60 amino acid residues in length. In certain embodiments, the endosomolytic peptide has about 7-10, 7-12, 7-15, 7-20, 7-30, 7-40, 7-50, or 7-60 amino acid residues in length.

Non-limiting examples of the endosomolytic peptides include GALA, INF-7, KALA, RALA, H5WYG and LAGA (Table 3). Lochmann et al., Drug delivery of oligonucleotides by peptides. *Eur. J. Pharm. Biopharm.* 58: 237-251.

In certain embodiments, the fusion polypeptide comprises an endosomolytic peptide comprising (or consisting essentially of, or consisting of) an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 99%, about 70%, about 75%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequence set forth in SEQ ID NO: 6 (Table I).

In certain embodiments, the fusion polypeptide comprises an endosomolytic peptide comprising (or consisting essentially of, or consisting of) an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 99%, about 70%, about 75%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequence set forth in any of SEQ ID NOs: 12, 13, 14, 15 and 16.

Cell-penetrating peptides

Cell-penetrating peptides (CPPs) can cross the cellular membrane. In certain embodiments, cell-penetrating peptides gain entry into the cell via endocytosis and/or direct translocation through the cellular membrane. Endocytosis occurs by various mechanisms, including clathrin-dependent endocytosis and clathrin-independent endocytosis.

Cell-penetrating peptides can be cationic, amphipathic, hydrophobic, anionic, hydrophilic, or non-amphipathic. Cell-penetrating peptides can be linear or cyclical. Cell-penetrating peptides can be random coiled, alpha-helical, or contain beta-sheets.

In certain embodiments, the present fusion polypeptide comprises a non-cationic cell-penetrating peptide.

In certain embodiments, the cell-penetrating peptide has up to 60, up to 50, up to 40, up to 30, up to 20, up to 18, up to 15, up to 12, up to 11, or up to 10, amino acid residues in length. In certain embodiments, the cell-penetrating peptide has about 10-20, 8-10, 8-12, 8-15, 8-20, 8-30, 8-40, 8-50, or 8-60 amino acid residues in length. In

certain embodiments, the cell-penetrating peptide has about 7-10, 7-12, 7-15, 7-20, 7-30, 7-40, 7-50, or 7-60 amino acid residues in length.

In certain embodiments, the fusion polypeptide comprises a cell-penetrating peptide comprising (or consisting essentially of, or consisting of) an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 99%, about 70%, about 75%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequence set forth in SEQ ID NOs: 3 or 4.

Non-limiting examples of cell-penetrating peptides also include the cell-penetrating peptides in Tables 4-9. Milletti, F., Cell-penetrating peptides: classes, origin, and current landscape, Drug Discovery Today, 2012, Volume 17, Numbers 15/16: 850-860, the content of which is incorporated herein by reference in its entirety.

Table 4

CPPs derived from heparan-, RNA- and DNA-binding proteins		
Cationic		
Heparan binding proteins		
RKKRRRESRKKRRRES	DPV3	SEQ ID NO: 27
GRPRESGKKRKRRLKP	DPV6	SEQ ID NO: 28
GKRKKKGKLGKKRDP	DPV7	SEQ ID NO: 29
GKRKKKGKLGKKRPRSR	DPV7b	SEQ ID NO: 30
RKKRRRESRRARRSPRHL	DPV3/10	SEQ ID NO: 31
SRRARRSPRESGKKRKRKR	DPV10/6	SEQ ID NO: 32
VKRGLKLRHVRPRVTRMDV	DPV1047	SEQ ID NO: 33
SRRARRSPRHLGSG	DPV10	SEQ ID NO: 34
LRRERQSRLRRERQSR	DPV15	SEQ ID NO: 35
GAYDLRRRERQSRLRRRERQSR	DPV15b	SEQ ID NO: 36
RNA binding proteins		
RKKRRQRRR	HIV-1 Tat	SEQ ID NO: 37
RRRRNRTRNRNRVR	FHV coat	SEQ ID NO: 38

TRQARRNRRRRWRERQR	HIV-1 Rev	SEQ ID NO: 39
TRRQRTRRARRNR	HTLV-II Rex	SEQ ID NO: 40
KMTRAQRRAAARRNRWTAR	BMV Gag	SEQ ID NO: 41
NAKTRRHERRRKLAIER	P22 N	SEQ ID NO: 42
MDAQTRRRERRAEKQAQWKAAN	λ N(1–22)	SEQ ID NO: 43
TAKTRYKARRAELIAERR	ϕ 21N(12–29)	SEQ ID NO: 44
TRRNKRNRRIQEQLNRK	Yeast PrP6	SEQ ID NO: 45
DNA binding proteins		
PRRRSSSRPVRRRRRPRVSRRRRRRGGRRRR	Protamine 1	SEQ ID NO: 46
Leucine zipper		
RIKAERKMRNRRIAASKSRKRKLERIAR	Human cJun	SEQ ID NO: 47
KRRIRRRERNKMAAAKSRNRRRELTDI	Human cFos	SEQ ID NO: 48
Transcription factors		
KRARNTAAARRSRARKLQRMKQ	Yeast GCN4	SEQ ID NO: 49
Homeoproteins		
RQIKIWFQNRRMKWKK	Penetratin	SEQ ID NO: 50
RVIRVWFQNKRCCKDKK	Islet-1	SEQ ID NO: 51
SKRTRQTYTRYQTLELEKEFHFNRYITRRRRIDI ANALSLSERQIKIWFQNRRMKSKKDR	Fushi-tarazu	SEQ ID NO: 52
SQIKIWFQNKRAKIKK	Engrailed-2	SEQ ID NO: 53
RQVTIWFQNRRVKEKK	HoxA-13	SEQ ID NO: 54
KQINNWFQNRKRHWK	Knotted-1	SEQ ID NO: 55
RHIKIWFQNRRMKWKK	PDX-1	SEQ ID NO: 56

Table 5

CPPs derived from signal peptides		
Amphipathic (I): signal peptide + NLS		
MGLGLHLLVLAALQGAKKKRKV	Ig(v)	SEQ ID NO: 57
MVSKIGSWILVLFVAMWSDVGLCKKRPKP	BPrPp(1–30)	SEQ ID NO: 58
MANLGYWLLALFVTMWTDVGLCKKRPKP	MPrPp(1–28)	SEQ ID NO: 59
AAVLLPVLLAAPVQRKRQKLP	K-FGF + NLS	SEQ ID NO: 60

Hydrophobic: signal peptide alone		
AAVLLPVLLAAP	K-FGF	SEQ ID NO: 61

Table 6

CPPs derived from antimicrobial peptides		
Pro-rich		
RRIRPRPPRLPRPRPLPFPRPG	Bac7	SEQ ID NO: 62
VDKGSYLPRPTPPRPIYNRN	Pyrrhocoricin	SEQ ID NO: 63
Amphipathic		
KCFQWQRNMRKVRGPPVSCIQR	Human lactoferrin (19–40)	SEQ ID NO: 64
TRSSRAGLQWPVGRVHRLLRK	Buforin 2	SEQ ID NO: 65
GIGAVLKVLTTGLPALISWIKRKRQQ	Melittin	SEQ ID NO: 66
GIGKWLHSAKKFGKAFVGEIMNS	Magainin 2	SEQ ID NO: 67
LLGDFFRKSKEKIGKEFKRIVQRIK- DFLRNLVPRTEEC	LL-37	SEQ ID NO: 68
RGGRLSYRRRFSTSTGR	SynB1	SEQ ID NO: 69
YKQCHKKGGKKGSG	Crotamine	SEQ ID NO: 70
ALWKTLLKKVLKAPKKRKRK	S4 ₁₃ -PV _{rev}	SEQ ID NO: 71
HARIKPTFRRLLKWYKGGKFW	L-2	SEQ ID NO: 72

Table 7

CPPs derived from viral proteins		
Unknown structure		
TKRRITPKDVIDVRSVTTEINT	Inv3	SEQ ID NO: 73
Amphipathic		
RQGAARVTSWLGRQLRIAGKRLEGRSK	E ^{ms}	SEQ ID NO: 74
NAATATRGRSAASRPTQRPRAPARSASRPR RPVQ	VP22	SEQ ID NO: 75
RHSRIGIIQQRRTNG	HIV-1 VPR 77–	SEQ ID NO: 76

	92	
KLIKGRTPIKFGKADCDRPPKHSQNGMGK	Ribotoxin2 L3 loop	SEQ ID NO: 77
PLSSIFSRIGDP	PreS2-TLM	SEQ ID NO: 78
Amphipathic (b-sheet)		
DPKGDPKGVTVTVTVTVTGKGDPKPD	VT5	SEQ ID NO: 79

Table 8

CPPs derived from various natural proteins		
Cationic		
RRIPNRRPRR	HRSV	SEQ ID NO: 80
RLRWR	AIP6	SEQ ID NO: 81
Amphipathic (I)		
MVRRFLVTLRIRACGPPRVRV	ARF(1-22)	SEQ ID NO: 82
MVTVLFRRRLRIRACGPPRVRV	M918	SEQ ID NO: 83
LLIILRRRIRKQAHASK	pVEC	SEQ ID NO: 84
Amphipathic (helical)		
LSTAADMQGVVTDGMASG	Azurin p18	SEQ ID NO: 85
LSTAADMQGVVTDGMASGLDKDYLPDD	Azurin p28	SEQ ID NO: 86
KFHTFPQTAIGVGAP	hCT18-32	SEQ ID NO: 87
Hydrophobic		
VPTLK (PMLKE, VPALR, VSALK, IPALK)	Bip	SEQ ID NO: 88
PFVYLI	C105Y	SEQ ID NO: 89
PIEVCMYREP	FGF12	SEQ ID NO: 90

Table 9

Designed CPPs and CPPs derived from peptide libraries		
Designed		
Cationic		
R8, R9, R10, R12	Polyarginine	

Amphipathic (cationic I)		
KETWWETWWTEWSQPKKRKV	Pep-1	SEQ ID NO: 91
GLAFLGFLGAAGSTMGAWSQPKKKRKV	MPG	SEQ ID NO: 92
Amphipathic (cationic II)		
GWTLNSAGYLLGKINLKALAALAKKIL	Transportan	SEQ ID NO: 93
AGYLLGHINLHHLAHLAibHHIL	TH	SEQ ID NO: 94
KLALKALKALKAALKLA	MAP	SEQ ID NO: 95
RRWWRRWRR	W/R	SEQ ID NO: 96
GLWRALWRLRLSLWRLWRA	CADY	SEQ ID NO: 97
LIRLWSHLIHIWFQNRRLKWKKK	EB-1	SEQ ID NO: 98
Amphipathic (anionic II)		
WEAALAEALAEALAEHLAEALAEALAA	GALA	SEQ ID NO: 99
LKTLTETLKELTKLTEL	MAP12	SEQ ID NO: 100
Amphipathic (zero-charge II)		
QLALQLALQALQAALQLA	MAP17	SEQ ID NO: 101
Amphipathic (Proline-rich)		
(PPR)3, (PPR)4, (PPR)5, (PPR)6	(PPR) _n	
(PRR)3, (PRR)4, (PRR)5, (PRR)6	(PRR) _n	
GPSQPTYPGDDAPVRDLIRFYRDLQRYLNVVTR HRY	aPP4R1	SEQ ID NO: 102
GPSQPTYPGDDAPVRDLIRFYRDLRRYLNVVTR HRY	aPP5R1	SEQ ID NO: 103
GPSQPTYPGDDAPVRDLRRFYRDLRRYLNVVTR HRY	aPP6R1	SEQ ID NO: 104
G(P _L XX) _n P _I	PoliProline- based	
VRLPPPVRLLPPPVRLLPPP	SAP	SEQ ID NO: 105
VELPPPVELPPPVELPPP	SAP(E)	SEQ ID NO: 106
Peptide libraries		
Support-vector machine model		
FKIYDKKVRTRVVKH	SVM1	SEQ ID NO: 107
RASKRDGSWVKKLHRILE	SVM2	SEQ ID NO: 108

KGTYKKKLMRIPLKGT	SVM3	SEQ ID NO: 109
LYKKGPAKKGRPPLRGWFH	SVM4	SEQ ID NO: 110
HSPIIPLGTRFVCHGVT	SVM5	SEQ ID NO: 111
YTAIAWVKAFIRKLRK	YTA2	SEQ ID NO: 112
IAWVKAFIRKLRKGPLG	YTA4	SEQ ID NO: 113
IAWVKAFIRKLRKGPLG	YTA4	SEQ ID NO: 114
Plasmid display		
Amphipathic		
RLSGMNEVLSFRWL	SG3	SEQ ID NO: 115
Phage display		
Hydrophobic		
SDLWEMMMVSLACQY	Pep-7	SEQ ID NO: 116
VTWTPQAWFQWV		SEQ ID NO: 117
GSPWGLQHHPRT	439a	SEQ ID NO: 118
GPFHFYQFLFPPV	435b	SEQ ID NO: 119
TSPLNIHNGQKL	HN-1	SEQ ID NO: 120
Other		
CAYHRLRRC		SEQ ID NO: 121
Phylomer library		
Cationic		
RCGRASRCRVRWMRRRI	BEN_1079	SEQ ID NO: 122
Other		
PYSRPHVQLWYPNRESCSLIRSLGP	BEN_0805	SEQ ID NO: 123
Peptide arrays		
Hydrophobic		
PLILLRLLRGQF	Pept1	SEQ ID NO: 124
PLIYLRLLRGQF	Pept2	SEQ ID NO: 125
KLWMRWYSPTRRYG	IVV-14	SEQ ID NO: 126

Nucleic acids

The present systems and methods deliver nucleic acids into eukaryotic cells, particularly higher eukaryotic cells.

The nucleic acid may be deoxyribonucleic acid (DNA), ribonucleic acid (RNA) or a DNA/RNA hybrid. The nucleic acid may be linear or circular (such as a plasmid). The nucleic acid may be single-stranded, double-stranded, branched or modified by the ligation of non-nucleic acid molecules. The nucleic acid may be natural, synthetic, or semi-synthetic. These nucleic acids may be of human, animal, plant, bacterial, viral, etc. origin.

Such nucleic acids include, but are not limited to, ESTs, PCR products, genomic DNA, cDNA, RNA, oligonucleotides and antisense constructs; such nucleic acids may be present within expression vectors. The nucleic acids include isolated naturally occurring as well as synthetic nucleic acids, and nucleic acids produced by recombinant technology. An RNA may be a single or double-stranded RNA and may be a small interference RNA (siRNA) or a ribozyme.

In certain embodiments, the nucleic acid is a plasmid DNA including a coding sequence for a transcription product or a protein of interest, together with flanking regulatory sequences effective to cause the expression of the protein in the transfected cells. Examples of flanking regulatory sequences are a promoter sequence sufficient to initiate transcription and a terminator sequence sufficient to terminate the gene product, by termination of transcription or translation. Suitable transcriptional or translational enhancers can be included in the exogenous gene construct to further assist the efficiency of the overall transfection process and expression of the protein in the transfected cells.

A marker or reporter gene encodes a gene product which can be easily assayed, as described herein. The presence of the product of the marker gene indicates that the cell is transfected and the amount of the product indicates how efficient the transfection process.

The nucleic acid may encompass both DNA and RNA from any source comprising natural and non-natural bases. The nucleic acid may contain one or more nucleotide analogs such as nucleotides comprising bases other than the five naturally occurring bases (adenine, guanine, thymine, cytosine and uracil). The monomers of the nucleic acid (e.g., nucleotides and/or nucleotide analogs) can be connected by phosphodiester linkages or modified linkages such as phosphotriester, phosphoramidate, siloxane, carbonate, carboxymethyl ester, acetamidate, carbamate, thioether, bridged phosphoramidate, bridged methylene phosphonate, bridged phosphoramidate, bridged phosphoramidate, bridged methylene phosphonate,

phosphorothioate, methylphosphonate, phosphorodithioate, bridged phosphorothioate or sulfone linkages, and combinations of such linkages.

Nucleic acids may have a variety of biological functions. They may encode proteins, comprise regulatory regions, function as inhibitors of gene or RNA expression (e.g., antisense DNA or RNA, or RNAi), function as inhibitors of proteins, function to inhibit cell growth or kill cells, catalyze reactions, or function in a diagnostic or other analytical assay.

Particular useful nucleic acids in the present invention comprise genes. Exemplary genes encode transcription factors, cytoskeleton proteins, hormones, oncogenes, metabolic enzymes, ion channels, and reporter genes. A reporter gene may be any fluorescent protein, any enzyme for which immunocytochemical determination is possible (beta-galactosidase, beta-lactamase, etc.), or any protein or epitope tagged protein for which specific antibodies are available. Gene products can be detected directly, as by the products of an enzyme or by antibody binding, or indirectly, as by linked enzyme assays or by effects which alter cell function. Altered cell function which can be detected include changes in the cell polarity, cell pH, cell morphology, or ability of a cell to bind certain compounds. Detection can be by fluorescence or luminescence.

The nucleic acid may comprise a gene so that the present systems and methods are used in gene therapy. The gene may be intended to overcome a gene deficiency or defect in the subject, i.e., where the subject fails to produce active, endogenous protein at all or within normal levels, and the gene introduced in the plasmid is intended to make up this deficiency. The gene may encode one or more polypeptides designed to treat any existing disease or condition. The gene may encode an antigenic peptide, capable of generating an immune response in humans or animals. In this particular embodiment, the present system and method help produce either vaccines or immunotherapeutic treatments applied to humans or to animals. The gene may encode an antisense RNA, an interfering RNA (such as a small interfering RNA (siRNA), a small hairpin RNA (shRNA)) and a microRNA (miRNA), a ribozyme, a mRNA, etc.

The nucleic acid may be contained within an expression vector. Thus, for example, a nucleic acid sequence may be included in any one of a variety of expression vectors for expressing a polypeptide, and more than one nucleic acid of interest may be included in one expression vector. Alternatively, parts of one gene or

nucleic acid may be included in separate vectors. In some embodiments, vectors include, but are not limited to, chromosomal, nonchromosomal and synthetic DNA sequences (e.g., derivatives of SV40, bacterial plasmids, phage DNA; baculovirus, yeast plasmids, vectors derived from combinations of plasmids and phage DNA, and derivatives of viral DNA).

Cells

The present system and method may deliver nucleic acids into any suitable types of cells. The cell may a eukaryotic cell. The cell may a mammalian cell, such as a human cell or a non-human mammalian cell (e.g., a non-human primate cell). These include a number of cell lines that can be obtained from American Tissue Culture Collection. In certain embodiments, the cell is infected with a pathogen, e.g. virus, bacteria, mycobacteria, fungi, unicellular organisms. In certain embodiments, the cell is a tumor cell.

In certain embodiments, the cell is present in a subject (e.g., a mammal). The mammal can be a human or a non-human primate. Non-human primates include, but are not limited to, chimpanzees, cynomolgous monkeys, spider monkeys, and macaques, e.g., Rhesus. The mammal can be a transgenic non-human mammal.

In certain embodiments, the cell may be removed and maintained in tissue culture in a primary, secondary, immortalized or transformed state. In certain embodiments, the cells are cultured cells or cells freshly obtained from a source (e.g., a tissue, an organ, a subject, etc.). The mammalian cell can be primary or secondary which means that it has been maintained in culture for a relatively short time after being obtained from an animal tissue. These include primary liver cells, primary muscle cells, primary myoblasts, etc.

In certain embodiments, the present system and method deliver nucleic acids into a stem cell or a progenitor cell. Stem cells are undifferentiated cells that have the ability both to self-renew, and to generate differentiated progeny (see Morrison et al. (1997) Cell 88:287-298). They are found in multicellular organisms. In mammals, there are two broad types of stem cells: embryonic stem cells, and adult stem cells, which are found in various tissues.

The stem cells may be bone marrow-derived stem cells (BMSCs), adipose-derived stem cells (ADSCs), neural stem cells (NSCs), blood stem cells, or

hematopoietic stem cells. Stem cells can also be from umbilical cord blood. Stem cells may be generated through somatic cell nuclear transfer or dedifferentiation.

The stem cells include, but are not limited to, a blood stem cell, an adipose stem cell, a bone marrow mesenchymal stem cell, a mesenchymal stem cell, a neural stem cell (NSC), a skin stem cell, an endothelial stem cell, a hepatic stem cell, a pancreatic stem cell, an intestinal epithelium stem cell, or a germ stem cell. In certain embodiments, mesenchymal stem cells are isolated from mesodermal organs, such as bone marrow, umbilical cord blood, and adipose tissue.

In certain embodiments, the stem cell is an induced pluripotent stem cell (iPS cell or iPSC). iPSC refers to a type of pluripotent stem cell artificially generated from a non-pluripotent cell, typically an adult somatic cell, or terminally differentiated cell, such as fibroblast, a hematopoietic cell, a myocyte, a neuron, an epidermal cell, or the like.

In certain embodiments, the present system and method deliver nucleic acids into a proliferating cell. In certain embodiments, the present system and method deliver nucleic acids into a T cell (including a primary T cell).

The cells can include autologous cells that are harvested from the subject being treated and/or biocompatible allogeneic or syngeneic cells, such as autologous, allogeneic, or syngeneic stem cells (e.g., mesenchymal stem cells), progenitor cells (e.g., connective tissue progenitor cells or multipotent adult progenitor cells) and/or other cells that are further differentiated.

In certain embodiments, cells are cultured prior to transfection. In certain embodiments, cells in the G2/M phase are transfected, where cells are synchronized by double-thymidine blockage, aphidocolin treatment or nocodazole treatment before transfection (Mortimer et al., *Gene Ther* 6: 401-411 (1999); Tseng et al, *Biochim Biophys Acta* 1445: 53-64).

In certain embodiments of the present method, the cells are contacted with the present system for a period of time, ranging from about 1 hour to about 30 days, from about 3 hours to about 20 days, from about 5 hours to about 10 days, from about 5 hours to about 5 days, from about 10 hours to about 3 days, from about 12 hours to about 48 hours, from about 12 hours to about 36 hours, or about 24 hours.

Kits

The present invention also provides kits comprising the present fusion polypeptide or the present system.

In some aspects, the present disclosure provides kits that include a suitable container containing the present fusion polypeptide or the present system. In some embodiments, the present fusion polypeptide or the present system is in a formulation, e.g., pharmaceutical composition. In addition to the fusion polypeptide or the present system, the kit can include informational material. The informational material can be descriptive, instructional, marketing or other material that relates to the methods described herein and/or the use of the fusion polypeptide or the present system for the methods described herein. For example, the informational material describes methods for administering the formulation to a subject or methods for transfecting a cell. The kit can also include a delivery device.

In one embodiment, the informational material can include instructions to administer the formulation in a suitable manner, e.g., in a suitable dose, dosage form, or mode of administration (e.g., a dose, dosage form, or mode of administration described herein).

The informational material of the kits is not limited in its form. In many cases, the informational material, e.g., instructions, is provided in printed matter, e.g., a printed text, drawing, and/or photograph, e.g., a label or printed sheet. However, the informational material can also be provided in other formats, such as Braille, computer readable material, video recording, or audio recording. In another embodiment, the informational material of the kit is a link or contact information, e.g., a physical address, email address, hyperlink, website, or telephone number, where a user of the kit can obtain substantive information about the formulation and/or its use in the methods described herein. Of course, the informational material can also be provided in any combination of formats.

In some embodiments, the individual components of the formulation can be provided in one container. Alternatively, it can be desirable to provide the components of the formulation separately in two or more containers. The different components can be combined, e.g., according to instructions provided with the kit. The components can be combined according to a method described herein, e.g., to prepare and administer a pharmaceutical composition.

In addition to the the present fusion polypeptide or the present system, the kit can include other ingredients, such as a solvent or buffer, a stabilizer or a preservative, and/or a second agent for treating a condition or disorder.

The present fusion polypeptide or the present system can be provided in any form, e.g., liquid, dried or lyophilized form.

EXAMPLE 1

The vector that is used for stem cell transfection requires high efficiency because the methods used to rapidly produce unlimited quantities of undifferentiated stem cells have not yet been perfected. In addition to possessing high efficiencies, these vectors need to be non-genotoxic in stem cells because they could potentially transform normal stem cells into cancer initiating cells. Thus, it is essential to ensure that the engineered stem cells do not incur not only somatic, but also genetic aberrations during the transfection process. Unfortunately, for demonstration of safety in stem cells, non-viral vectors have been mainly evaluated for their impact on metabolic activity without considering impact on membrane integrity, differentiation ability, genetic integrity, and gene dysregulation.

The objective of this research was to develop an efficient vector that can be used for genetic modification of stem cells without any significant negative somatic or genetic impact.

To achieve the objective, two types of designer biomimetic vectors (DBVs) were engineered; targeted and non-targeted. The targeted vectors were composed of four repeating units of histone H2A to condense DNA (H4), a pH-dependent endosomolytic fusogenic peptide GALA (G), and either a Vascular Endothelial Growth Factor Receptor 1 (VEGFR-1) agonist targeting peptide (Vago) or antagonist peptide (Vanta). The rationale for targeting VEGFR-1 is that this receptor is overexpressed on the surface of stem cells and internalizes via receptor mediated endocytosis. The non-targeted vectors are composed of the same motifs which are mentioned above but instead of the VEGFR-1 targeting peptide, they have non-cationic cell penetrating peptides such as Pep1 (tryptophan-rich cluster with high affinity for membranes) and MPG (derived from the fusion sequence of the HIV glycoprotein 41). While many other cell-penetrating peptides are reported in literature (e.g., Tat), the rationale behind choosing these two peptides are: 1) non-cationic nature, 2) high efficiency in membrane fusion and cellular entry and 3) negligible

cytotoxicity^{13, 14, 15, 16, 17}. The role of the cell penetrating peptides is to facilitate internalization of the vector through the stem cell membrane. To evaluate efficiency and safety of the vectors, Adipose-Derived MSCs (ADSCs) were selected for this study because in the clinical setting, they can be obtained from patients in large amounts using minimally painful procedures (unlike bone marrow-derived). The following widely used commercially available non-viral vectors were selected as controls: GeneIn™, Lipofectamine® LTX with Plus, Attractene, FuGENE® HD and jetPRIME®. A commercially available adenoviral vector (Ad-GFP) was used as a viral vector control. This research addressed two significant deficiencies that currently exist. The first is the low efficiency of non-viral vectors in MSC transfection, and the second is a lack of comprehensive toxicity data related to the cell proliferation rate, membrane integrity, micronuclei formation (genotoxicity), gene dysregulation and cell differentiation. The results of this study revealed that the VEGFR-1 targeted recombinant fusion vector could transfect mesenchymal stem cells with high efficiency (>50%) without showing any genotoxicity or negative impact on gene function or ability to differentiate. Overall, the results of this study show that use of receptors as ports for cellular entry is a safer approach for stem cell transfection in comparison to vectors that enter through cellular membrane. The developed vector could be used to transfect any mammalian cell line that overexpresses VEGFR-1 including all types of mesenchymal stem cells.

Materials and Methods

Genetic engineering and production of recombinant vectors

We used standard genetic engineering techniques similar to our previous reports in order to clone, express, and purify the DBVs^{18, 19, 20}. In brief, the genes encoding H4G, MPG-H4G, Pep1-H4G, Vago-H4G, and Vanta-H4G with 6x-histidine tag at the c-terminus, were designed and then chemically synthesized by Integrated DNA Technologies (Coralville, IA, US). The corresponding amino acid sequences of the vectors are shown in **Table 1**. The genes were restriction digested by NdeI and XhoI enzymes and cloned into a pET21b bacterial expression vector (Novagen®, EMD Millipore, MA, US). The fidelity of each gene sequence to the original design was verified by DNA sequencing.

To express the vectors, the expression plasmids were transformed into the LOBSTR BL21(DE3) E. coli expression strain (Kerafast Inc., MA, US). The protein

expression protocol is optimized for the production of highly cationic vectors in *E. coli* as described previously by our group ²¹. In brief, one colony was picked from the LB agar plate and inoculated overnight in a 5ml Miller's LB media supplemented with 100 µg/mL carbenicillin (Sigma-Aldrich, MO, US). The next day, the starter culture was transferred into 500mL terrific broth (TB) supplemented with 100 µg/mL carbenicillin. The culture was incubated at 37°C under vigorous shaking until the OD₆₀₀ reached 0.4-0.6. To induce protein expression, isopropyl β-D-1-thiogalactopyranoside (IPTG, Teknova, CA, US) was added to the culture at the final concentration of 1 mM. After 2.5-4 hours of induction, the *E. Coli* pellet was collected by centrifugation at 5000 g, weighed and stored in -80°C freezer.

To purify the peptides, a method based on Ni-NTA immobilized metal affinity chromatography (QIAGEN, MD, US) was developed. A lysis buffer was formulated beforehand, containing 8 M urea, 2 M NaCl, 100 mM NaH₂PO₄, 10 mM Tris, 1% (v/v) Triton X-100, and 10 mM imidazole. The bacterial pellet was lysed by the lysis buffer (5 mL buffer per 1 gram pellet) for one hour at room temperature under vigorous stirring. Then, the supernatant was collected by centrifuging the slurry for one hour, at 20,000 rpm, 4°C. Meanwhile, the Ni-NTA resin was washed with 10 mL distilled/deionized water and preconditioned with 2 mL of lysis buffer. Afterwards, the supernatant was mixed with the preconditioned Ni-NTA resin and incubated on ice with gentle shaking. After one hour of incubation, the mixture was diluted with 3 times lysis buffer and passed through a 10-mL polypropylene filter column (Bio-Rad Inc., US) by vacuum driven filtration. The column was washed by 100 mL of lysis buffer followed by 50 mL wash buffer (5 M Urea, 1.5 M NaCl, 100 mM NaH₂PO₄, 10 mM Tris and 40 mM imidazole). Finally, the purified vector was eluted by 5 mL of elution buffer (3 M Urea, 0.5 M NaCl, 100 mM NaH₂PO₄, 10 mM Tris and 300 mM imidazole) and collected in 500 µL fractions. The concentration of the peptide within each fraction was measured by the Nanodrop 2000 spectrophotometer (Thermo Fisher Scientific, US). The purity of each peptide was determined by SDS-PAGE analysis.

Peptide desalting and preparation of stock solution

To desalt, a disposable PD-10 desalting column with Sephadex G-25 resin (GE Healthcare's Life Sciences, MA, US) was preconditioned with 15 mL of 10mM L-Glu/ L-Arg buffer (pH 5.8-6.0). Then, each purified peptide fraction was loaded onto the column and eluted with additional 5mL of buffer driven by gravity. The

concentration of each peptide was measured by Nanodrop 2000 spectrophotometer (Thermo Fisher Scientific, US) using the molecular weight and corresponding extinction coefficient as calculated by the ProtParam tool from the ExPASy Bioinformatics Resource Portal (<http://web.expasy.org/protparam/>). The conductivity of the peptide solution was determined by Laser Doppler Velocimetry using Malvern Nano-ZS Zetasizer (Malvern Instruments, UK).

Nanoparticle formation and particle size, charge and shape analysis

The DNA/peptides nanoparticles were formed by the Flash Mixing method¹⁹. In brief, the required amount of each peptide to condense 1 μ g of pEGFP plasmid DNA (pDNA) at various N:P ratios was calculated beforehand. For example, to prepare a N:P ratio of 1, the required amounts of H4G, MPG-H4G, Pep1-H4G, Vago-H4G and Vanta-H4G were 1.17 μ g, 1.22 μ g, 1.29 μ g, 1.27 μ g, and 1.35 μ g, respectively. Then, pEGFP was diluted to a volume of 50 μ L using distilled/deionized water. Concurrently, predetermined amount of each peptide was diluted to 50 μ L volume using distilled/deionized water and placed in another microfuge tube. The peptide solution was added to the pDNA solution rapidly and flash mixed. After 5-10 minutes of incubation, the nanoparticle size was measured by Dynamic Light Scattering and surface charge by Laser Doppler Velocimetry using Malvern Nano-ZS Zetasizer (Malvern Instruments, UK). To make nanoparticles with the commercial transfection reagents including GeneIn™ (MTI-GlobalStem, MD, US), Lipofectamine® LTX with Plus (Thermo Fisher Scientific, MA, US), Attractene (QIAGEN, MD, US), FuGENE® HD (Promega Corporation, WI, US) and jetPRIME® (Polyplus-transfection, France), we followed the corresponding manufacturers' protocols. Once nanoparticles were formed, the surface charges were measured in 5mM NaCl solution. The data are presented as mean $\pm$ s.d. (n=3). Each mean is the average of 15 measurements while n represents the number of independent batches prepared for the measurements.

To study the morphology of the nanoparticles, transmission electron microscopy (TEM) was utilized¹⁹. First, nanoparticles were formed and then one drop of the mixture was loaded onto a carbon type B coated copper grid. As soon as the sample dried on the surface, the solution of 1% sodium phosphotungstate was added to stain the nanoparticles. The detailed images were recorded by 1200EX electron microscope (JEOL, US).

ADSC Characterization

The ADSCs (Lonza, NJ, US) were cultured in ADSC™ Growth Medium Bullet kit (Lonza, NJ, US) which contains the basal media and the necessary supplements for proliferation of human adipose derived mesenchymal stem cells. ADSCs were characterized for cell cycle and VEGFR-1 expression by flow cytometry. The cell cycle study was performed using propidium iodide (PI) DNA staining protocol. In brief, cells were seeded in 96-well plates at the density of 6000 cells per well. After 16, 20, 24, 26, 28 hours of incubation with ADSC™ Growth Medium Bulletkit at 37 °C and 5% CO₂, cells were detached through trypsinization. Cells were then fixed by 70% cold ethanol. After 1 hour, cells were collected by centrifugation, re-suspended in PBS and treated with 0.5 mg/mL Rnase A. Finally, cells were stained by PI (10 µg/mL) for 1 hour. The cell cycle distribution was determined by flow cytometry (Beckman Coulter GALLIOS Cytometer, CA, US).

To determine the level of VEGFR-1 expression, ADSCs were detached by Accutase® Cell Detachment Solution (Innovative Cell Technologies, CA, US). Cells were fixed by 4% formaldehyde solution in PBS and then permeabilized by 0.1% Tween 20/PBS solution. Cells were washed and re-suspended in the staining buffer (0.3M glycine and 10% normal goat serum in PBS solution). 2 µL of Anti-VEGFR-1 rabbit monoclonal antibody conjugated with Alexa Fluor® 488 (abcam, MA, US) was added to each sample. Rabbit monoclonal IgG conjugated with Alexa Fluor® 488 (abcam, MA, US) was used as isotype control. Samples were incubated overnight at 4°C and then washed extensively with PBS. The expression level of VEGFR-1 was determined by flow cytometry (Beckman Coulter GALLIOS Cytometer, CA, US). The unstained sample was also included as a negative control.

Evaluation of cell transfection efficiency

The day before transfection, ADSCs were seeded in 96-well tissue culture plates at the density of 6000 cells per well and incubated for 24 hours. In a microfuge tube, nanoparticles were prepared at various N:P ratios as described above in a total volume of 50 µL and incubated for 5-10 minutes at room temperature. Each tube was further supplemented with 200 µL of ADSC basal media, 1µM dexamethasone (Sigma-Aldrich, MO, US) and 1X ITS Liquid Media. A 100X ITS solution includes 1.0 mg/mL recombinant human insulin, 0.55 mg/mL human transferrin and 0.5

$\mu\text{g/mL}$ sodium selenite (Sigma-Aldrich, MO, US). Next, the old media in each well was removed and replaced with the 250 μL nanoparticle mixture. Twenty four hours post transfection, the media in each well was replaced with 200 μL full growth media and the cells were allowed to grow for another twenty four hours. The green fluorescent protein (GFP) expression was visualized and qualitatively evaluated by a fluorescent microscope (Olympus, FL, US). To quantify GFP expression and percent transfection, cells were trypsinized and analyzed by flow cytometry (Beckman Coulter CytoFLEX Cytometer, CA, US). The ratio of GFP positive cells to untransfected cells was calculated by Kaluza flow analysis software (Beckman Coulter, CA, US).

To measure the transfection efficiency of commercially available transfection reagents including GeneIn™, Lipofectamine® LTX with Plus, Attractene, FuGENE® HD and jetPRIME®, cells were seeded in 96-well plates at the density of 6,000 cells/well. Twenty four hours later, cells were transfected following each manufacturer's cell transfection protocol.

To measure transduction efficiency of adenoviruses, cells were seeded as above. Adenovirus particles encoding GFP (Ad-GFP) were purchased from Baylor College of Medicine (TX, US), and the transduction process was performed according to the manufacturer's protocol. In brief, the multiplicity of infection (MOI) was calculated based on viral titer (plaque-forming units, PFU/mL). The Ad-GFP particles were mixed thoroughly with 300 μL of ADSC basal media. Next, the old media in each well was replaced by the transduction mixture. Four hours post transduction, the media in each well was replaced by the full growth media and the GFP expression was quantified after forty eight hours by flow cytometry as described above. The data are presented as mean $\pm$ s.d. (n=3).

Evaluation of vectors' impact on cell proliferation rate, membrane integrity and morphology

The impact of each vector on ADSC proliferation rates was evaluated by the WST-1 cell proliferation assay. Cells were seeded in the 96-well plates at the density of 6,000 cells per well. After twenty four hours of incubation, ADSCs were transfected with vectors as described above. Forty eight hours post-transfection, the old media was replaced with 100 μL of fresh media containing 10 μL WST-1 reagent (1:10 dilution). After one hour of incubation at 37 °C / 5% CO₂, the absorbance of

each well was measured by Infinite® M200 PRO NanoQuant microplate reader (Tecan, Switzerland) at 440nm/600nm. The absorbance of each treatment was normalized to the negative control (untreated cells) to measure the percentage of cell viability.

To evaluate the impact of each vector on ADSC membrane integrity, a lactate dehydrogenase (LDH) release assay (Roche, IN, US) was performed using manufacturer's kit and protocol. In brief, cells were seeded and transfected as described above. Cells were incubated in ADSC basal media for 48 hours post transfection since the LDH reagent is not compatible with serum. Media in each well was removed and centrifuged at 250g for 5 minutes to pellet the debris. The supernatants were collected into a 96-well plate with 100 µL per well. Next, 100 µL LDH reagent was added into each well and incubated for 30 minutes at room temperature. The absorbance at wavelengths of 490nm and 600nm was measured using Infinite® M200 PRO NanoQuant (Tecan, Switzerland) microplate reader. The media, without contacting any cells, served as the background control. The media from the untransfected cells was used as the negative control (spontaneous LDH release). The media from the cells incubated with the 2% Triton X-100 was served as the positive control (maximum LDH release). After subtracting the background control, the percentage of impact on membrane integrity was calculated as follows: %membrane integrity= (Positive-Treatment)/ (Positive-Negative) × 100. The data are presented as mean±s.d. (n=3).

The morphology of ADSCs before and after transfection was studied by using phase-contrast microscopy (Olympus, FL, US).

Evaluation of vectors' impact on micronuclei formation (genotoxicity)

To quantify the percentage of micronuclei formation, cells were seeded and transfected as described above. Twenty four hours post-transfection (equivalent to 1-1.5 doubling time), cells were harvested and stained using an In Vitro MicroFlow® Kit (Litron Lab., NY). The staining was performed according to the manufacturer's protocol with several modifications. Briefly, cells were detached, transferred into a microfuge tube, and centrifuged for 6 min at 300g. The supernatant was removed and the pellet was placed on ice for 20 min. Next, ADSCs were resuspended in 50 µL of ethidium monoazide (EMA) solvent (Dye A). EMA is a DNA staining fluorescent dye that cannot pass through the cell membrane of live cells. As a result, it can only stain

the late apoptotic or dead cells helping to distinguish them from live cells. After 30 min of incubation with EMA, cells were washed by the Kit's wash buffer, lysed by lysis buffer, and treated with RNase enzyme. Cells were then exposed to SYTOX green fluorescent dye that stains all nuclei and micronuclei. The lysis and SYTOX green staining process were performed at 37 °C while samples were protected from light. After staining, samples were analyzed by CytoFlex Flow Cytometer (Beckman Coulter, Brea, CA) using an optimized acquisition protocol according to the guideline of In Vitro Microflow® Kit (**Figures 1A-1G**). The detailed information about the gating protocol can be found elsewhere ²². Briefly, the process started by gating all events from side scatter vs. forward scatter plots (**Figure 1A**) and continued with the second plot in which the doublet nuclei were discriminated and excluded by FITC width vs. FITC area plot (**Figure 1B**). Next, the SYTOX Green positive events were selected (**Figure 1C**) and the two different dot plots represented in **Figures 1D and 1E** illustrate nuclei and micronuclei populations with the correct size and pattern. This excludes other interfering events, such as smaller fluorescent particles, green fluorescent protein aggregates, and stained plasmids or nanoparticles. **Figure 1F** shows exclusion of the EMA-positive events which originated from dead or late apoptotic cells. At this point, the number and percentage of micronuclei and nuclei shown in **Figure 1G** can be quantified. In general, micronuclei are defined as events showing 1/10 to 1/100 of the mean intensity of SYTOX Green fluorescence found in nuclei of viable (i.e. EMA-negative) cells. The gating protocols were kept unchanged during the analysis and for each sample, at least 1000 EMA negative nuclei events were counted. Accordingly, %MN= Number of MN/ Number of viable nuclei × 100. The data are presented as mean±s.d. (n=4).

Determination of vectors' impact on gene regulation (microarray analysis)

The effects of vectors on the expression of 84 genes associated with cell growth regulation were analyzed by using the Human Genes RT² Profiler™ PCR Array (Qiagen, MD, US). The names of the tested genes are as follows: SERPINB5, MYCN, ABL1, AKT1, APC, ATM, BAX, BCL2, BCL2L1, BCR, BRCA1, BRCA2, CASP8, CCND1, CDH1, CDK4, CDKN1A, CDKN2A, CDKN2B, CDKN3, CTNNB1, E2F1, EGF, ELK1, ERBB2, ESR1, ETS1, FHIT, FOS, FOXD3, HGF, HIC1, HRAS, IGF2R, JAK2, JUN, JUNB, JUND, KIT, KITLG, KRAS, MCL1, MDM2, MEN1, MET, MGMT, MLH1, MOS, MYB, MYC, NF1, NF2, NFKB1,

NFKBIA, NRAS, PIK3C2A, PIK3CA, PML, PRKCA, RAF1, RARA, RASSF1, RB1, REL, RET, ROS1, RUNX1, RUNX3, S100A4, SH3PXD2A, SMAD4, SRC, STAT3, STK11, TGFB1, TNF, TP53, TP73, TSC1, VHL, WT1, WWOX, XRCC1, ZHX2. ADSCs were seeded in the 96-well plates at the density of 6,000 cells per well and then transfected with selected DBVs. For adenovirus, ADSCs were seeded in a 6-well plate at the density of 100,000 cells per well and incubated for twenty four hours. Cells were transduced by Ad-GFP at MOI of 5,000 and 50,000 in a serum free media (ADSC basal media). Four hours post transduction, the media was removed and replaced with full growth media. Forty eight hours after, ADSCs were collected and the GFP positive cells were separated from the general population by the Moflo XDP Cell Sorter (Beckman Coulter, CA, US). The GFP positive cells were reseeded in a 6-well plate at the density of 45,000 cells per well and allowed to fully recover from the process until they reached 80% confluency (4 to 8 days). The mRNAs of transfected and untransfected cells were extracted by RNeasy Mini Kit (Qiagen, MD, US). The genome DNA was eliminated by the RNase-Free DNase Set (Qiagen, MD, US) during the RNA isolation process. The concentration and purity of mRNA were evaluated by measuring the absorbance at wavelength 260 nm and 280 nm. Concurrently, an agarose gel (1%) electrophoresis was performed to examine the mRNA integrity. Then, 0.5 µg of mRNA was reverse transcribed into complementary DNA (cDNA) by RT² First Strand Kit (Qiagen, MD, US). The cDNA of each sample with RT² SYBR Green ROX PCR Master mix (Qiagen, MD, US) was loaded onto the PCR array. The real-time PCR reactions were performed using StepOnePlus™ Real-Time PCR System (Thermo Fisher Scientific, MA, US). The program settings on temperature cycling were followed as instructed by the manufacturer. The raw data and gene profile expression was analyzed by “Double Delta Ct Method” using the manufacturer’s online software tool (<http://pcrdataanalysis.sabiosciences.com/pcr/arrayanalysis.php>). Here, five housekeeping genes (ACTB, B2M, GAPDH, HPRT1 and RPLP0) were used as controls. All experiments were performed in triplicates while a two-fold change in RNA levels served as the cut-off point (*, $p < 0.05$).

Evaluation of vectors’ impact on ADSC differentiation

To examine whether the transfection process had a negative impact on ADSC differentiation, the cells were induced to differentiate into adipocytes. ADSCs were

transfected with the developed vectors and after 48 h post-transfection, were harvested and sorted by flow cytometry according to their respective GFP expression. The sorted GFP-positive cells were then reseeded in 96-well plates at the density of 10,000 cells per well and incubated at 37 °C with ADSC full media. The media was changed every other day until cells reached maximum confluency. At this point, the ADSC full growth media was removed and replaced with adipogenesis differentiation media cocktail (Lonza Inc., NJ) containing 1 μ M dexamethasone, 0.5 mM isobutyl-methylxanthine (IBMX), 1 μ g/ml insulin, and 100 μ M indomethacin. The differentiation media was gently replaced every 3 days for 12 days. Next, ADSCs were washed by PBS and stained with AdipoRedTM fluorescent staining reagent (Lonza Inc., NJ). The production of intracellular oil vesicles was visualized by fluorescent microscopy (Olympus Co., USA) and the percentage of differentiated ADSCs was quantified by flow cytometry. Untransfected ADSCs were subjected to the same differentiation protocol and used as the positive control. The data are presented as mean $\pm$ s.d. (n=3).

Results and Discussion

The concept of engineering recombinant fusion vectors for gene delivery dates back to the late 1990s ²³. However, due to significant technical difficulties related to recombinant production of highly cationic vectors and formulation of stable and efficient nanoparticles, recombinant fusion vectors remained ineffective for more than a decade (reviewed in reference ²⁴). Since 2006, we have worked to overcome these challenges and through the use of several innovative approaches, have successfully created highly efficient targeted fusion vectors for various gene delivery applications including the targeting of different cancer cell types or compartments within the cell ^{25, 26, 27, 28, 29}. We have previously reported the structure of a DBV composed of four repeating units of histone H2A (H4) for efficient condensation of DNA into nanosize particles and a pH-dependent fusogenic peptide (GALA) for disruption of endosome membranes facilitating the escape of cargo into the cytoplasm. Due to the presence of an inherent nuclear localization signal in the structure of histone H2A ³⁰, the vector also uses microtubules to actively transport the nanoparticles towards the cell nuclear membrane ²⁰. To make the above mentioned vector (i.e., H4G) suitable for targeted gene transfer to HER2 positive mammalian cells (e.g., SKOV-3), a HER2 targeting affibody was fused with the vector sequence (**Figure 2A**) ²⁹. We have demonstrated

that this vector can target and transfect SKOV-3 cancer cells above a 95% efficiency³¹. To make this vector suitable for transfection of stem cells, a primary cell line without HER2 expression, we replaced the HER2 targeting peptide in the vector structure with the VEGFR1 targeting peptides and cell penetrating peptides (**Figure 2B**). The sequences of the VEGFR targeting peptides (agonist and antagonist) are previously reported and also shown in **Table 1**^{32,33}. To achieve the objective, we first genetically engineered the DBVs as described below.

Genetic engineering and production of fusion vectors

Considering that the above mentioned DBVs are highly cationic, their production in *E. coli* expression systems is marred by low expression yield which complicates the possibility of obtaining pure products. For example, SlyD and ArnA endogenous *E. coli* proteins are considered the major culprits that co-purify with the low-expressing DBVs during metal affinity chromatography³⁴. The inability to produce highly pure vectors and in sufficient quantities are among the major obstacles that significantly hampered the progress of this field of research. To overcome this obstacle, we developed and previously reported an optimized protocol for the recombinant production of cationic fusion vectors²¹. Using this protocol, all constructs were expressed in an *E. coli* expression system, purified by Ni-NTA affinity columns and analyzed for purity by SDS-PAGE. The results of this study showed that by using *E. coli* BL21(DE3) LOBSTR strain in combination with the developed stringent expression and Ni-NTA purification methods, highly pure products in one purification step (>95% purity) could be obtained (**Figure 7**). In the next step, we examined the ability of the vectors to condense pDNA into nanosize particles.

Nanoparticle formation and particle size, charge and shape analysis

We performed a peptide desalting step before forming nanoparticles. The desalting step is important as it helps remove the excess ions from the system. This procedure stabilizes the nanoparticles' diameters by minimizing the possibility of inter-particle salt bridge formation and ensuing aggregation. In addition, presence of excess ions in the media interferes with the electrostatic interactions between cationic residues in the vector sequence and anionic residues in the pDNA resulting in formation of pseudo-condensed DNA. Therefore, we performed a desalting step to

significantly reduce the ionic strength of DBV solution which brought down the solution conductivity from 33.7 ± 0.6 mS/cm to 0.45 ± 0.01 mS/cm without compromising solubility. We have previously shown that this level of conductivity is equivalent to that of a 5mM NaCl solution³⁵. The low conductivity value allows for efficient condensation of pDNA by DBVs and production of stable nanoparticles. The purified/desalted DBVs were then complexed with pDNA (i.e., pEGFP) at various N:P ratios and characterized in terms of size, surface charge and morphology. The results of this study showed that all DBVs were able to condense pEGFP into floccus, spherical particles with sizes of less than 100nm and surface charges below +15mV (**Figure 2C-E**). The analysis of data showed that all nanoparticles beyond the N:P 4 ratio were statistically the same in terms of size and charge ($p > 0.05$). Maintaining the nanoparticle surface charge below +20mV is critically important as it has been shown that the potential for genetic aberrations (genotoxicity) increases when the surface charge goes beyond +20mV³⁶. This goal could be reached due to the unique structure of the histone H2A in the DBV sequence. Histone H2A is a basic peptide with the amino acid sequence of SGRGKQGKARAKAKTRSSRAGLQFPVGRVHRLLRKG (SEQ ID NO: 248). Even though only 33% of amino acid residues in the Histone H2A sequence are cationic, it can efficiently condense pDNA into nanosize particles. This efficiency in DNA condensation is attributed to the alpha-helix secondary structure at the H2A N-terminal domain³⁰. As a result, less amount of vector is needed to efficiently condense pDNA into compact nanoparticles.

The commercial vectors used in this study were able to generate nanoparticles with surface charges ranging from +30mV to +80mV (**Figure 2F**). While this high surface charge guarantees production of stable nanoparticles even in the presence of serum, there remains significant potential for toxicity in primary mammalian cell lines such as stem cells.

Characterization of ADSCs in terms of cell cycle and VEGFR-1 expression

Before cell transfection, we performed a cell cycle analysis to determine the optimum time for transfection of ADSCs since non-viral vectors can mainly transfect dividing cells that are in the mitotic state. For this purpose, we analyzed the cell cycle status of the ADSCs from 16 to 28 hours post-seeding. This study revealed that the optimum time for transfecting ADSCs is 24 hours post-seeding because at this point,

significant numbers of ADSCs are in G2-M phase where the nuclear membrane starts dissolving (**Figure 3A-B**). Furthermore, we characterized the ADSCs in terms of VEGFR-1 expression to confirm that this receptor is expressed on the surface of ADSCs in abundance. This is important since our targeted DBVs are expected to rely on these receptors for entry into the cells. The results of this study showed a very high expression of VEGFR-1 on the surface of the ADSCs (**Figure 3C**). The VEGFR-1 expression level in ADSCs appeared to be even higher than in A431 (human squamous carcinoma) cancer cells which are known to have high expression levels of VEGFR-1³⁸.

Evaluation of transfection efficiency, cell proliferation rate, morphology and membrane integrity

Learning from the studies mentioned above, we initiated the ADSC transfection studies. Therefore, we used the DBVs (N:P 5) to transfect ADSCs with pEGFP twenty-four hours post-cell seeding. As controls, we also transfected the ADSCs with commercial non-viral and viral vectors to help us better understand the efficiencies of current available vector technologies. Using fluorescent microscopy, we first qualitatively evaluated the transfection rates of the different vectors and noticed there were noticeable differences among the vectors' efficiencies (**Figures 8A, 8B and 9**). This prompted us to use flow cytometry in order to quantify the percentage of transfected cells in each group. For practical purposes and to assist in identifying the most efficient vector, we drew a line at 25% efficiency. This means that the constructs that could transfect ADSCs at rates higher than 25% were considered efficient. It is noteworthy that ADSCs are primary cells and are considered hard to transfect; unlike, easy to transfect cells such as HEK293 or HeLa (**Figure 10**). The results of this study demonstrated that the H4G and Vanta-H4G vectors carrying 0.4 and 0.5 μ g pEGFP were among the most efficient DBVs with Vanta-H4G surpassing 50% transfection efficiency (**Figure 4A**). A complementary cell transfection study using U87 glioblastoma, which does not express the VEGFR-1 receptor³⁹, confirmed the ability of Vanta-H4G to transfect VEGFR-1 positive ADSCs but not U87 cells (**Figure 11**). Among the non-viral commercial vectors, GeneIn™ carrying 0.2, 0.3 and 0.5 μ g of pEGFP was the most efficient (**Figures 4B**).

One curious observation was that we did not see significant cell transfection rates with the Pep1-H4G and MPG-H4G. Muller et al. (2012), have previously

emphasized that not only does the type of cell line determine the cell penetration efficacy of the Pep1 and MPG peptides, but also the chemical nature of the peptides' C-terminus¹⁶. This means that either the ADSC is not a suitable cell model for transfection by Pep1 and MPG, or the proposed sequences may not have been designed in proper order. If the former is true, then the MPG-H4G and Pep1-H4G vectors should be able to effectively transfect other mammalian cell lines. To examine this hypothesis, we selected Pep1-H4G carrying 0.5 μ g pEGFP as an example along with a model fast growing cancer cell line such as SKOV-3 (ovarian cancer). Interestingly, the results showed that Pep1-H4G could transfect SKOV-3 cells up to 35% (**Figure 12**). This rate of transfection efficiency is far more than what we observed in ADSCs (i.e., <5%) (**Figure 4A**). This shows that the cell type played a significant role in limiting the efficiency of Pep1-H4G and MPG-H4G. To examine whether the positing of Pep1 and MPG at the C-terminus would make a difference, we genetically engineered H4G-Pep1 and H4G-MPG. Unfortunately, due to the co-expression and co-purification of prematurely terminated H4G-Pep1 and H4G-MPG peptide sequences, we could not obtain pure products in order to test the latter hypothesis. Nonetheless, our data shows that ADSCs may not be easily transfected with vectors that are decorated with Pep1 and MPG cell penetrating peptides (CPPs) and perhaps other types of CPPs could produce better results.

Another interesting observation was the inability of the Vago-H4G to efficiently transfect ADSCs. We believe that this could be due to the presence of the three lysine residues in the Vago sequence, especially presence of one at the N-terminus and one at the C-terminus. Cationic charged lysine residues could interact with pDNA inhibiting the protrusion of the VEGFR-1 agonist peptide from the surface of the nanoparticles rendering them unavailable for receptor binding. Considering that a non-cationic high affinity VEGFR-1 agonist is not developed yet, this would be an interesting venue to pursue in order to design the next generation of VEGFR-1 targeted DBVs for stem cell transfection.

Another unexpected observation was the need to use Ad-GFP at extremely high MOIs (>5K) in order to transfect ADSCs beyond 50% (**Figure 4C**). Adenoviral vectors are known to be very efficient in transfecting mammalian cells and can render beyond 50% efficiency at MOIs as low as 50⁴⁰. The fact that such high numbers of adenoviral particles are needed to achieve a high transfection efficiency indicates that the coxsackie adenovirus receptor (CAR) is not expressed in abundance on the surface

of ADSCs. Consequently, the downside of using adenoviral vectors at such high MOIs to transfect stem cells is not only the elevated costs, but also the presence of large amounts of viral proteins inside the stem cells which could induce immune response after reintroduction into a patient's body.

In the next step, we evaluated the impact of the vectors on ADSC proliferation rate. Considering that the formazan based assays such as MTT, MTS, and WST-1 possess potential for side reactions and ambiguities ⁴¹, we only eliminated the vectors from the pool that had more than a 25% negative impact on cell proliferation rate. We set this level of tolerance for screening purposes as well as to narrow down the field for more in-depth toxicity studies as later described. The cell proliferation rate study showed that only H4G (0.4 and 0.5 μ g pEGFP) and Vanta-H4G (0.4 μ g pEGFP) had more than 25% efficiencies and acceptable negative impacts on ADSC proliferation rate (i.e., <25%). GeneIn™, carrying 0.2 μ g of pEGFP, appeared to be the only viable vector that met our strict efficiency/toxicity guideline for transfecting ADSCs (**Figures 4D and E**). The adenoviral vector rather than showing negative impact on cell proliferation rates at high MOIs, it actually induced cell proliferation (**Figure 4F**). This could be explained by the fact that toxic substances in low concentrations occasionally stimulate cellular metabolic activity. In order to protect themselves from such toxicities, cells upregulate their enzymatic activities at the initial stages. Cells will start to die when the concentration of toxic substances, in this case AD-GFP, exceeds their level of tolerance.

We further characterized the screened and selected vectors from the studies mentioned above in terms of their impact on the cell membrane integrity during transfection. Considering the associated errors with the method and the ability of the cells to recover from the assault, again we set our level of tolerance at 25% negative impact on cell membrane integrity for screening purposes. Given that the non-targeted, positively charged H4G and GeneIn™ vectors enter the cells through binding and temporarily disrupting the cell membranes, it is important to investigate whether the cellular entry process results in significant damage to the membrane integrity. Here, we performed an LDH release assay which showed both H4G and Vanta-H4G having minimal impact on the ADSCs membrane integrity (**Figure 4G**). This minimal disturbance could be attributed to the low surface positive charge associated with nanoparticles formed through complexation of pEGFP with either H4G or Vanta-H4G. The substantial release of LDH enzyme after transfection of the

cells with GeneIn™ was somewhat expected as it bears a significantly high surface positive charge (**Figure 2F**).

At this stage, we also carefully examined the morphology of the ADSCs by a light microscope to ensure that the selected vectors did not induce significant changes to the cells' morphology. The observed pictures clearly show the deleterious effects of certain vector concentrations on the ADSCs, resulting in shrinkage and lysis of the cells. The cell morphology study also confirmed that our selected vectors did not alter the morphology of ADSCs as witnessed by the maintenance of their spindle-like shapes (**Figures 13 and 14**).

Evaluation of vectors' impact on micronuclei formation (genotoxicity) and gene dysregulation

In addition to the tests that evaluate the somatic damages to stem cells during and post transfection such as LDH release and cell proliferation assays, it is also critically important to look at the potential aberrations to the genome of the stem cells. In recent years, the need for the evaluation of genotoxicity of gene delivery systems has been highlighted in several published articles^{42, 43, 44}. Furthermore, US Food and Drug Administration and International Conference on Harmonization in a published online record (<https://www.fda.gov/downloads/drugs/guidances/ucm074931.pdf>), recommend researchers and industries to report a geno-safety profile of pharmaceutical formulation ingredients including nanocarriers⁴⁵. Characterizing micronuclei formation requires an in vitro assay that uses the generation of nuclear blebs and micronuclei in the cytoplasm of interphase cells as an approximation of the cell's genetic instability upon exposure to the reagents. Here, we adapted a flow cytometry based method that could help quantitatively measure the micronuclei formation in transfected cells. From the efficiency/toxicity studies shown above, we identified that the H4G (0.4 and 0.5µg pDNA) and Vanta-H4G (0.4µg pDNA) are the most suitable vectors for ADSC transfection. To examine their genotoxicity, ADSCs were transfected with these vectors and the percentages of micronuclei formation were determined. For the negative control, we used the H4G vector carrying 0.3µg pDNA and as the positive control, we used GeneIn™ carrying 0.5µg of pDNA. Ad-GFP (MOI: 5K and 50K), which bears a negative surface charge and transfects ADSCs via CAR, was also used as negative controls. The selection of the vector controls was based on the data presented in **Figure 4** which shows high toxicity for

GeneIn™ (0.5µg pDNA) and low toxicity for H4G (0.3µg pDNA) and Ad-GFP. Bryce et al. (2007), have previously established that a genotoxic substance would increase the percentage of micronuclei by at least three folds higher than the untreated control group ²². Based on this guideline, the results of this study showed that H4G (0.5µg pDNA) and GeneIn™ (0.5µg pDNA) produced significantly higher numbers of micronuclei in transfected ADSCs. Therefore, both vectors were considered genotoxic (*t-test, $p < 0.05$), while all other vectors were non-genotoxic ($p > 0.05$) (**Figure 5A**). The result of this study helped us eliminate the H4G (0.5µg) from the selected vectors despite the fact that the LDH release assay, WST-1 assay, and cell morphology studies had shown that it was acceptable. It was also very interesting to see that the GeneIn™ carrying 0.2µg pDNA did not show any significant genotoxicity despite the previous observations that showed it had some somatic toxicity.

We further examined the effect of DBVs on up/down regulation of genes in ADSCs. Ideally, it is preferred not to observe any significant dysregulation of the host's endogenous genes. Post transfection, we sorted out the strong GFP-positive cells, reseeded, and performed a PCR microarray assay to examine the extent of gene dysregulation in transfected cells. As shown in **Figure 5B**, we did not observe any significant change in the genetic pathways of the cells that were transfected with the H4G vector carrying 0.3µg of pDNA. ADSCs that were transfected with H4G (0.4µg pDNA) showed dysregulation in three genes out of the eighty four tested. Interestingly, in this group, the S100A4 tumor suppressor gene was upregulated whereas the FOS/TNF gene pathway was downregulated. The FOS gene is a transcription factor, whose expression is most often positively correlated with TNF expression. It has been reported that the up-regulation of the FOS/TNF pathway could increase the probability of mesenchymal stem cell transformation towards malignancy ⁴⁶. Considering that there is no negative report on downregulation of FOS/TNF pathway, it may be safe to conclude that such downregulation may reduce the probability of malignant transformation. Similar to the cells in the H4G treated group, cells that were transfected with Vanta-H4G (0.4µg pDNA), also exhibited down-regulation of the FOS/TNF pathway. Additionally, it was observed that another signaling pathway; i.e., KITLG/KIT, was up-regulated in this group. Both VEGF/VEGFR and KITLG/KIT signaling pathways play an essential role in stem cell hematopoiesis and new blood vessel formation ^{47, 48}. Reports also indicate that these pathways share multiple gene cross-talks during signal transduction ^{48, 49}. Since the

Vanta-H4G complex competes with VEGF in media for VEGFR-1 binding, the ADSC turns on the alternative KITLG/KIT pathway to adapt to the change. The upregulation of the KITLG/KIT pathway is genetic level evidence supporting the cellular entry of the Vanta-H4G/pDNA nanoparticles through VEGFR binding. The PCR microarray data also showed that few genes were dysregulated within the adenovirus-transduced groups and there is a direct correlation between the MOI and number of dysregulated genes. Furthermore, it was noticeable that in addition to the upregulated BCL2 gene (anti-apoptotic), the genes that promote cell division and growth were down-regulated (HGF, KIT, MYB). The combination of these changes point to potential toxicity of the Ad-GFP to stem cells at such high MOIs. This observation provides genetic level evidence in support of our discussion for **Figure 4F**. Overall, the results of genotoxicity assay and microarray analysis shows that none of the selected vectors through the screening process had a significant detrimental effect on the genome of the transfected stem cells validating our approach.

Evaluation of vectors' impact on stem cell differentiation

After learning that the H4G (0.3 and 0.4 μ g pDNA) and Vanta-H4G (0.4 μ g pDNA) groups were not genotoxic, we examined whether they, by any means, negatively affected the ADSCs potential for differentiation. This is important because the objective for the significant number of stem cell engineering studies is to ultimately differentiate them into a tissue. For this purpose, we first transfected the ADSCs with the above mentioned vectors using pEGFP, sorted out the ADSCs that were strongly positive in GFP expression, and then reseeded for differentiation. Here, we sorted the strong GFP-positive cells because these cells received the maximum number of the vector/pDNA nanocomplexes; thereby, demonstrating a higher probability of negative effects. The results of this study showed that none of the vectors negatively affected the ADSCs and the transfected cells could differentiate into adipocytes similar to that of the untreated cells (t-test, $p>0.05$) (**Figure 6**). These observations demonstrate that the developed DBVs could indeed be used for efficient and safe genetic modification of ADSCs without any negative effect on their differentiation into the desired tissue.

Conclusions

The goal of this research was to develop a vector that is not only efficient in stem cell transfection, but also has the ability to maintain such efficiencies without inducing somatic or genetic toxicity. Overall, the efficiency and toxicity data show that among the developed DBVs, the VEGFR-1 targeted Vanta-H4G is not only the most efficient vector for ADSC transfection (~50% efficiency), but also one without any significant negative impact on physical integrity, metabolic activity, genetic composition, and cell differentiation. Considering that the adenoviral vector which is also a targeted vector, could efficiently transfect stem cells with minimal short-term toxicity, it may be safe to conclude that the best approach towards transfecting stem cells efficiently and safely is through receptor targeting rather than entry through a cellular membrane. The developed Vanta-H4G could potentially be used to transfect any mammalian cell line that overexpresses VEGFR-1.

In Example 1, the terms “vector” or “fusion vector” are used interchangeably with “fusion polypeptide”.

EXAMPLE 2

We seeded ADSCs, BMSCs, and NSCs in 96-well plates and transfected them with Vanta-H4G in complexation with 0.4 μ g of pEGFP. The results of this study showed that Vanta-H4G can transfect all three cell lines with high efficiency confirming its broad application in stem cell engineering (**Figure 15**).

Transfection of ADSCs, BMSCs and NSCs by using Vanta-H4G in complexation with 0.4 μ g of pEGFP. This figure shows that Vanta-H4G can transfect all three cell lines with high transfection efficiency, ranging from, e.g., about 30% to about 50% (such as about 30%, about 37%, about 50%, etc.).

We also examined the efficiency of “Lipofectamine Stem” and “Lipofectamine 3000” (ThermoFisher Scientific) for transfecting stem cells.

Transfection of ADSCs by Lipofectamine Stem

Following the vendor’s protocol, ADSCs were seeded at the density of 6000 cells per well (n=3) in a 96-well plate. 100 ng pEGFP was complexed with 0.4 μ l

Reagent in Opti-MEM media. Cells were transfected and observed under fluorescent microscope 48 hours post transfection. The results of this study showed that Lipofectamine Stem could not transfect stem cells efficiently. Based on the fluorescent microscopy images, the transfection efficiency was estimated to be below 5% and was not analyzed further due to its very low efficiency.

Transfection of ADSCs by Lipofectamine 3000

Lipofectamine 3000 was purchased from ThermoFisher Scientific. Following vendor's protocol, the following numbers of ADSCs were seeded in a 96-well plate: 10,000/well; 20,000/well; and 40,000/well. Based on the vendor's recommendation, 100ng of plasmid DNA (pEGFP) was complexed with Lipofectamine 3000 and used to transfect ADSCs. The percentages of transfected ADSCs as well as cell viability were determined by flow cytometry. As shown in Figures 16A-16B, the highest rate of transfection efficiency was observed when 10,000 cells were seeded in a 96-well plate and transfected with 100 ng of pEGFP. The transfection efficiency ranged from about 0.8% to about 8%. These results show that Lipofectamine 3000 is not only inefficient but also toxic and not a suitable vector for stem cell transfection.

Recently, the leading commercial non-viral vectors have been shown to be genotoxic. Nomani A., Chen X. and Hatefi A., Evaluation of genotoxicity and mutagenic effects of vector/DNA nanocomplexes in transfected mesenchymal stem cells by flow cytometry, *Acta Biomaterialia* 74 (2018) 236–246.

EXAMPLE 3

Genetic engineering and production of recombinant vectors

We use standard genetic engineering techniques similar to our previous reports in order to clone, express, and purify the DBVs^{18, 19, 20}. In brief, the genes encoding IGFR-H4G, FGFR-H4G, EGFR-H4G, PDGFR-H4G, INTEGRIN-H4G with 6x-histidine tag at the c-terminus, were designed and are then chemically synthesized. The corresponding amino acid sequences of the vectors are shown in **Table 1**. The genes are restriction digested by NdeI and XhoI enzymes and cloned into a pET21b bacterial expression vector (Novagen®, EMD Millipore, MA, US). The fidelity of each gene sequence to the original design is verified by DNA sequencing.

To express the vectors, the expression plasmids are transformed into the LOBSTR BL21(DE3) E. coli expression strain (Kerafast Inc., MA, US). The protein

expression protocol is optimized for the production of highly cationic vectors in *E. coli* as described previously by our group ²¹. In brief, one colony is picked from the LB agar plate and inoculated overnight in a 5ml Miller's LB media supplemented with 100 µg/mL carbenicillin (Sigma-Aldrich, MO, US). The next day, the starter culture is transferred into 500mL terrific broth (TB) supplemented with 100 µg/mL carbenicillin. The culture is incubated at 37°C under vigorous shaking until the OD₆₀₀ reached 0.4-0.6. To induce protein expression, isopropyl β-D-1-thiogalactopyranoside (IPTG, Teknova, CA, US) is added to the culture at the final concentration of 1 mM. After 2.5-4 hours of induction, the *E. Coli* pellet is collected by centrifugation at 5000 g, weighed and stored in -80°C freezer.

To purify the peptides, a method based on Ni-NTA immobilized metal affinity chromatography (QIAGEN, MD, US) is developed. A lysis buffer is formulated beforehand, containing 8 M urea, 2 M NaCl, 100 mM NaH₂PO₄, 10 mM Tris, 1% (v/v) Triton X-100, and 10 mM imidazole. The bacterial pellet is lysed by the lysis buffer (5 mL buffer per 1 gram pellet) for one hour at room temperature under vigorous stirring. Then, the supernatant is collected by centrifuging the slurry for one hour, at 20,000 rpm, 4°C. Meanwhile, the Ni-NTA resin is washed with 10 mL distilled/deionized water and preconditioned with 2 mL of lysis buffer. Afterwards, the supernatant is mixed with the preconditioned Ni-NTA resin and incubated on ice with gentle shaking. After one hour of incubation, the mixture is diluted with 3 times lysis buffer and passed through a 10-mL polypropylene filter column (Bio-Rad Inc., US) by vacuum driven filtration. The column is washed by 100 mL of lysis buffer followed by 50 mL wash buffer (5 M Urea, 1.5 M NaCl, 100 mM NaH₂PO₄, 10 mM Tris and 40 mM imidazole). Finally, the purified vector is eluted by 5 mL of elution buffer (3 M Urea, 0.5 M NaCl, 100 mM NaH₂PO₄, 10 mM Tris and 300 mM imidazole) and collected in 500 µL fractions. The concentration of the peptide within each fraction is measured by the Nanodrop 2000 spectrophotometer (Thermo Fisher Scientific, US). The purity of each peptide is determined by SDS-PAGE analysis.

Peptide desalting and preparation of stock solution

To desalt, a disposable PD-10 desalting column with Sephadex G-25 resin (GE Healthcare's Life Sciences, MA, US) is preconditioned with 15 mL of 10mM L-Glu/ L-Arg buffer (pH 5.8-6.0). Then, each purified peptide fraction is loaded onto the column and eluted with additional 5mL of buffer driven by gravity. The

concentration of each peptide is measured by Nanodrop 2000 spectrophotometer (Thermo Fisher Scientific, US) using the molecular weight and corresponding extinction coefficient as calculated by the ProtParam tool from the ExPASy Bioinformatics Resource Portal (<http://web.expasy.org/protparam/>). The conductivity of the peptide solution is determined by Laser Doppler Velocimetry using Malvern Nano-ZS Zetasizer (Malvern Instruments, UK).

Nanoparticle formation and particle size, charge and shape analysis

The DNA/peptides nanoparticles are formed by the Flash Mixing method¹⁹. In brief, the required amount of each peptide to condense 1 μ g of pEGFP plasmid DNA (pDNA) at various N:P ratios is calculated beforehand. Then, pEGFP is diluted to a volume of 50 μ L using distilled/deionized water. Concurrently, predetermined amount of each peptide is diluted to 50 μ L volume using distilled/deionized water and placed in another microfuge tube. The peptide solution is added to the pDNA solution rapidly and flash mixed. After 5-10 minutes of incubation, the nanoparticle size is measured by Dynamic Light Scattering and surface charge by Laser Doppler Velocimetry using Malvern Nano-ZS Zetasizer (Malvern Instruments, UK). To make nanoparticles with the commercial transfection reagents including GeneIn™ (MTI-GlobalStem, MD, US), Lipofectamine® LTX with Plus (Thermo Fisher Scientific, MA, US), Attractene (QIAGEN, MD, US), FuGENE® HD (Promega Corporation, WI, US) and jetPRIME® (Polyplus-transfection, France), we follow the corresponding manufacturers' protocols. Once nanoparticles are formed, the surface charges are measured in 5mM NaCl solution. The data are presented as mean $\pm$ s.d. (n=3). Each mean is the average of 15 measurements while n represents the number of independent batches prepared for the measurements.

To study the morphology of the nanoparticles, transmission electron microscopy (TEM) is utilized¹⁹. First, nanoparticles are formed and then one drop of the mixture is loaded onto a carbon type B coated copper grid. As soon as the sample dry on the surface, the solution of 1% sodium phosphotungstate is added to stain the nanoparticles. The detailed images are recorded by 1200EX electron microscope (JEOL, US).

ADSC, BMSC, NSC Characterization

The ADSCs, BMSCs (Lonza, NJ, US) and NSCs (ATCC, VA, US) were cultured in their corresponding growth medium which contains the basal media and the necessary supplements for proliferation of human mesenchymal and neural stem cells.

ADSCs, BMSCs and NSCs were characterized for cell cycle and VEGFR-1, IGFR-1, EGFR, and FGFR-2 expression by flow cytometry. The cell cycle study was performed using propidium iodide (PI) DNA staining protocol. In brief, cells were seeded in 96-well plates at the density of 6000 cells per well. After 16, 20, 24, 26, 28 hours of incubation with growth medium at 37 °C and 5% CO₂, cells were detached through trypsinization. Cells were then fixed by 70% cold ethanol. After 1 hour, cells were collected by centrifugation, re-suspended in PBS and treated with 0.5 mg/mL Rnase A. Finally, cells were stained by PI (10 µg/mL) for 1 hour. The cell cycle distribution was determined by flow cytometry (Beckman Coulter GALLIOS Cytometer, CA, US).

To determine the level of VEGFR-1 expression, ADSCs were detached by Accutase® Cell Detachment Solution (Innovative Cell Technologies, CA, US). Cells were fixed by 4% formaldehyde solution in PBS and then permeabilized by 0.1% Tween 20/PBS solution. Cells were washed and re-suspended in the staining buffer (0.3M glycine and 10% normal goat serum in PBS solution). 2 µL of Anti-VEGFR-1 rabbit monoclonal antibody conjugated with Alexa Fluor® 488 (abcam, MA, US) was added to each sample. Rabbit monoclonal IgG conjugated with Alexa Fluor® 488 (abcam, MA, US) was used as isotype control. Samples were incubated overnight at 4°C and then washed extensively with PBS. The expression level of VEGFR-1 was determined by flow cytometry (Beckman Coulter GALLIOS Cytometer, CA, US). The unstained sample was also included as a negative control.

To examine the potential application of the developed vector in transfecting bone marrow-derived stem cells (BMSCs) and neural stem cells (NSCs), we characterized these cell lines in terms of VEGFR-1 expression. In addition, we evaluated the expression levels of other growth factor receptors such as insulin-growth factor receptor-1 (IGFR-1), epidermal growth factor receptor (EGFR) and basic fibroblast growth factor receptor (FGFR-2). Using fluorescently labeled antibodies against these receptors, we labeled the cells and analyzed the expression of receptors by flow cytometry. For this experiment, stem cells were incubated with

Anti-VEGFR-1, Anti-IGFR-1, Anti-EGFR, and Anti-FGFR-2 monoclonal antibodies conjugated with Alexa Fluor® 488. Monoclonal IgG conjugated with Alexa Fluor® 488 was used as isotype control. The expression level of each receptor was determined by flow cytometry. The unstained sample was used as negative control. The results of this experiment showed that almost all ADSCs, BMSCs and NSCs express VEGFR-1, FGFR-2, EGFR, and IGFR-1 receptors. Although at different densities, these receptors are expressed in high copy numbers on the surfaces of these cell lines.

Evaluation of cell transfection efficiency

The day before transfection, ADSCs and BMSCs and NSCs are seeded in 96-well tissue culture plates at the densities of 6000, 6000 and 25,000 cells per well, respectively. In a microfuge tube, nanoparticles are prepared at various N:P ratios as described above in a total volume of 50 μ L and incubated for 5-10 minutes at room temperature. Each tube is further supplemented with 200 μ L of basal media (without serum), 1 μ M dexamethasone (Sigma-Aldrich, MO, US) and 1X ITS Liquid Media. A 100X ITS solution includes 1.0 mg/mL recombinant human insulin, 0.55 mg/mL human transferrin and 0.5 μ g/mL sodium selenite (Sigma-Aldrich, MO, US). Next, the old media in each well is removed and replaced with the 250 μ L nanoparticle mixture. Twenty-four hours post transfection, the media in each well is replaced with 200 μ L full growth media and the cells are allowed to grow for another twenty-four hours. The green fluorescent protein (GFP) expression is visualized and qualitatively evaluated by a fluorescent microscope (Olympus, FL, US). To quantify GFP expression and percent transfection, cells are trypsinized and analyzed by flow cytometry (Beckman Coulter CytoFLEX Cytometer, CA, US). The ratio of GFP positive cells to untransfected cells is calculated by Kaluza flow analysis software (Beckman Coulter, CA, US). The data are presented as mean $\pm$ s.d. (n=3).

Evaluation of vectors' impact on cell proliferation rate, membrane integrity and morphology

The impact of each vector on ADSC, BMSC and NSC proliferation rates is evaluated by the WST-1 cell proliferation assay. Cells are seeded in the 96-well plates. After twenty four hours of incubation, cells are transfected with vectors as described above. Forty eight hours post-transfection, the old media is replaced with

100 μ L of fresh media containing 10 μ L WST-1 reagent (1:10 dilution). After one hour of incubation at 37 °C / 5% CO₂, the absorbance of each well is measured by Infinite® M200 PRO NanoQuant microplate reader (Tecan, Switzerland) at 440nm/600nm. The absorbance of each treatment is normalized to the negative control (untreated cells) to measure the percentage of cell viability.

To evaluate the impact of each vector on cell membrane integrity, a lactate dehydrogenase (LDH) release assay (Roche, IN, US) is performed using manufacturer's kit and protocol. In brief, cells were seeded and transfected as described above. Cells are incubated in stem cell basal media for 48 hours post transfection since the LDH reagent is not compatible with serum. Media in each well is removed and centrifuged at 250g for 5 minutes to pellet the debris. The supernatants are collected into a 96-well plate with 100 μ L per well. Next, 100 μ L LDH reagent is added into each well and incubated for 30 minutes at room temperature. The absorbance at wavelengths of 490nm and 600nm is measured using Infinite® M200 PRO NanoQuant (Tecan, Switzerland) microplate reader. The media, without contacting any cells, serves as the background control. The media from the untransfected cells is used as the negative control (spontaneous LDH release). The media from the cells incubated with the 2% Triton X-100 serves as the positive control (maximum LDH release). After subtracting the background control, the percentage of impact on membrane integrity is calculated as follows: %membrane integrity= (Positive-Treatment)/ (Positive-Negative) $\times$ 100. The data are presented as mean $\pm$ s.d. (n=3).

The morphology of stem cells before and after transfection is studied by using phase-contrast microscopy (Olympus, FL, US).

Evaluation of vectors' impact on micronuclei formation (genotoxicity)

To quantify the percentage of micronuclei formation, cells are seeded and transfected as described above. Twenty four hours post-transfection (equivalent to 1-1.5 doubling time), cells are harvested and stained using an In Vitro MicroFlow® Kit (Litron Lab., NY). The staining is performed according to the manufacturer's protocol with several modifications. Briefly, cells are detached, transferred into a microfuge tube, and centrifuged for 6 min at 300g. The supernatant is removed and the pellet is placed on ice for 20 min. Next, cells are resuspended in 50 μ L of ethidium monoazide (EMA) solvent (Dye A). EMA is a DNA staining fluorescent dye that cannot pass

through the cell membrane of live cells. As a result, it can only stain the late apoptotic or dead cells helping to distinguish them from live cells. After 30 min of incubation with EMA, cells are washed by the Kit's wash buffer, lysed by lysis buffer, and treated with RNase enzyme. Cells are then exposed to SYTOX green fluorescent dye that stains all nuclei and micronuclei. The lysis and SYTOX green staining process is performed at 37 °C while samples were protected from light. After staining, samples are analyzed by CytoFlex Flow Cytometer (Beckman Coulter, Brea, CA) using an optimized acquisition protocol according to the guideline of In Vitro Microflow® Kit. The detailed information about the gating protocol can be found elsewhere²². Briefly, the process starts by gating all events from side scatter vs. forward scatter plots and continues with the second plot in which the doublet nuclei are discriminated and excluded by FITC width vs. FITC area plot. Next, the SYTOX Green positive events are selected. This excludes other interfering events, such as smaller fluorescent particles, green fluorescent protein aggregates, and stained plasmids or nanoparticles. In general, micronuclei are defined as events showing 1/10 to 1/100 of the mean intensity of SYTOX Green fluorescence found in nuclei of viable (i.e. EMA-negative) cells. The gating protocols are kept unchanged during the analysis and for each sample, at least 1000 EMA negative nuclei events are counted. Accordingly, %MN= Number of MN/ Number of viable nuclei × 100. The data are presented as mean±s.d. (n=4).

Determination of vectors' impact on gene regulation (microarray analysis)

The effects of vectors on the expression of 84 genes associated with cell growth regulation are analyzed by using the Human Genes RT² Profiler™ PCR Array (Qiagen, MD, US). The names of the tested genes are as follows: SERPINB5, MYCN, ABL1, AKT1, APC, ATM, BAX, BCL2, BCL2L1, BCR, BRCA1, BRCA2, CASP8, CCND1, CDH1, CDK4, CDKN1A, CDKN2A, CDKN2B, CDKN3, CTNNB1, E2F1, EGF, ELK1, ERBB2, ESR1, ETS1, FHIT, FOS, FOXD3, HGF, HIC1, HRAS, IGF2R, JAK2, JUN, JUNB, JUND, KIT, KITLG, KRAS, MCL1, MDM2, MEN1, MET, MGMT, MLH1, MOS, MYB, MYC, NFI, NF2, NFKB1, NFKBIA, NRAS, PIK3C2A, PIK3CA, PML, PRKCA, RAF1, RARA, RASSF1, RB1, REL, RET, ROS1, RUNX1, RUNX3, S100A4, SH3PXD2A, SMAD4, SRC, STAT3, STK11, TGFB1, TNF, TP53, TP73, TSC1, VHL, WT1, WWOX, XRCC1, ZHX2. Stem cells are seeded in the 96-well plates and then transfected with selected

DBVs. Four hours post transduction, the media is removed and replaced with full growth media. Forty eight hours after, cells are collected and the GFP positive cells are separated from the general population by the Moflo XDP Cell Sorter (Beckman Coulter, CA, US). The GFP positive cells are reseeded in a 6-well plate at the density of 45,000 cells per well and allowed to fully recover from the process until they reach 80% confluency (4 to 8 days). The mRNAs of transfected and untransfected cells are extracted by RNeasy Mini Kit (Qiagen, MD, US). The genome DNA is eliminated by the RNase-Free DNase Set (Qiagen, MD, US) during the RNA isolation process. The concentration and purity of mRNA are evaluated by measuring the absorbance at wavelength 260 nm and 280 nm. Concurrently, an agarose gel (1%) electrophoresis is performed to examine the mRNA integrity. Then, 0.5 µg of mRNA is reverse transcribed into complementary DNA (cDNA) by RT² First Strand Kit (Qiagen, MD, US). The cDNA of each sample with RT² SYBR Green ROX PCR Master mix (Qiagen, MD, US) is loaded onto the PCR array. The real-time PCR reactions are performed using StepOnePlus™ Real-Time PCR System (Thermo Fisher Scientific, MA, US). The program settings on temperature cycling are followed as instructed by the manufacturer. The raw data and gene profile expression is analyzed by "Double Delta Ct Method" using the manufacturer's online software tool (<http://pcrdataanalysis.sabiosciences.com/pcr/arrayanalysis.php>). Here, five housekeeping genes (ACTB, B2M, GAPDH, HPRT1 and RPLP0) are used as controls. All experiments are performed in triplicates while a two-fold change in RNA levels served as the cut-off point (*, $p < 0.05$).

Evaluation of vectors' impact on ADSC differentiation

To examine whether the transfection process has a negative impact on stem cell differentiation, the cells are induced to differentiate into adipocytes. Cells are transfected with the developed vectors and after 48 h post-transfection, are harvested and sorted by flow cytometry according to their respective GFP expression. The sorted GFP-positive cells are then reseeded in 96-well plates and incubated at 37 °C with stem cell full media. The media is changed every other day until cells reached maximum confluency. At this point, the stem cells' full growth media is removed and replaced with adipogenesis differentiation media cocktail (Lonza Inc., NJ) containing 1 µM dexamethasone, 0.5 mM isobutyl-methylxanthine (IBMX), 1 µg/ml insulin, and 100 µM indomethacin. The differentiation media is gently replaced every 3 days for 12 days. Next, ADSCs are washed by PBS and stained with AdipoRed™ fluorescent

staining reagent (Lonza Inc., NJ). The production of intracellular oil vesicles is visualized by fluorescent microscopy (Olympus Co., USA) and the percentage of differentiated stem cells is quantified by flow cytometry. Untransfected stem cells are subjected to the same differentiation protocol and used as the positive control. The data are presented as mean $\pm$ s.d. (n=3).

Table 1: The amino acid sequences of the designed recombinant vectors for stem cell transfection.

Name	Cell Targeting Peptide	Cell Penetrating Peptide	DNA Condensing Motif (H4)	Fusogenic Peptide (GALA)
H4G	N/A	N/A	(SGRGKQGGKARA KAKTRSSRAGLQFP VGRVHRLLRK) ₄ (SEQ ID NO: 5)	WEAALAEAL AEALAEHLAE ALAEALEALA A (SEQ ID NO: 6)
MPG-H4G	N/A	GALFLGFLGAA GSTMGAWSQPK KKRKV (SEQ ID NO: 3)	(SGRGKQGGKARA KAKTRSSRAGLQFP VGRVHRLLRK) ₄ (SEQ ID NO: 5)	WEAALAEAL AEALAEHLAE ALAEALEALA A (SEQ ID NO: 6)
Pep1-H4G	N/A	KETWWETWWT EWSQPKKKRKV (SEQ ID NO: 4)	(SGRGKQGGKARA KAKTRSSRAGLQFP VGRVHRLLRK) ₄ (SEQ ID NO: 5)	WEAALAEAL AEALAEHLAE ALAEALEALA A (SEQ ID NO: 6)
Vago-H4G	KLTWQELYQ LKYKGI (SEQ ID NO: 1)	N/A	(SGRGKQGGKARA KAKTRSSRAGLQFP VGRVHRLLRK) ₄ (SEQ ID NO: 5)	WEAALAEAL AEALAEHLAE ALAEALEALA A (SEQ ID NO: 6)
Vanta-H4G	NGYEIEWYS WVTHGMY (SEQ ID NO: 2)	N/A	(SGRGKQGGKARA KAKTRSSRAGLQFP VGRVHRLLRK) ₄ (SEQ ID NO: 5)	WEAALAEAL AEALAEHLAE ALAEALEALA A (SEQ ID NO: 6)
IGFR-H4G	LLGDFFRKSK EKIGKEFKRI VQRIKDFLRN LVPRTES (SEQ ID NO: 17)	N/A	(SGRGKQGGKARA KAKTRSSRAGLQFP VGRVHRLLRK) ₄ (SEQ ID NO: 5)	WEAALAEAL AEALAEHLAE ALAEALEALA A (SEQ ID NO: 6)
FGFR-H4G	MQLPLAT (SEQ ID NO: 18)	N/A	(SGRGKQGGKARA KAKTRSSRAGLQFP VGRVHRLLRK) ₄ (SEQ ID NO: 5)	WEAALAEAL AEALAEHLAE ALAEALEALA A (SEQ ID NO: 6)
EGFR-H4G	YHWYGYTPQ NVI (SEQ ID NO: 19)	N/A	(SGRGKQGGKARA KAKTRSSRAGLQFP VGRVHRLLRK) ₄	WEAALAEAL AEALAEHLAE ALAEALEALA

Name	Cell Targeting Peptide	Cell Penetrating Peptide	DNA Condensing Motif (H4)	Fusogenic Peptide (GALA)
			(SEQ ID NO: 5)	A (SEQ ID NO: 6)
PDGF R-H4G	IPLPPPSRPFFK (SEQ ID NO: 20)	N/A	(SGRGKQGGKARA KAKTRSSRAGLQFP VGRVHRLLRK)4 (SEQ ID NO: 5)	WEAALAEALAEALAEHLAEALAEALEALA A (SEQ ID NO: 6)
INTEGRIN-H4G	RGDSPASSKP (SEQ ID NO: 21)	N/A	(SGRGKQGGKARA KAKTRSSRAGLQFP VGRVHRLLRK)4 (SEQ ID NO: 5)	WEAALAEALAEALAEHLAEALAEALEALA A (SEQ ID NO: 6)

Table 2

Vector	Amino Acid Sequence
H4G (SEQ ID NO: 7)	SGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLRLKSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLRLKSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLRLKSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLRLKGGWEAALAEALAEALAEHLAEALAEALEALAA
MPG-H4G (SEQ ID NO: 8)	GALFLGFLGAAGSTMGAWSQPKKKRKVSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLRLKSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLRLKSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLRLKSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLRLKGGWEAALAEALAEALAEHLAEALAEALEALAA
Pep1-H4G (SEQ ID NO: 9)	KETWWETWWTEWSQPKKKRKVSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLRLKSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLRLKSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLRLKGGWEAALAEALAEALAEHLAEALAEALEALAA
Vago-H4G (SEQ ID NO: 10)	KLTWQELYQLKYKGIGGGSGGGSGGGSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLRLKSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLRLKSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLRLKSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLRLKGGWEAALAEALAEALAEHLAEALAEALEALAA

Vector	Amino Acid Sequence
Vanta-H4G (SEQ ID NO: 11)	NGYEIEWYSWVTHGMYGGGSGGGSGGGSGRGKQGGKARAKAKTRSSR AGLQFPVGRVHRLLRKSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHR LLRKSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLLRKSGRGKQGG KARAKAKTRSSRAGLQFPVGRVHRLLRKGGGWEAALAEALAEALAEHL AEALAEALEALAA
IGFR-H4G (SEQ ID NO: 22)	LLGDFFRKSKKEKIGKEFKRIVQRIKDFLRNLVPRTESGGGSGGGSGGGSGR GKQGGKARAKAKTRSSRAGLQFPVGRVHRLLRKSGRGKQGGKARAKA KTRSSRAGLQFPVGRVHRLLRKSGRGKQGGKARAKAKTRSSRAGLQFPV GRVHRLLRKSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLLRKGGG WEAALAEALAEALAEHLAEALAEALEALAA
FGFR-H4G (SEQ ID NO: 23)	MQLPLATGGGSGGGSGGGSGRGKQGGKARAKAKTRSSRAGLQFPVGRV HRLLRKSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLLRKSGRGKQ GGKARAKAKTRSSRAGLQFPVGRVHRLLRKSGRGKQGGKARAKAKTRS SRAGLQFPVGRVHRLLRKGGGWEAALAEALAEALAEHLAEALAEALEA LAA
EGFR-H4G (SEQ ID NO: 24)	YHWYGYTPQNVIGGGSGGGSGGGSGRGKQGGKARAKAKTRSSRAGLQF PVGRVHRLLRKSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLLRK SRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLLRKSGRGKQGGKARAK AKTRSSRAGLQFPVGRVHRLLRKGGGWEAALAEALAEALAEHLAEALA EALAEALAA
PDGFR-H4G (SEQ ID NO: 25)	IPLPPSRPFFKGGSGGGSGGGSGRGKQGGKARAKAKTRSSRAGLQFPV GRVHRLLRKSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLLRKGS RKQGGKARAKAKTRSSRAGLQFPVGRVHRLLRKSGRGKQGGKARAKA KTRSSRAGLQFPVGRVHRLLRKGGGWEAALAEALAEALAEHLAEALAE ALEALAA
INTEGRIN-H4G (SEQ ID NO: 26)	RGDSPASSKPGGGSGGGSGGGSGRGKQGGKARAKAKTRSSRAGLQFPV GRVHRLLRKSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLLRKGS RKQGGKARAKAKTRSSRAGLQFPVGRVHRLLRKSGRGKQGGKARAKA KTRSSRAGLQFPVGRVHRLLRKGGGWEAALAEALAEALAEHLAEALAE ALEALAA

Table 3

Peptide	Amino Acid Sequence	SEQ ID NO:
INF-7	GLFEAIEGFIENGWEGMIDGWYG	SEQ ID NO: 12
KALA	WEAKLAKALAKALAKHLAKALAKALACEA	SEQ ID NO: 13
RALA	WEARLARALARALARHLARALARALRAGEA	SEQ ID NO: 14
H5WYG	GLFHAIHFIHGGWHGLIHGWYG	SEQ ID NO: 15
LAGA	WEAALAEALALAEKEALALAEALALAA	SEQ ID NO: 16

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GENERAL METHODS

Standard methods in molecular biology are described Sambrook, Fritsch and Maniatis (1982 & 1989 2nd Edition, 2001 3rd Edition) *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY; Sambrook and Russell (2001) *Molecular Cloning, 3rd ed.*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY; Wu (1993) *Recombinant DNA*, Vol. 217, Academic Press, San Diego, CA). Standard methods also appear in Ausbel, *et al.* (2001) *Current Protocols in Molecular Biology, Vols.1-4*, John Wiley and Sons, Inc. New York, NY, which describes cloning in bacterial cells and DNA mutagenesis (Vol. 1), cloning in mammalian cells and yeast (Vol. 2), glycoconjugates and protein expression (Vol. 3), and bioinformatics (Vol. 4).

Methods for protein purification including immunoprecipitation, chromatography, electrophoresis, centrifugation, and crystallization are described (Coligan, *et al.* (2000) *Current Protocols in Protein Science*, Vol. 1, John Wiley and Sons, Inc., New York). Chemical analysis, chemical modification, post-translational modification, production of fusion proteins, glycosylation of proteins are described (see, *e.g.*, Coligan, *et al.* (2000) *Current Protocols in Protein Science*, Vol. 2, John Wiley and Sons, Inc., New York; Ausubel, *et al.* (2001) *Current Protocols in Molecular Biology*, Vol. 3, John Wiley and Sons, Inc., NY, NY, pp. 16.0.5-16.22.17; Sigma-Aldrich, Co. (2001) *Products for Life Science Research*, St. Louis, MO; pp. 45-89; Amersham Pharmacia Biotech (2001) *BioDirectory*, Piscataway, N.J., pp. 384-391). Production, purification, and fragmentation of polyclonal and monoclonal antibodies are described (Coligan, *et al.* (2001) *Current Protocols in Immunology*, Vol. 1, John Wiley and Sons, Inc., New York; Harlow and Lane (1999) *Using Antibodies*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY; Harlow and Lane, *supra*). Standard techniques for characterizing ligand/receptor interactions are available (see, *e.g.*, Coligan, *et al.* (2001) *Current Protocols in Immunology*, Vol. 4, John Wiley, Inc., New York).

INCORPORATION BY REFERENCE

All references cited herein are incorporated by reference to the same extent as if each individual publication, database entry (*e.g.* Genbank sequences or GeneID entries), patent application, or patent, was specifically and individually indicated to be incorporated by reference. This statement of incorporation by reference is intended by Applicants, pursuant to 37 C.F.R. §1.57(b)(1), to relate to each and every individual publication, database entry (*e.g.* Genbank sequences or GeneID entries), patent application, or patent, each of which is clearly identified in compliance with 37 C.F.R. §1.57(b)(2), even if such citation is not immediately adjacent to a dedicated statement of incorporation by reference. The inclusion of dedicated statements of incorporation by reference, if any, within the specification does not in any way weaken this general statement of incorporation by reference. Citation of the references herein is not intended as an admission that the reference is pertinent prior art, nor does it constitute any admission as to the contents or date of these publications or documents.

The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and the accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. Various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims. The entire disclosure of each of the patent documents, including certificates of correction, patent application documents, scientific articles, governmental reports, websites, and other references referred to herein is incorporated by reference herein in its entirety for all purposes. In case of a conflict in terminology, the present specification controls.

EQUIVALENTS

The invention can be embodied in other specific forms without departing from the spirit or essential characteristics thereof. The foregoing embodiments are to be considered in all respects illustrative rather than limiting on the invention described herein. In the various embodiments of the methods and systems of the present invention, where the term comprises is used with respect to the recited steps or components, it is also contemplated that the methods and systems consist essentially of, or consist of, the recited steps or components. Further, it should be understood that the order of steps or order for performing certain actions is immaterial so long as the invention remains operable. Moreover, two or more steps or actions can be conducted simultaneously.

In the specification, the singular forms also include the plural forms, unless the context clearly dictates otherwise. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. In the case of conflict, the present specification will control.

All percentages and ratios used herein, unless otherwise indicated, are by weight.

What is claimed is:

1. A fusion polypeptide, comprising:
 - (i) a cell surface receptor-binding peptide;
 - (ii) a nucleic acid-binding polypeptide; and
 - (iii) an endosomolytic peptide.
2. The fusion polypeptide of claim 1, wherein the cell surface receptor-binding peptide is a vascular endothelial growth factor receptor (VEGFR)-binding peptide.
3. The fusion polypeptide of claim 2, wherein the VEGFR-binding peptide is an antagonist of VEGFR.
4. The fusion polypeptide of claim 2, wherein the VEGFR-binding peptide is an agonist of VEGFR.
5. The fusion polypeptide of claim 2, wherein the VEGFR-binding peptide comprises an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 1.
6. The fusion polypeptide of claim 2, wherein the VEGFR-binding peptide comprises an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 2.
7. The fusion polypeptide of claim 1, wherein the cell surface receptor-binding peptide is an insulin-like growth factor receptor (IGFR)-binding peptide.
8. The fusion polypeptide of claim 7, wherein the IGFR-binding peptide comprises an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 17.
9. The fusion polypeptide of claim 1, wherein the cell surface receptor-binding peptide is a fibroblast growth factor receptor (FGFR)-binding peptide.

10. The fusion polypeptide of claim 9, wherein the FGFR-binding peptide comprises an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 18.
11. The fusion polypeptide of claim 1, wherein the cell surface receptor-binding peptide is an epidermal growth factor receptor (EGFR)-binding peptide.
12. The fusion polypeptide of claim 11, wherein the EGFR-binding peptide comprises an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 19.
13. The fusion polypeptide of claim 1, wherein the cell surface receptor-binding peptide is a platelet-derived growth factor receptor (PDGFR)-binding peptide.
14. The fusion polypeptide of claim 13, wherein the PDGFR-binding peptide comprises an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 20.
15. The fusion polypeptide of claim 1, wherein the cell surface receptor-binding peptide is an integrin-binding peptide.
16. The fusion polypeptide of claim 15, wherein the integrin-binding peptide comprises an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 21.
17. The fusion polypeptide of claim 1, wherein the nucleic acid-binding polypeptide comprises repeats of a histone, a histone variant, or a fragment thereof.
18. The fusion polypeptide of claim 1, wherein the nucleic acid-binding polypeptide comprises repeats of a fragment of histone H2A.
19. The fusion polypeptide of claim 1, wherein the nucleic acid-binding polypeptide comprises 1 to 10 repeats of a N-terminal fragment of histone H2A, and wherein the fragment has 15-50 amino acid residues in length.

20. The fusion polypeptide of claim 1, wherein the nucleic acid-binding polypeptide comprises 4 repeats of a N-terminal fragment of histone H2A, and wherein the fragment has about 37 amino acid residues in length.
21. The fusion polypeptide of claim 1, wherein the nucleic acid-binding polypeptide comprises a nuclear localization sequence.
22. The fusion polypeptide of claim 1, wherein the nucleic acid-binding polypeptide comprises an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 5.
23. The fusion polypeptide of claim 1, wherein the endosomolytic peptide is GALA, INF-7, KALA, RALA, or H5WYG.
24. The fusion polypeptide of claim 1, wherein the endosomolytic peptide comprises an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 6.
25. The fusion polypeptide of claim 1, wherein the cell surface receptor-binding peptide is located at the N-terminus of the fusion polypeptide.
26. The fusion polypeptide of claim 1, wherein the endosomolytic peptide is located at the C-terminus of the fusion polypeptide.
27. The fusion polypeptide of claim 1, comprising an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 10 or SEQ ID NO: 11.
28. The fusion polypeptide of claim 1, comprising an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, or SEQ ID NO: 26.
29. The fusion polypeptide of claim 1, comprising an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 7.

30. A fusion polypeptide, comprising:
- (i) a cell-penetrating peptide;
 - (ii) a nucleic acid-binding polypeptide; and
 - (iii) an endosomolytic peptide.
31. The fusion polypeptide of claim 30, wherein the cell-penetrating peptide is Pep1.
32. The fusion polypeptide of claim 30, wherein the cell-penetrating peptide is MPG.
33. The fusion polypeptide of claim 30, wherein the cell-penetrating peptide comprises an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 3.
34. The fusion polypeptide of claim 30, wherein the cell-penetrating peptide comprises an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 4.
35. The fusion polypeptide of claim 30, wherein the nucleic acid-binding polypeptide comprises repeats of a histone, a histone variant, or a fragment thereof.
36. The fusion polypeptide of claim 30, wherein the nucleic acid-binding polypeptide comprises repeats of a fragment of histone H2A.
37. The fusion polypeptide of claim 30, wherein the nucleic acid-binding polypeptide comprises 1 to 10 repeats of a N-terminal fragment of histone H2A, and wherein the fragment has 15-50 amino acid residues in length.
38. The fusion polypeptide of claim 30, wherein the nucleic acid-binding polypeptide comprises 4 repeats of a N-terminal fragment of histone H2A, and wherein the fragment has about 37 amino acid residues in length.
39. The fusion polypeptide of claim 30, wherein the nucleic acid-binding polypeptide comprises a nuclear localization sequence.

40. The fusion polypeptide of claim 30, wherein the nucleic acid-binding polypeptide comprises an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 5.
41. The fusion polypeptide of claim 30, wherein the endosomolytic peptide is GALA, INF-7, KALA, RALA, or H5WYG.
42. The fusion polypeptide of claim 30, wherein the endosomolytic peptide comprises an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 6.
43. The fusion polypeptide of claim 30, wherein the cell-penetrating peptide is located at the N-terminus of the fusion polypeptide.
44. The fusion polypeptide of claim 30, wherein the endosomolytic peptide is located at the C-terminus of the fusion polypeptide.
45. The fusion polypeptide of claim 30, comprising an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 8 or SEQ ID NO: 9.
46. The fusion polypeptide of claim 30, comprising an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 7.
47. A system for transfection of a nucleic acid into a cell, comprising:
 - (a) the fusion polypeptide of claims 1 or 30; and
 - (b) a nucleic acid.
48. The system of claim 47, wherein the fusion polypeptide and the nucleic acid are suspended in an aqueous medium with a conductivity no greater than 10 mS/cm.
49. The system of claim 48, wherein the aqueous medium has a conductivity no greater than 2 mS/cm.

50. The system of claim 48, wherein the aqueous medium has a conductivity of about 0.45 mS/cm.
51. The system of claim 47, wherein the system further comprises dexamethasone, insulin (or its fragment), transferrin (or its fragment), a selenite, or combinations thereof.
52. The system of claim 47, wherein the system further comprises about 0.1 µg/ml to about 0.6 µg/ml dexamethasone, about 5 µg/ml to about 20 µg/ml insulin (or its fragment), about 3 µg/ml to about 10 µg/ml transferrin (or its fragment), and about 0.003 µg/ml to about 0.010 µg/ml selenite.
53. The system of claim 47, wherein the N:P ratio ranges from about 1:1 to about 12:1.
54. The system of claim 47, wherein the N:P ratio is about 5:1.
55. A method of transfecting a nucleic acid into a cell, the method comprising contacting the cell with the system of claim 47.
56. The method of claim 55, wherein the cell is a stem cell.
57. The method of claim 55, wherein the contacting step occurs *in vitro*.
58. A kit comprising the fusion polypeptide of claims 1 or 30.
59. A kit comprising the system of claim 47.

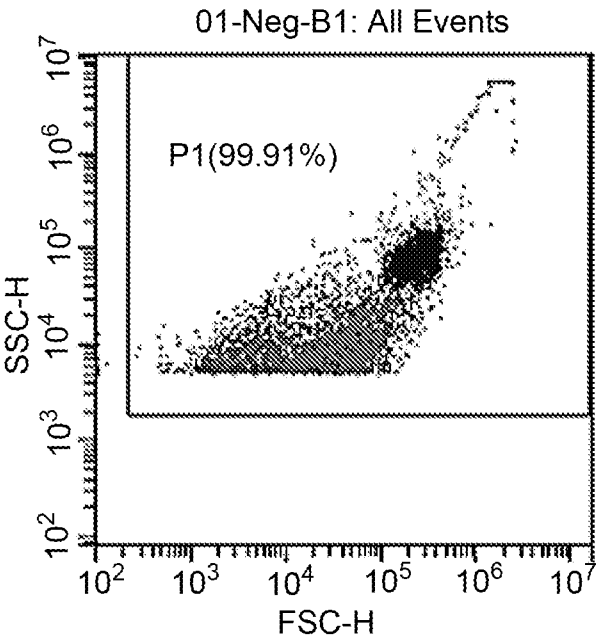


Figure 1A

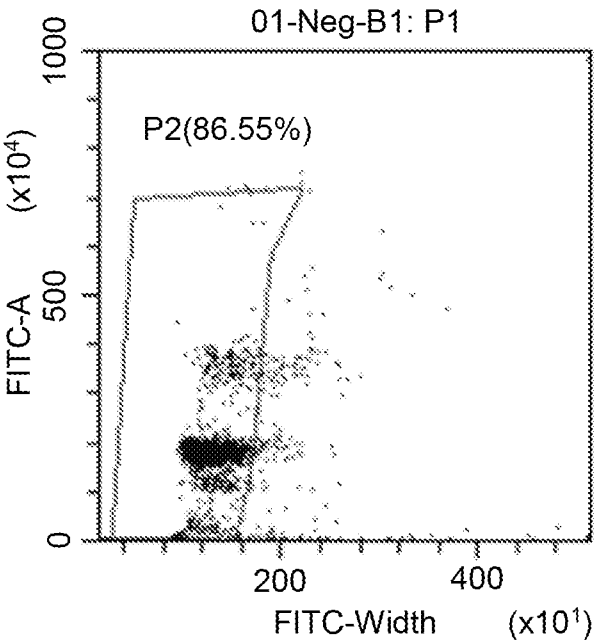


Figure 1B

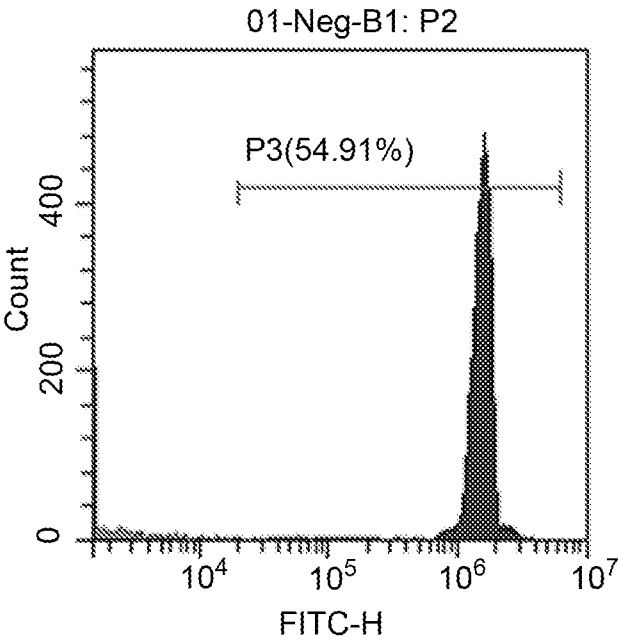


Figure 1C

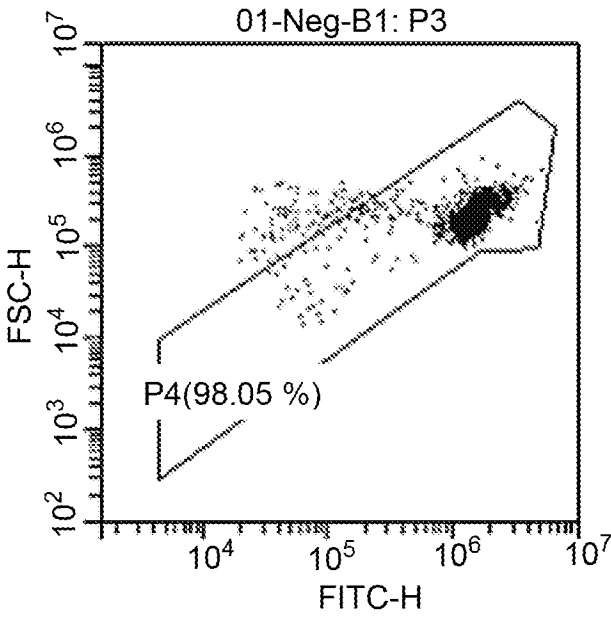


Figure 1D

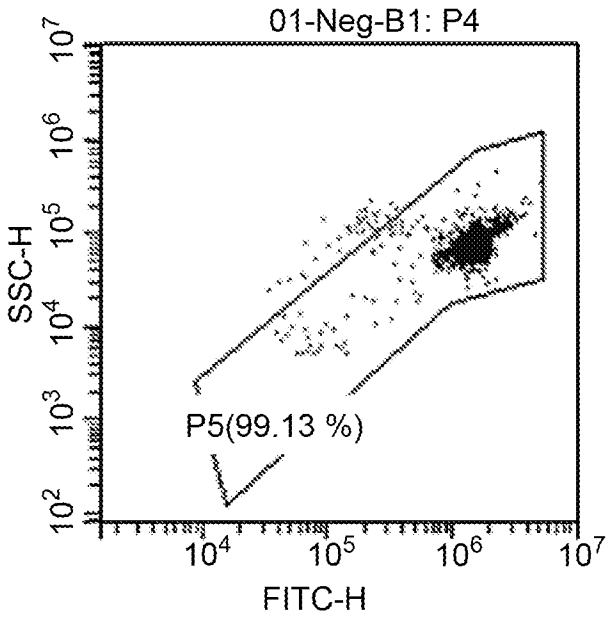


Figure 1E

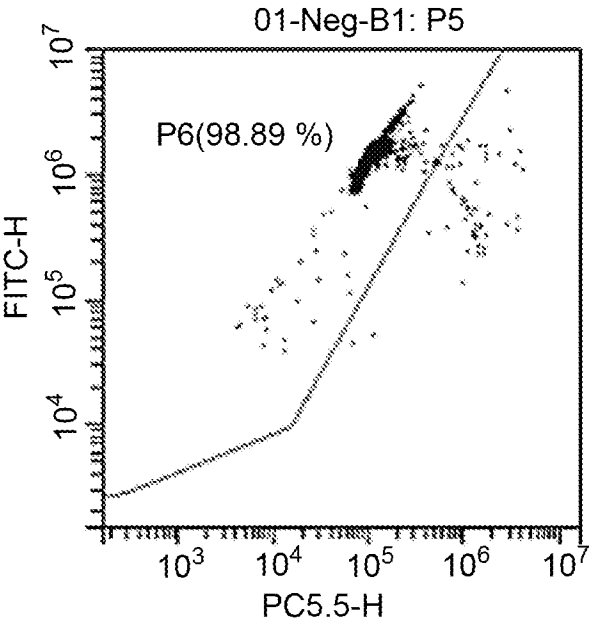


Figure 1F

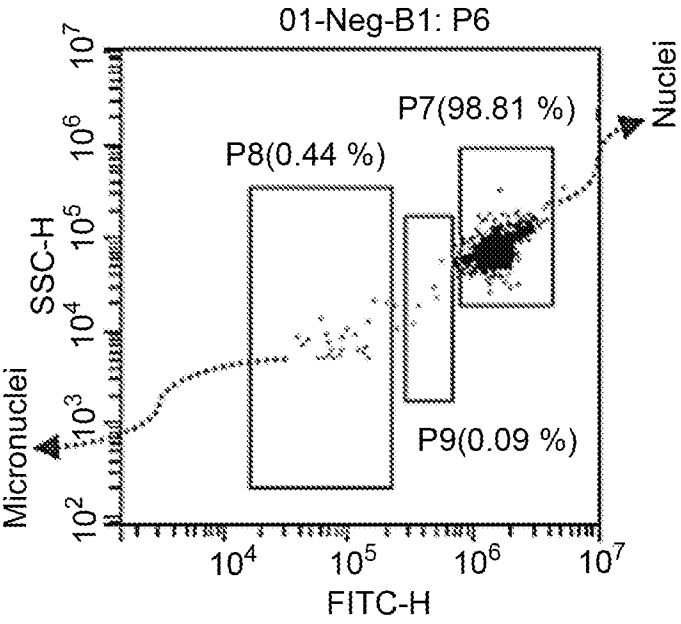


Figure 1G

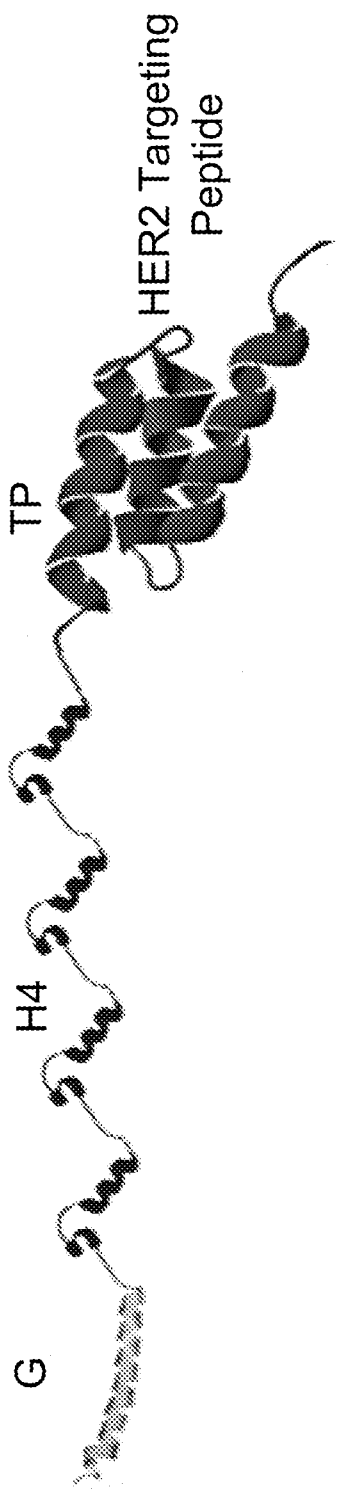


Figure 2A

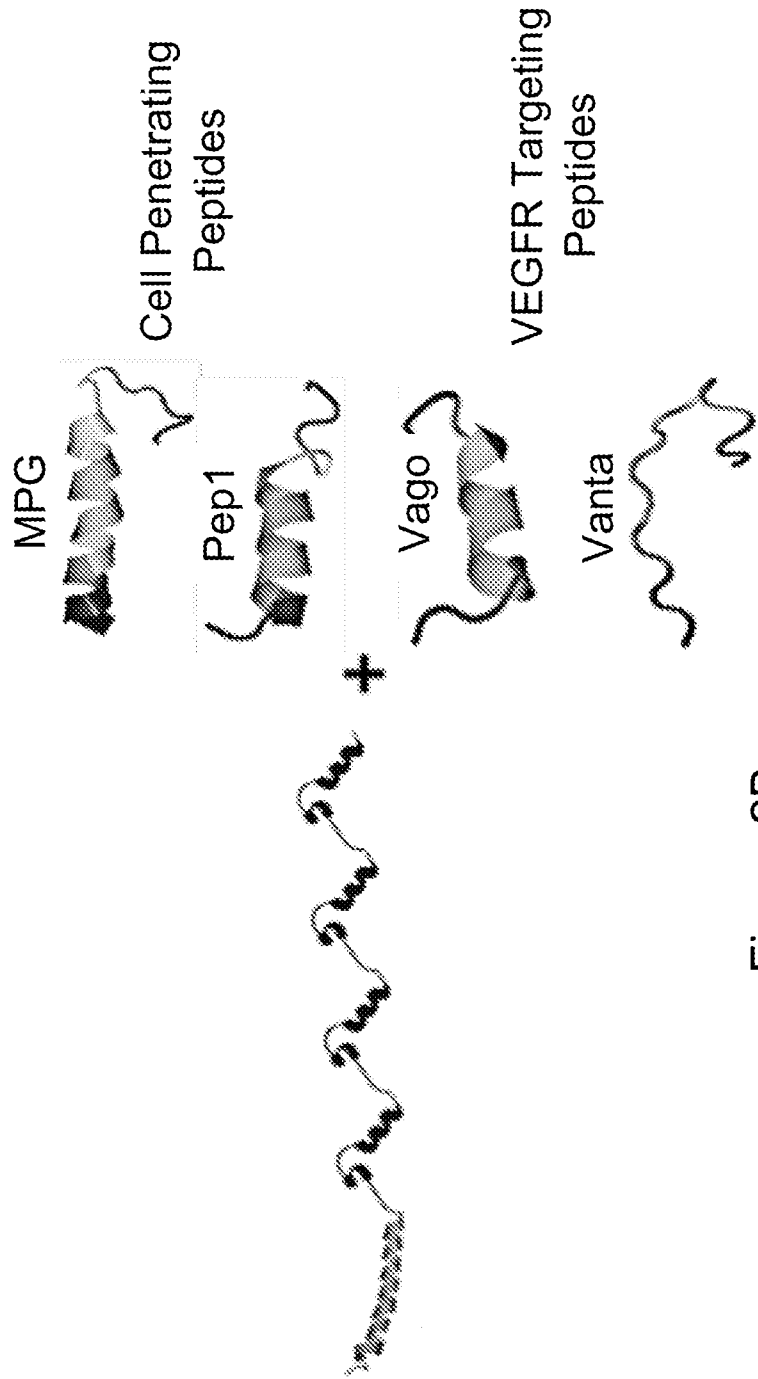


Figure 2B

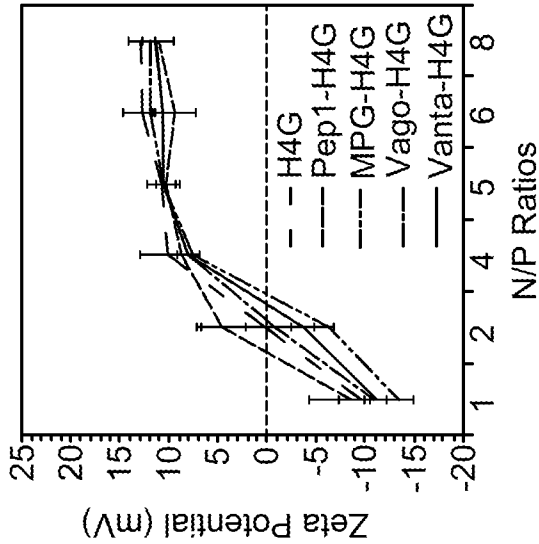


Figure 2D

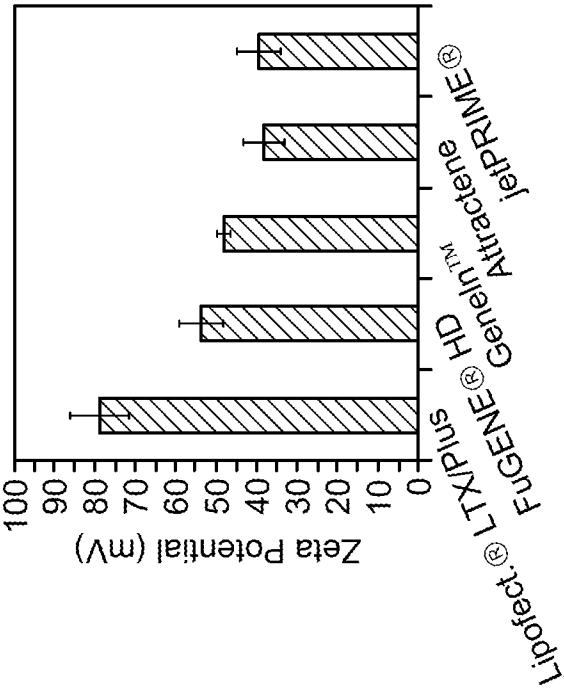


Figure 2F

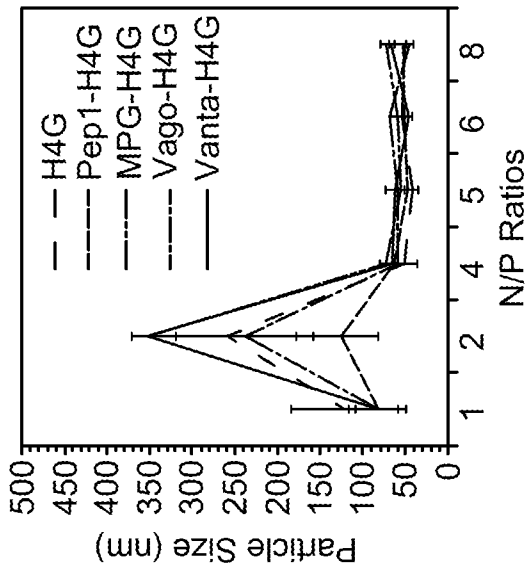


Figure 2C

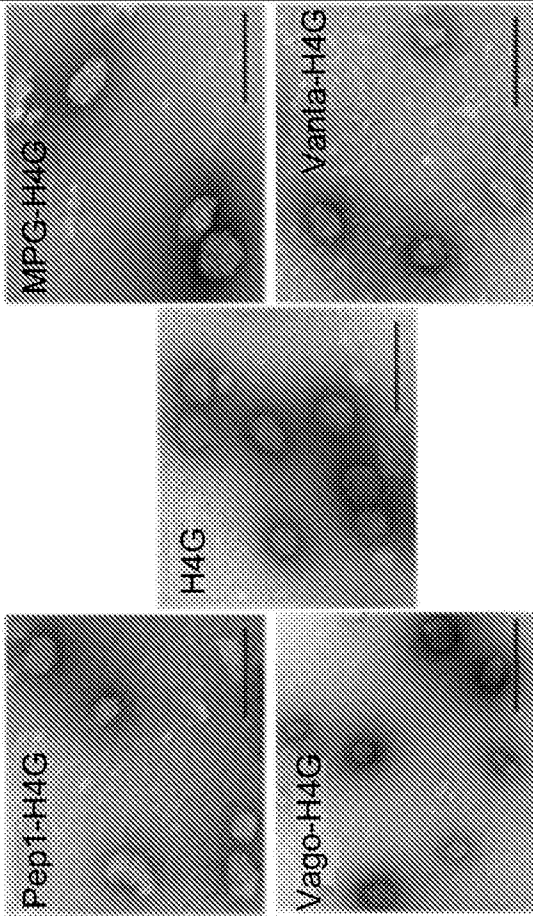


Figure 2E

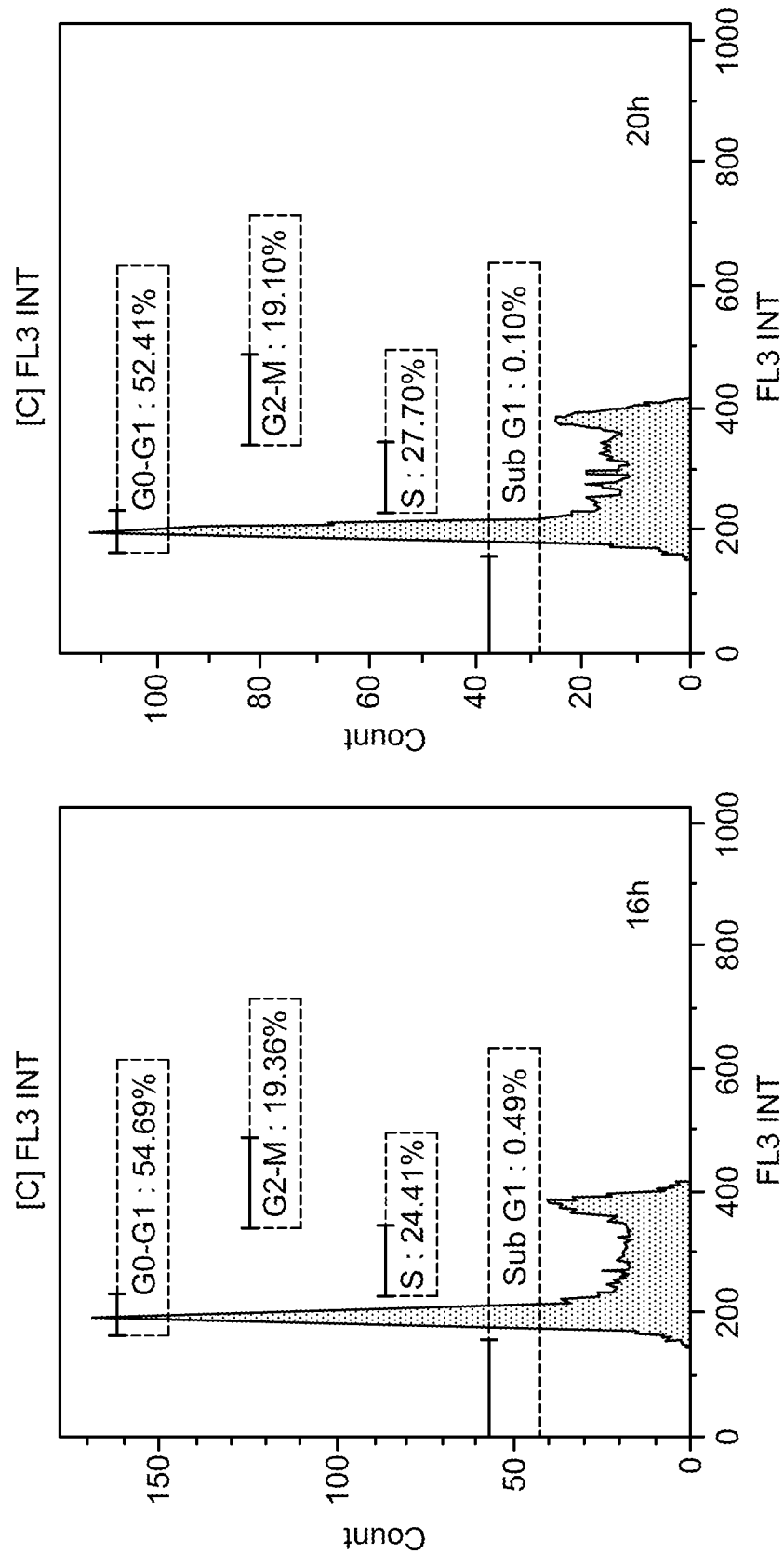


Figure 3A

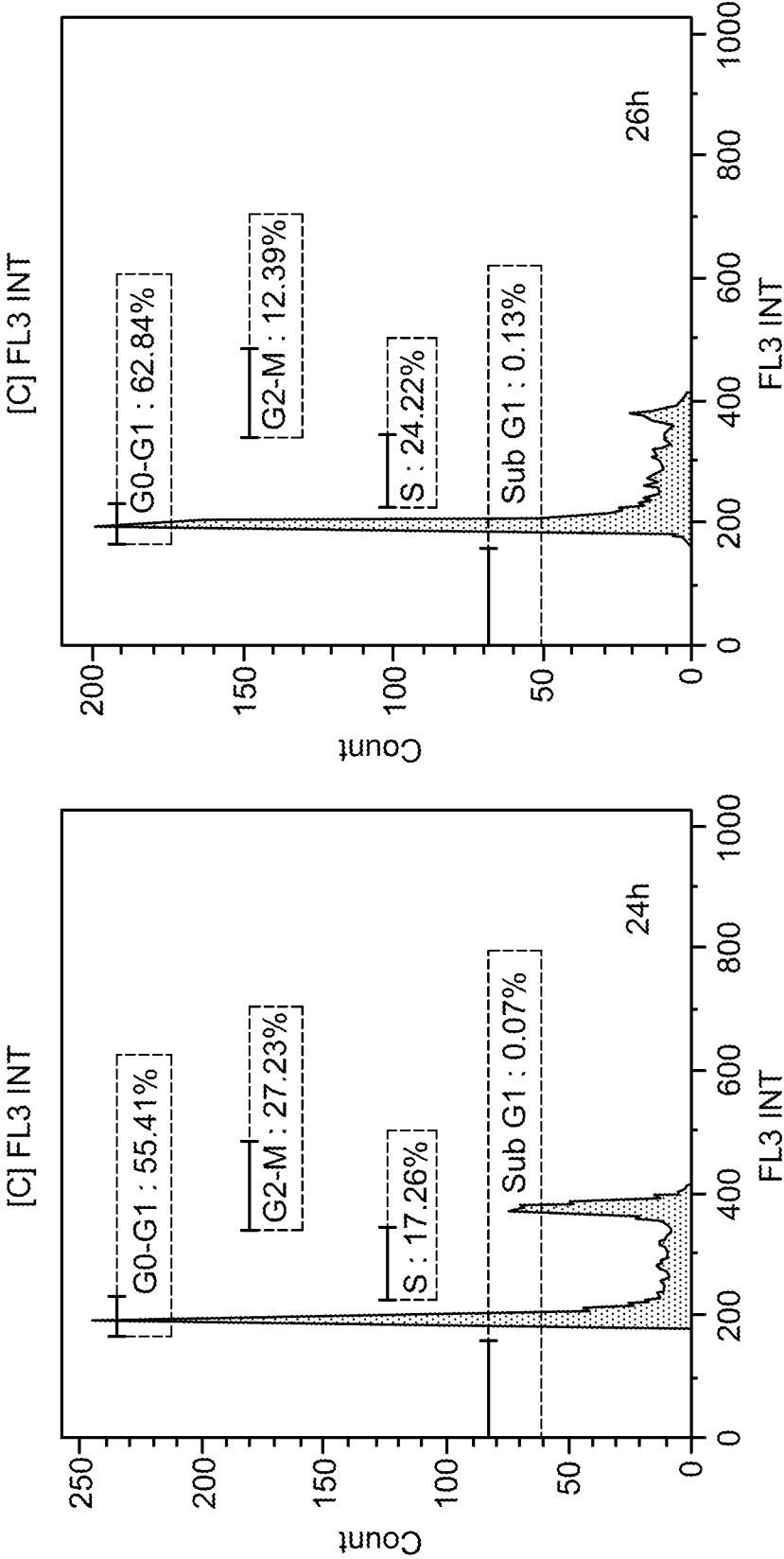


Figure 3A (continued)

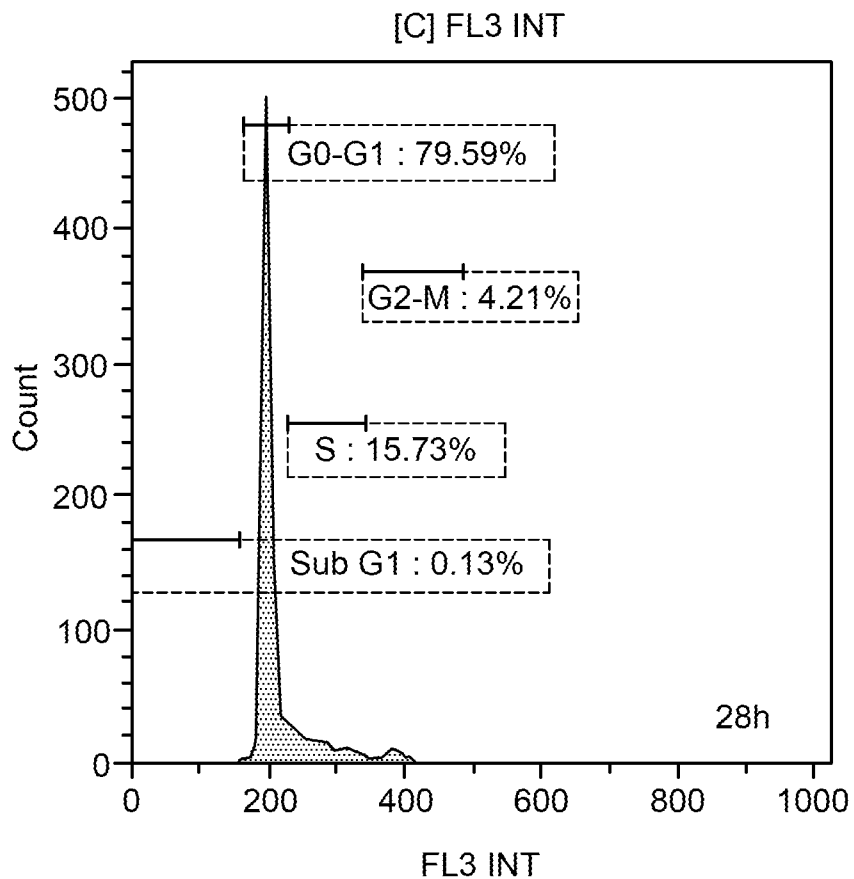


Figure 3A (continued)

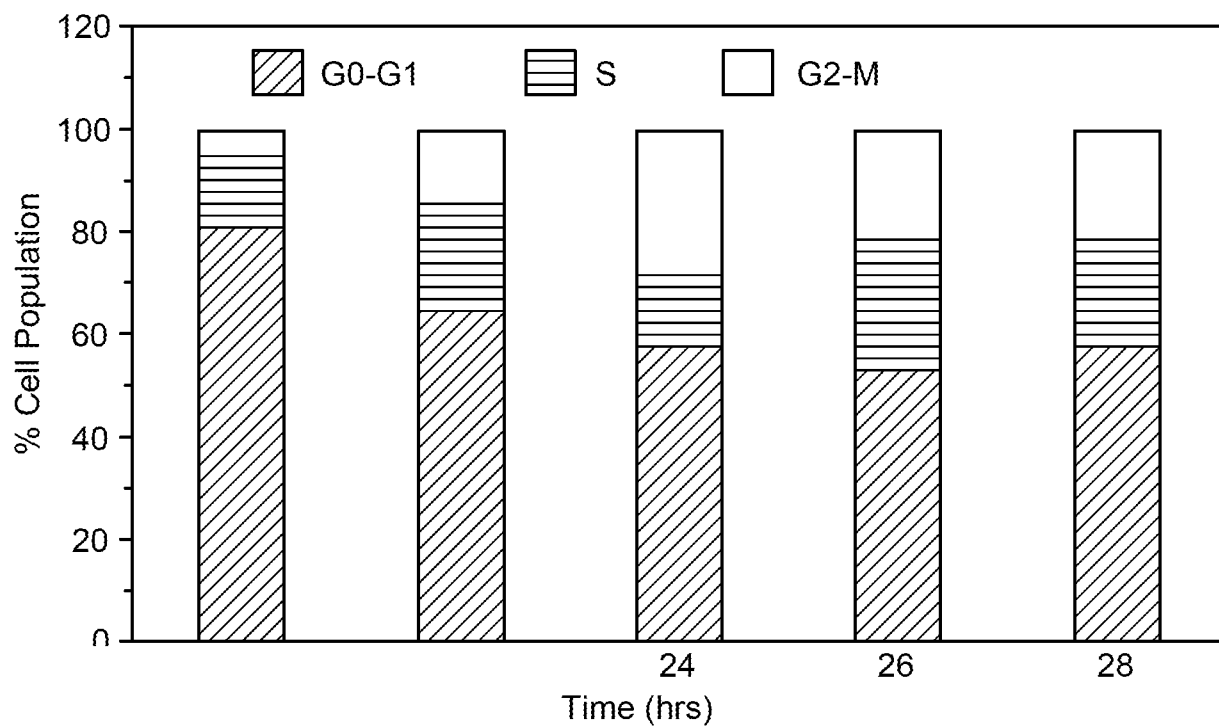


Figure 3B

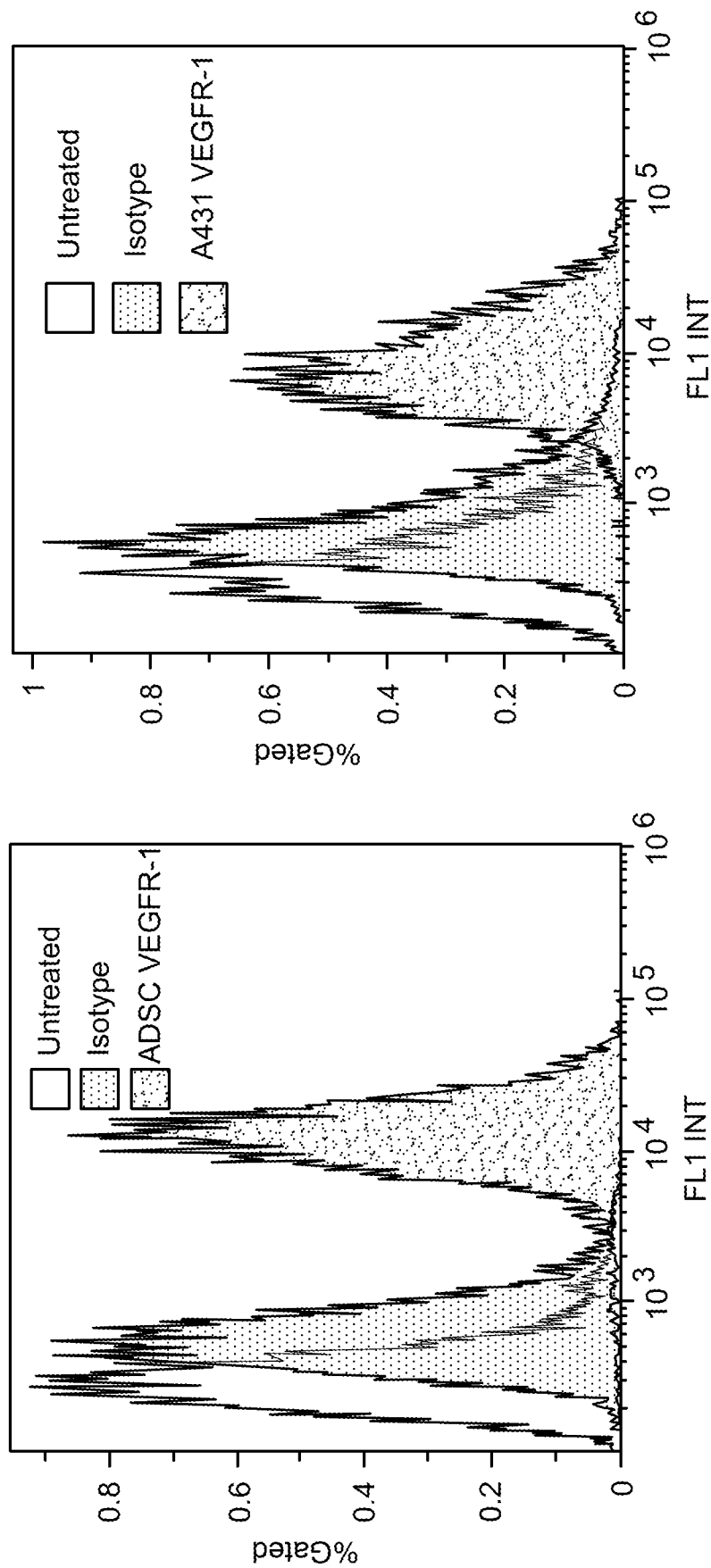


Figure 3C

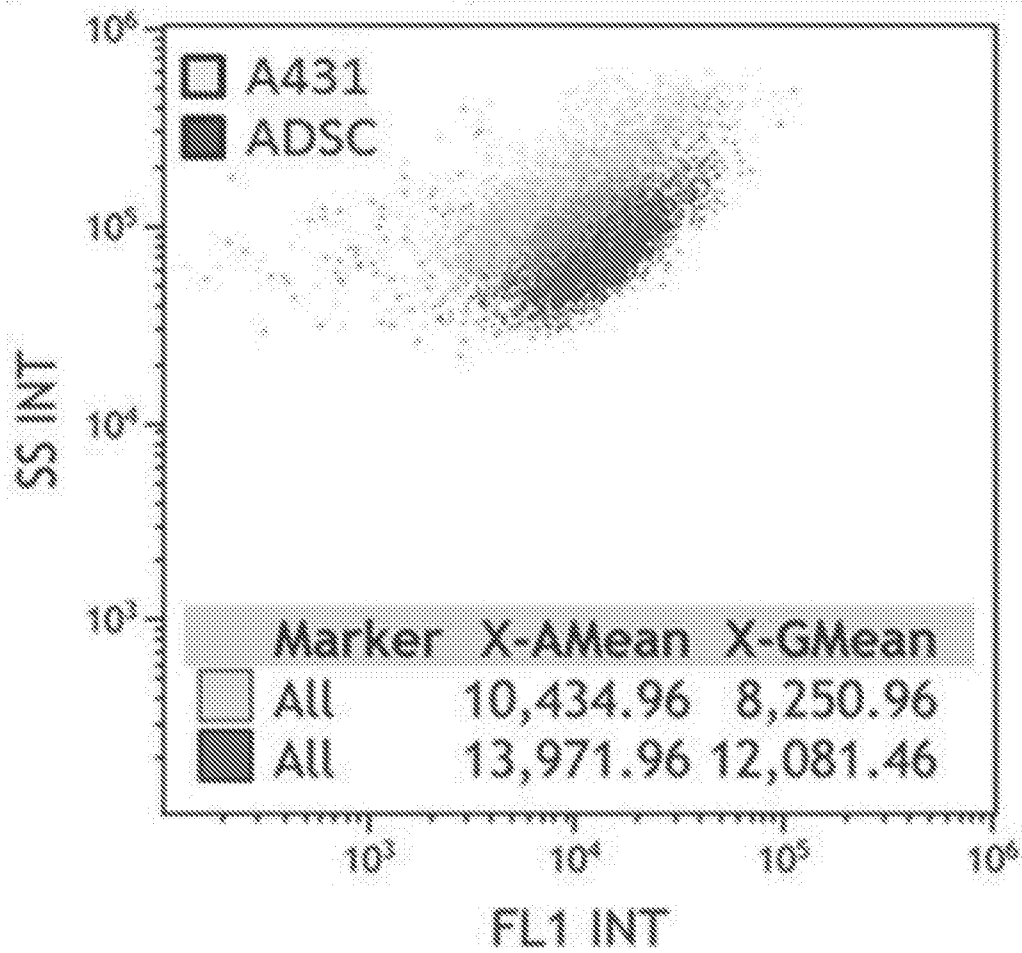


Figure 3C (continued)

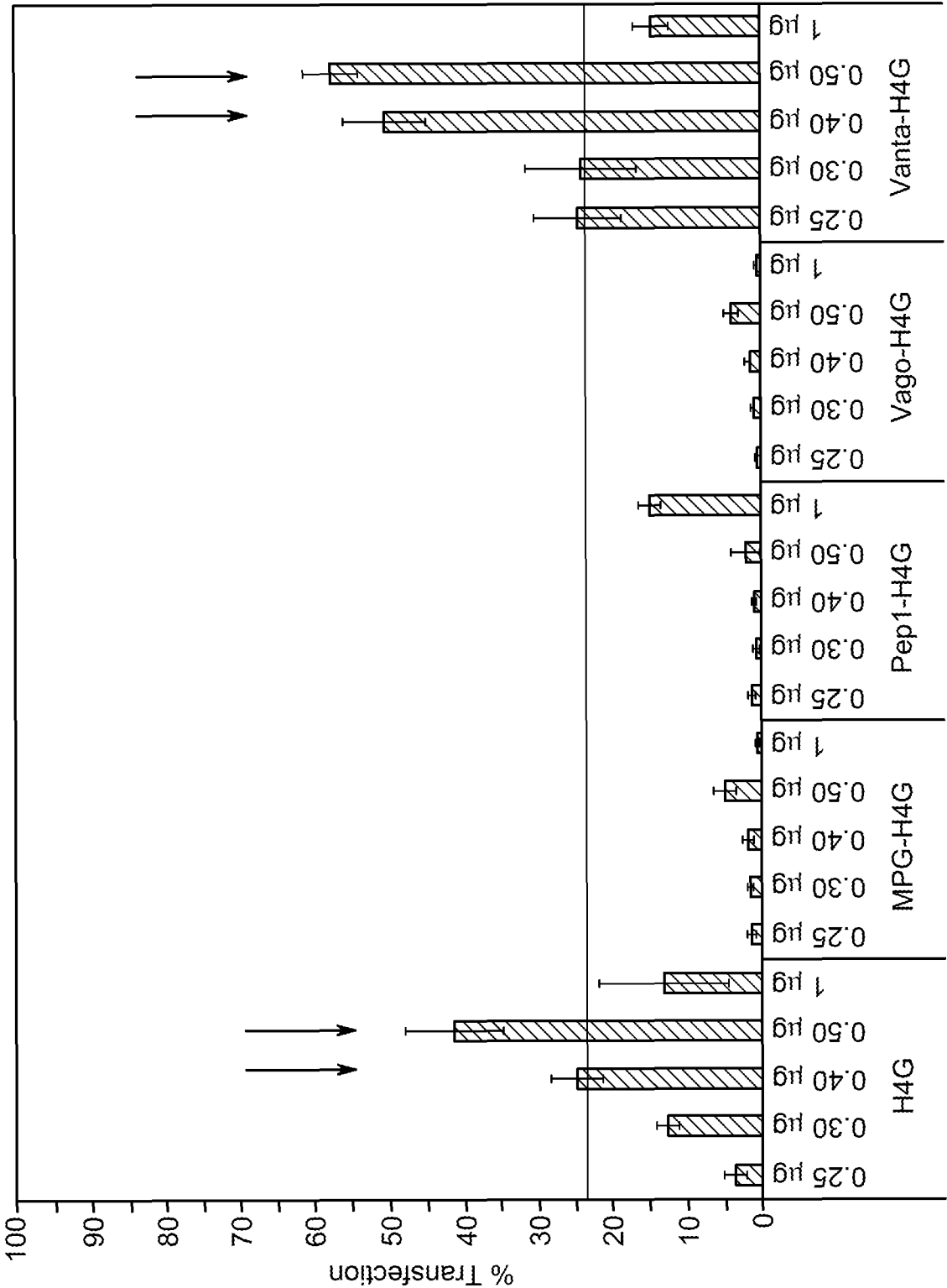


Figure 4A

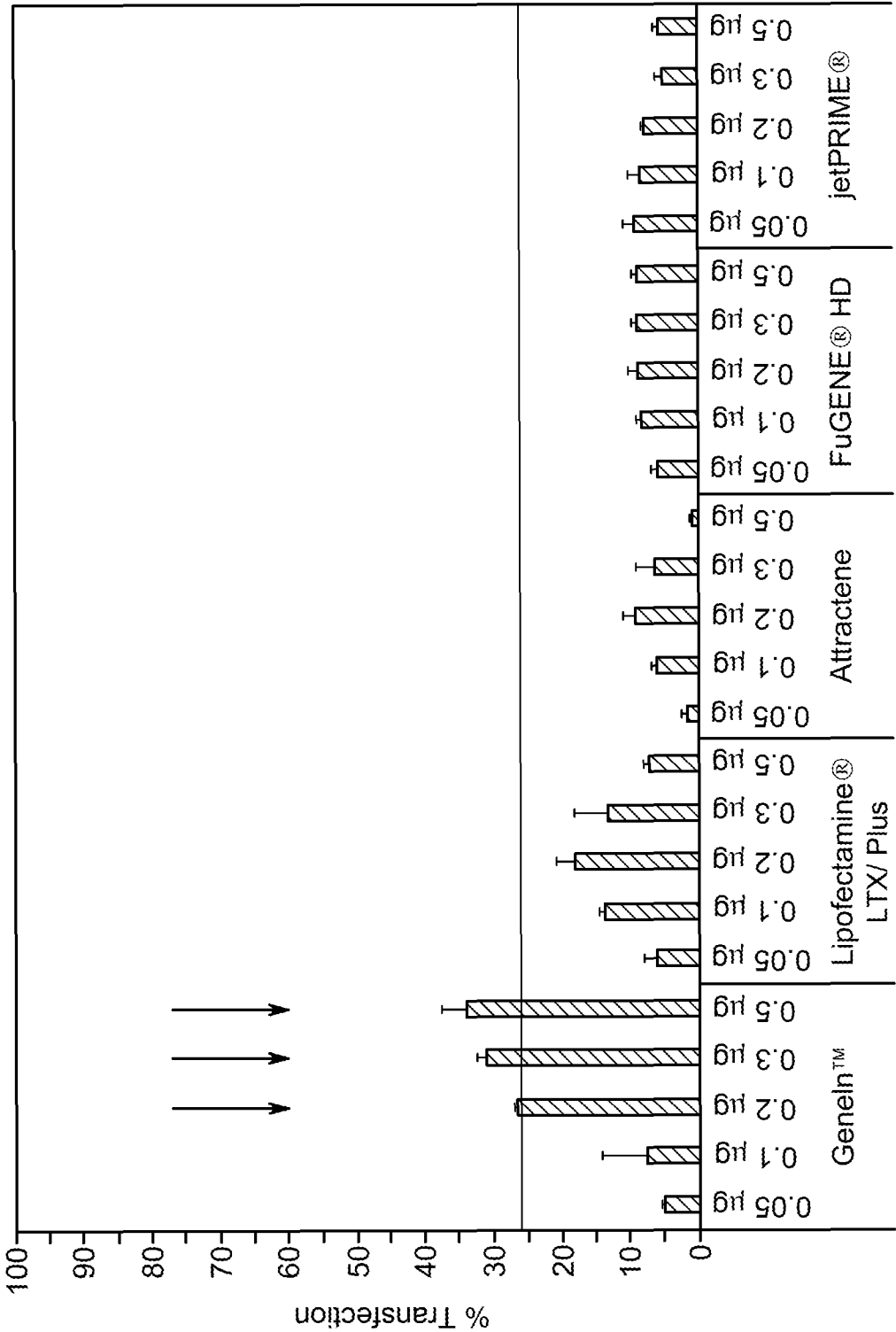


Figure 4B

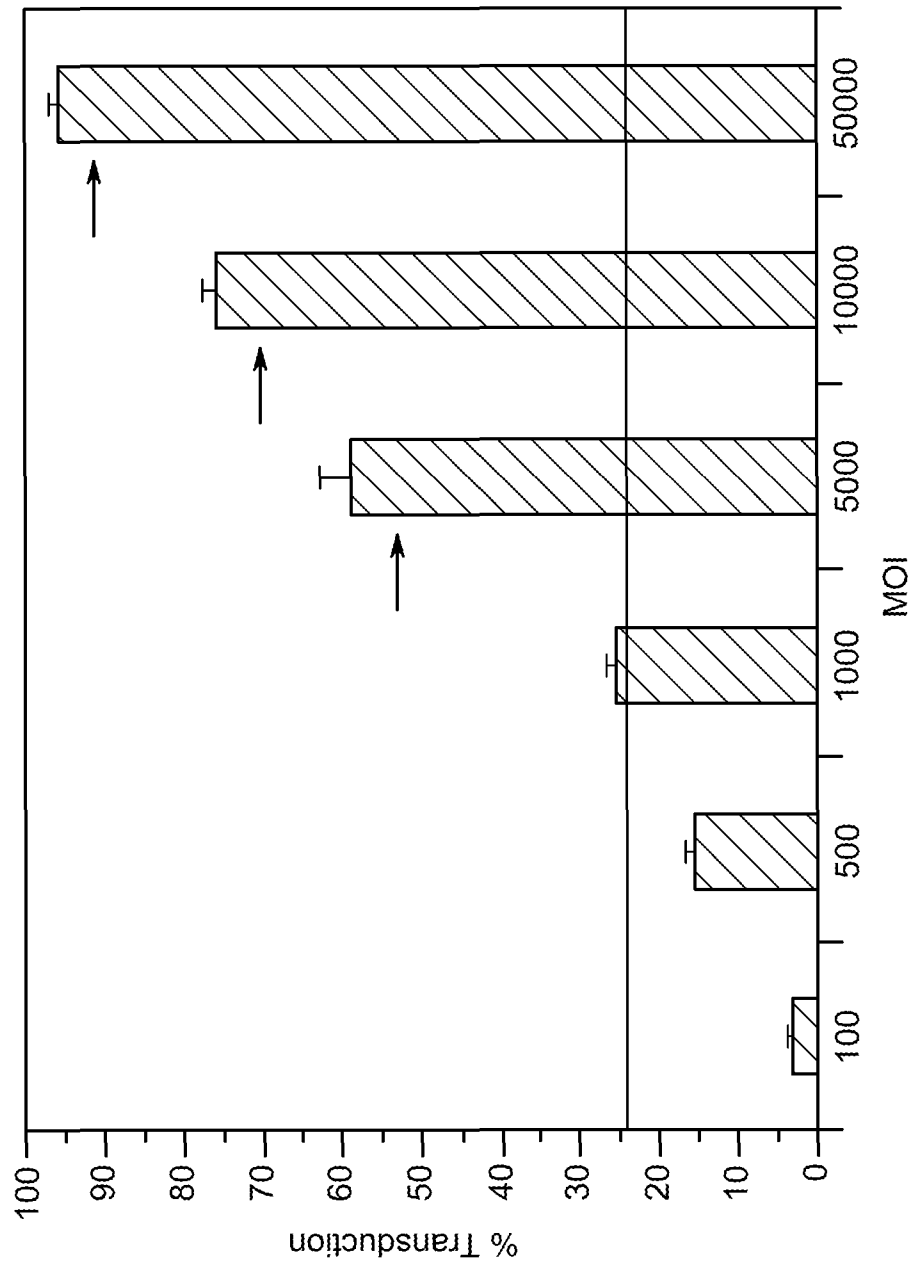


Figure 4C

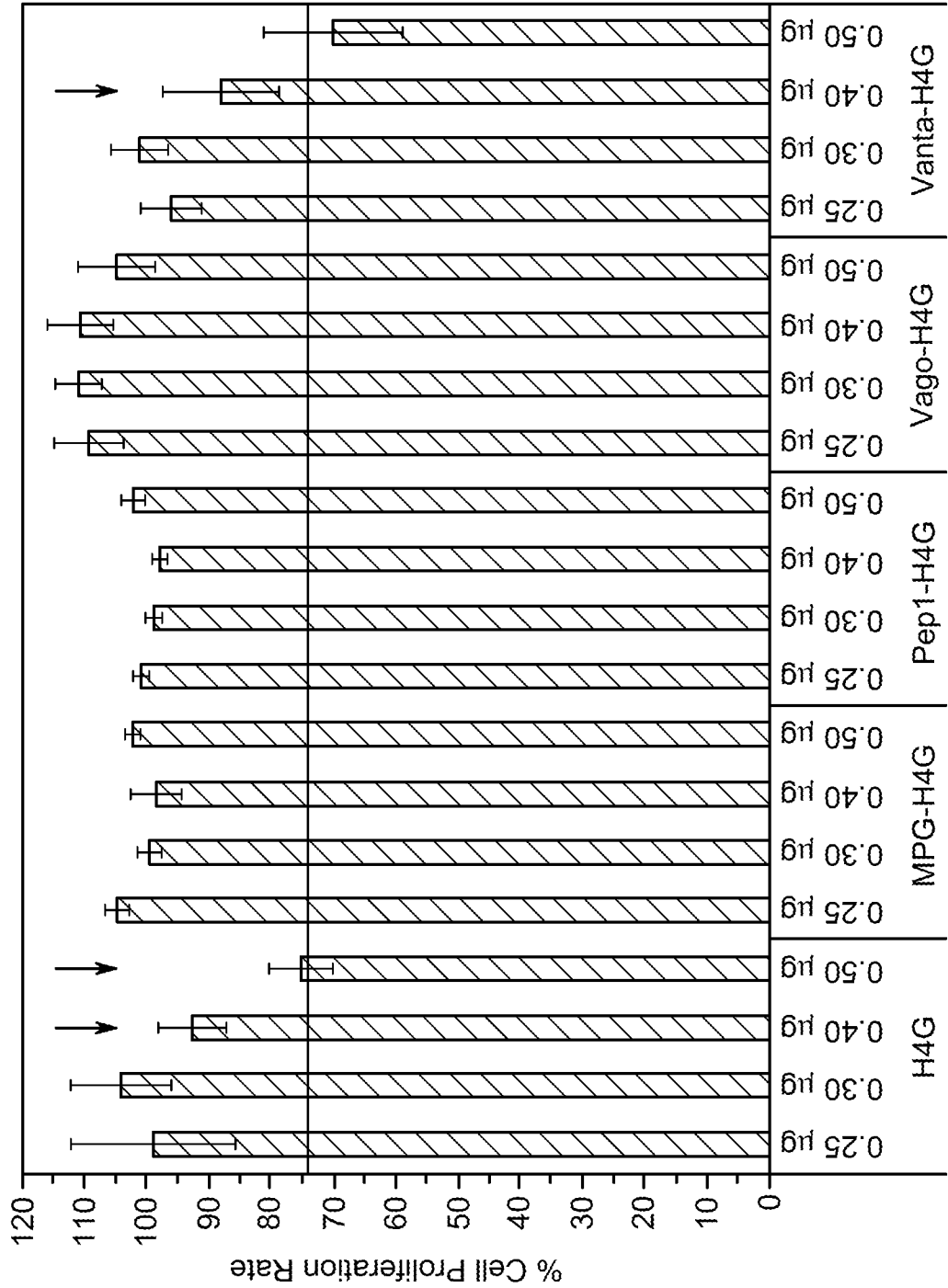


Figure 4D

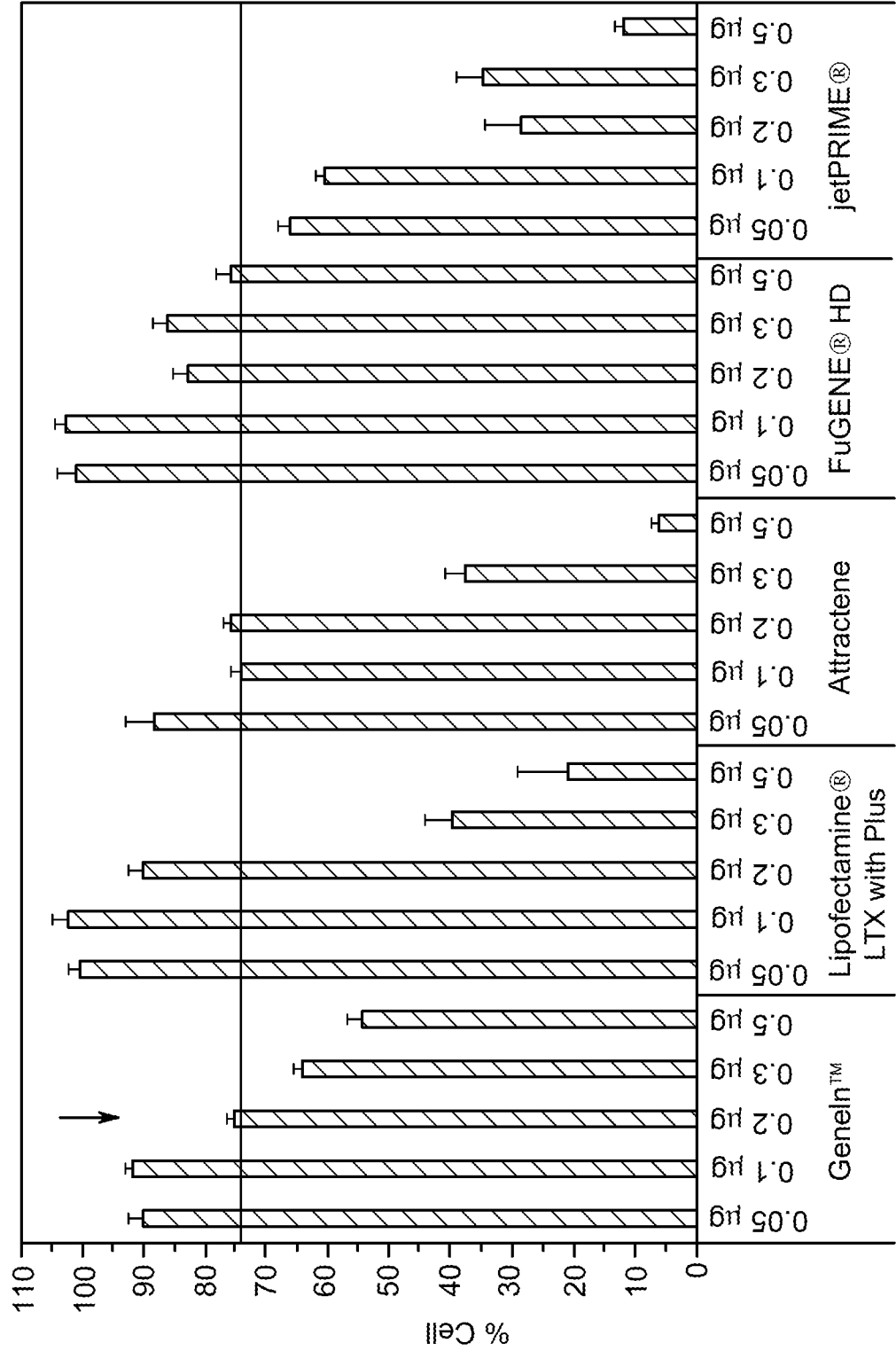


Figure 4E

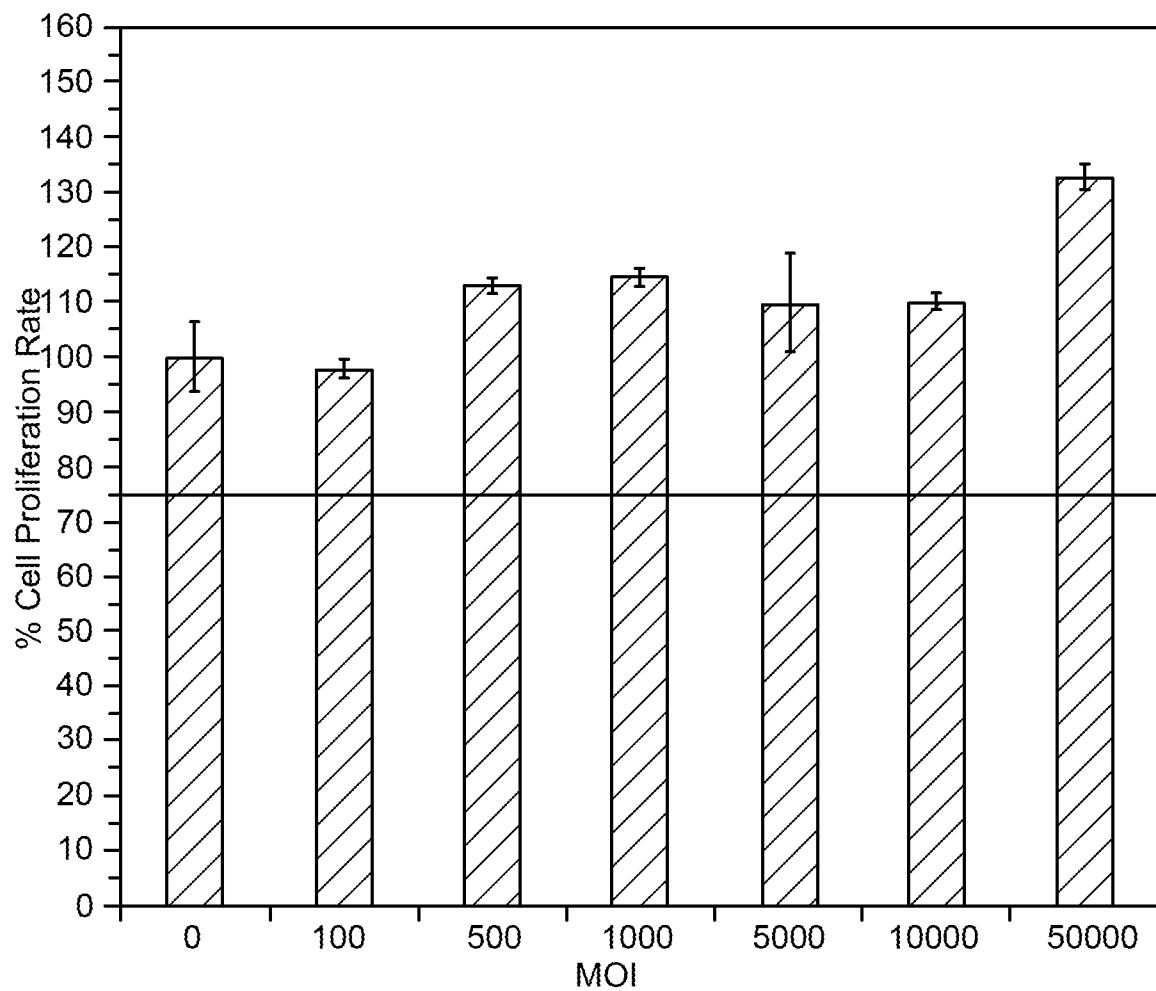


Figure 4F

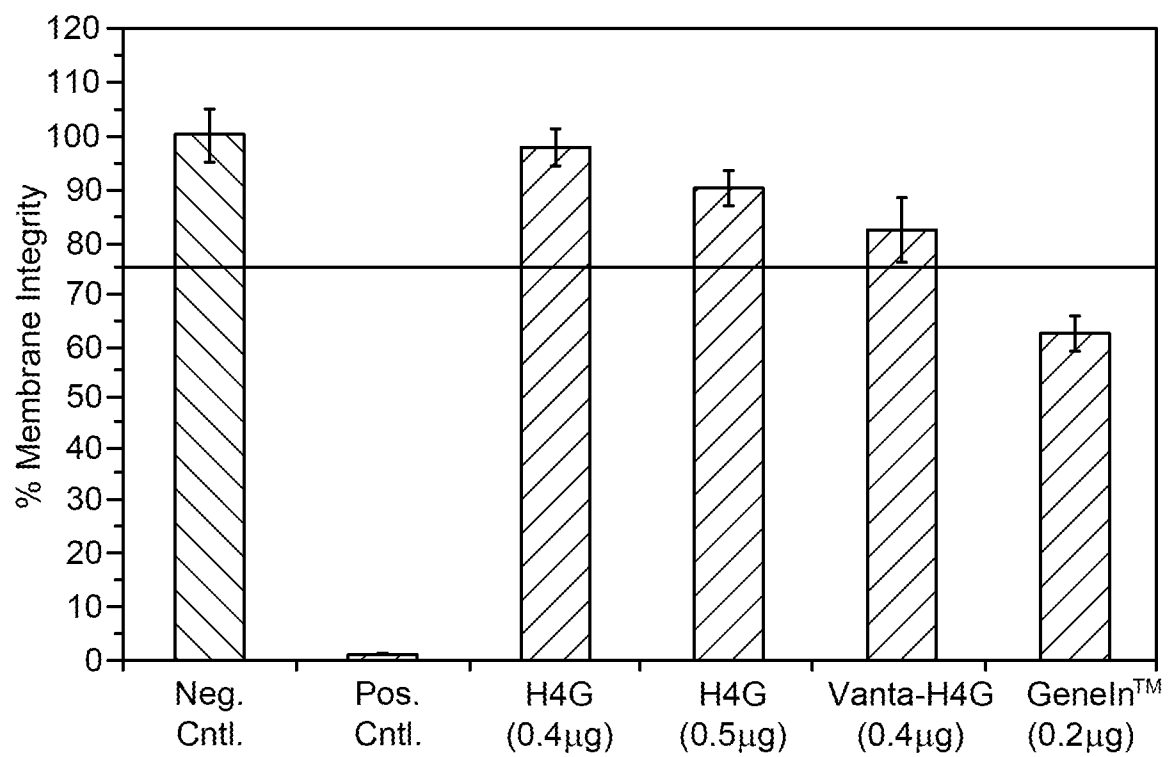


Figure 4G

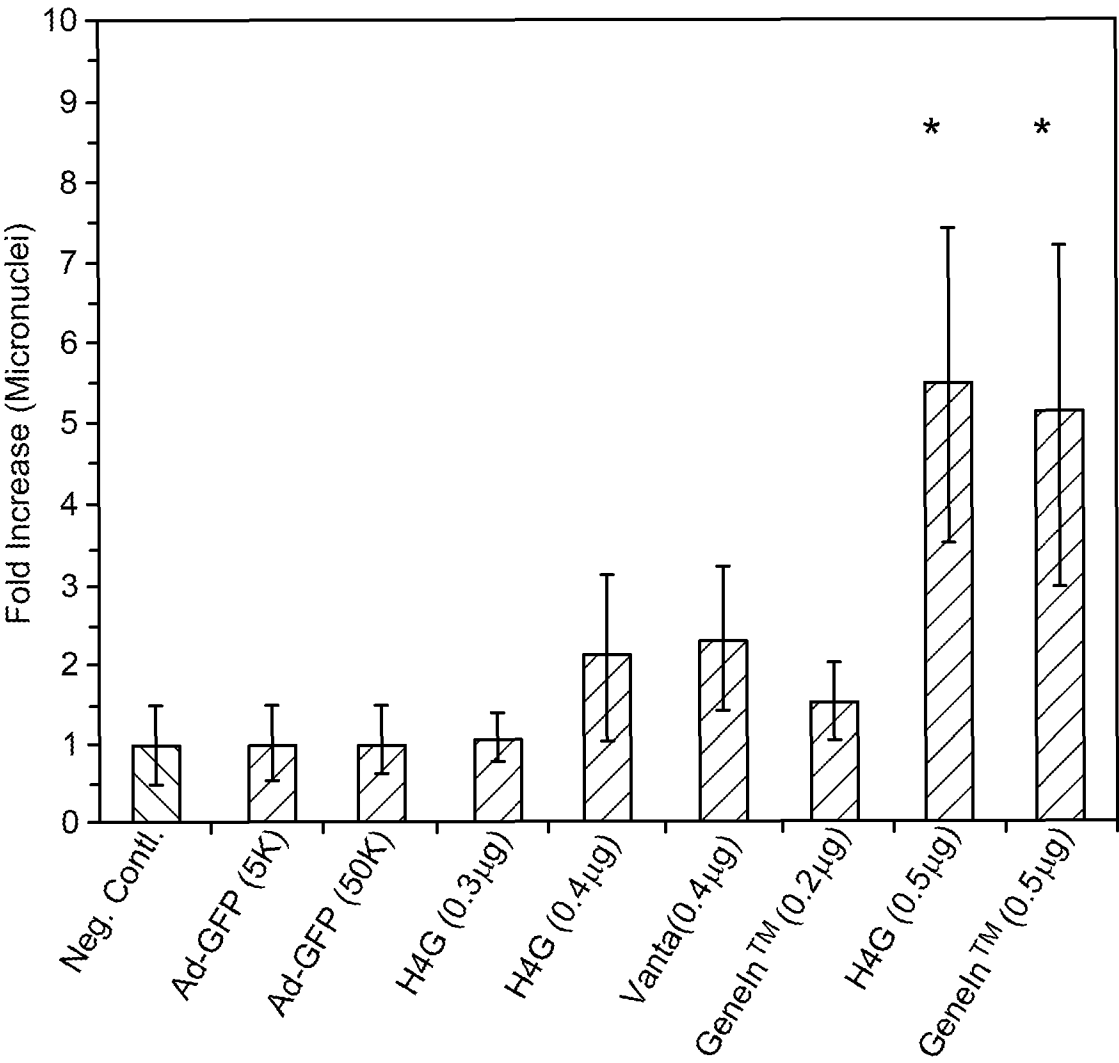


Figure 5A

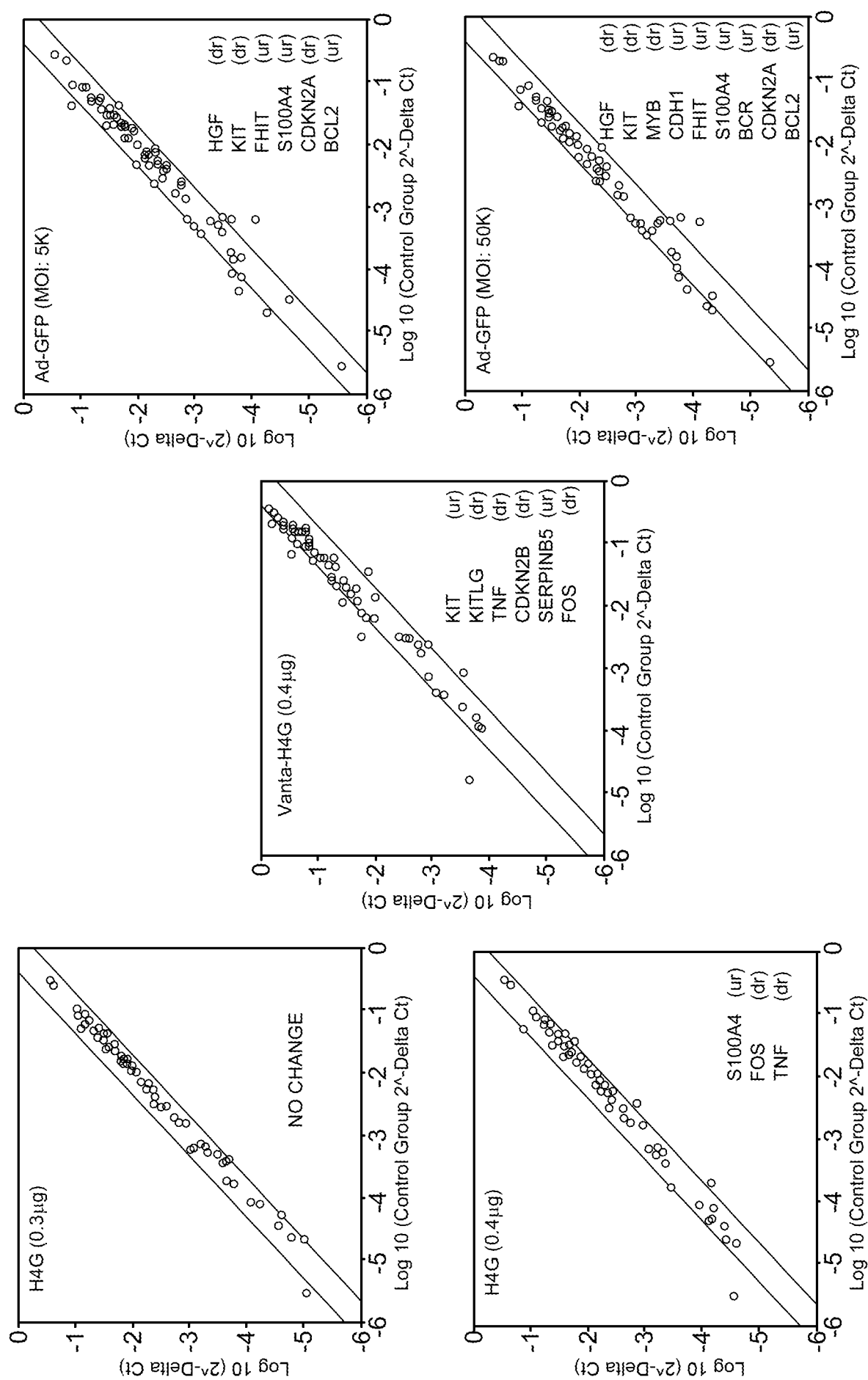


Figure 5B

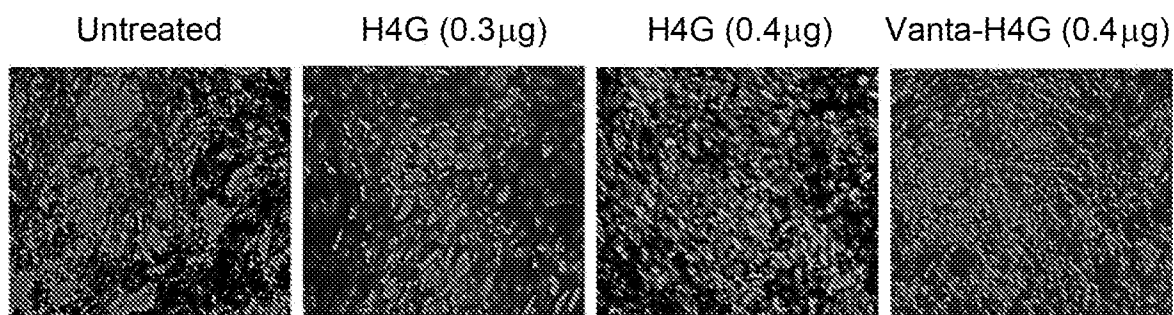


Figure 6A

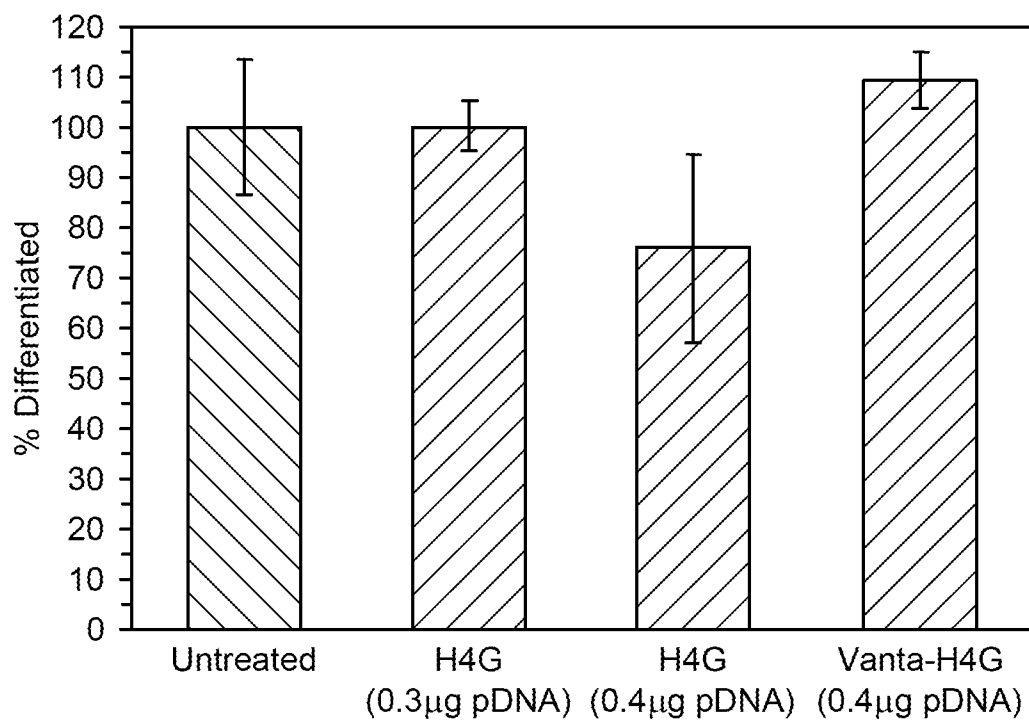


Figure 6B

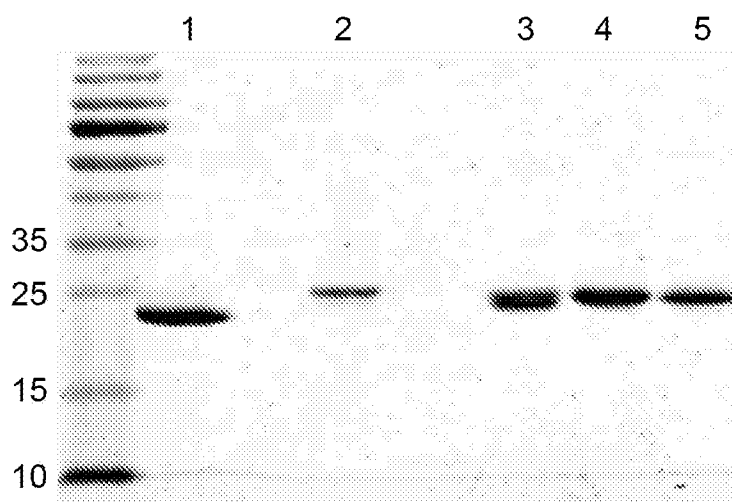


Figure 7

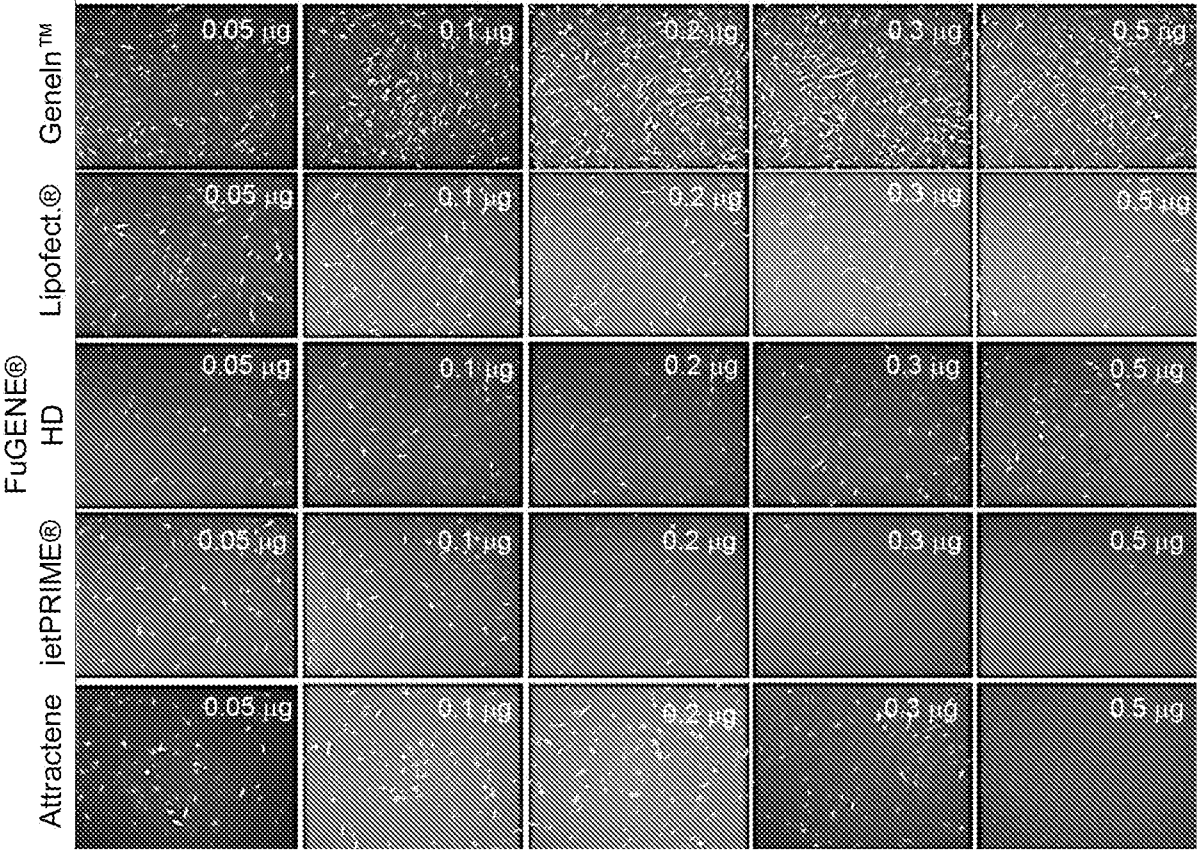


Figure 8A

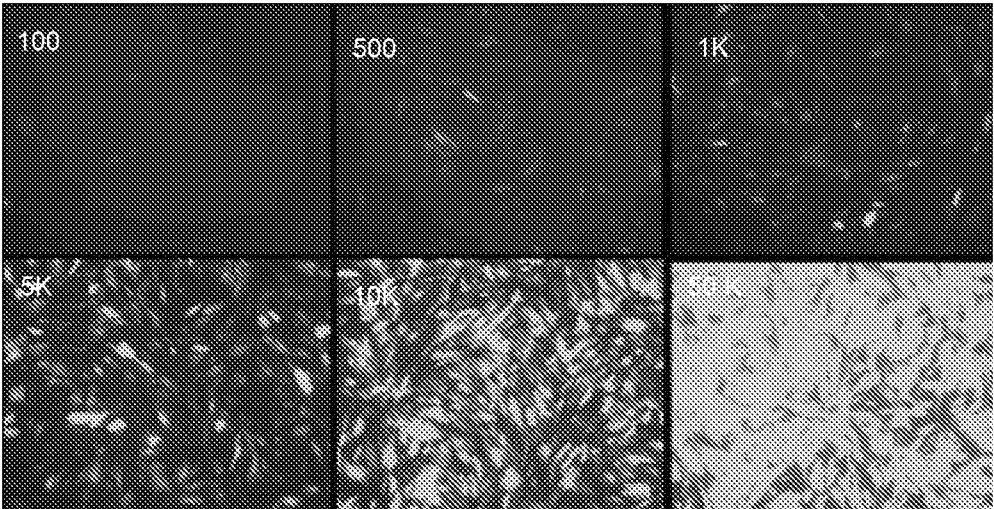


Figure 8B

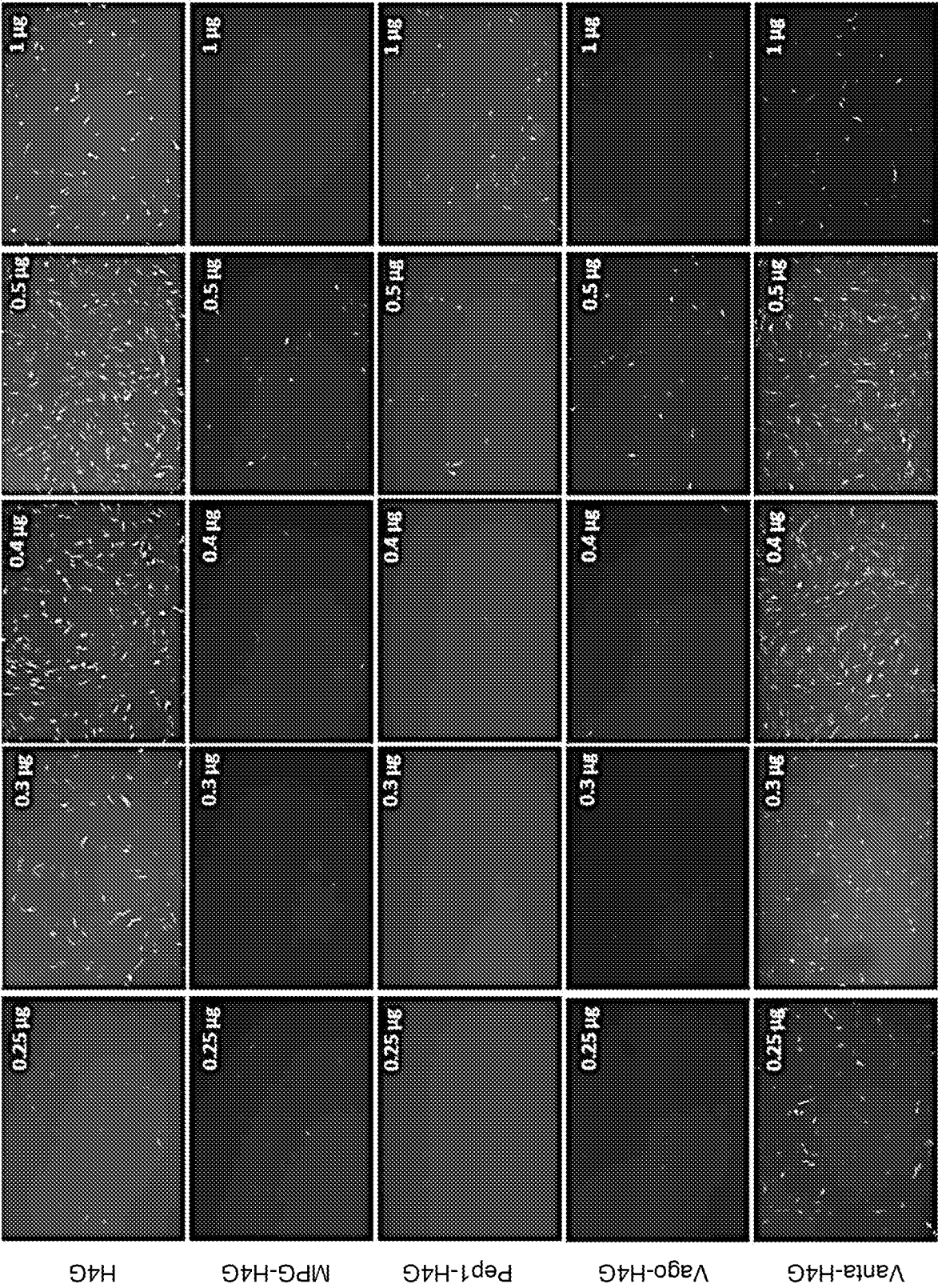


Figure 9

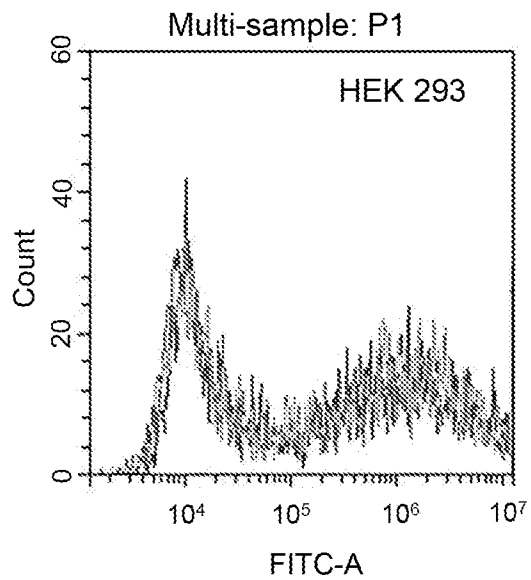


Figure 10A

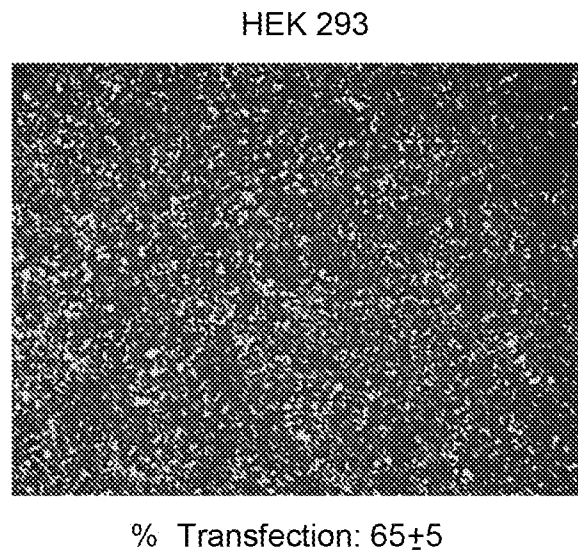


Figure 10B

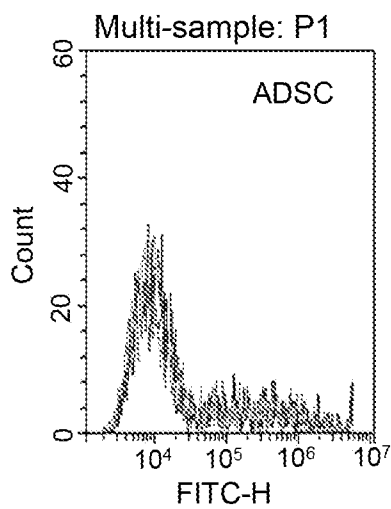


Figure 11A

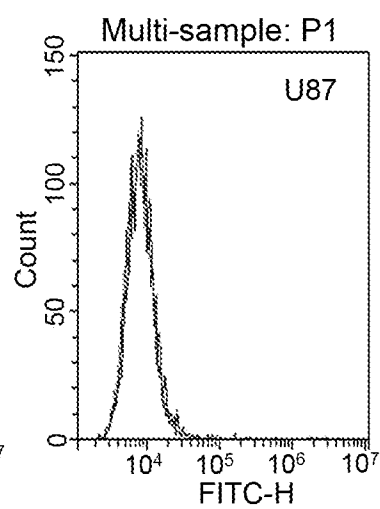


Figure 11B

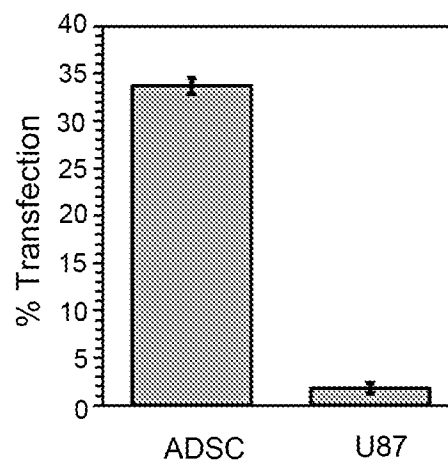


Figure 11C

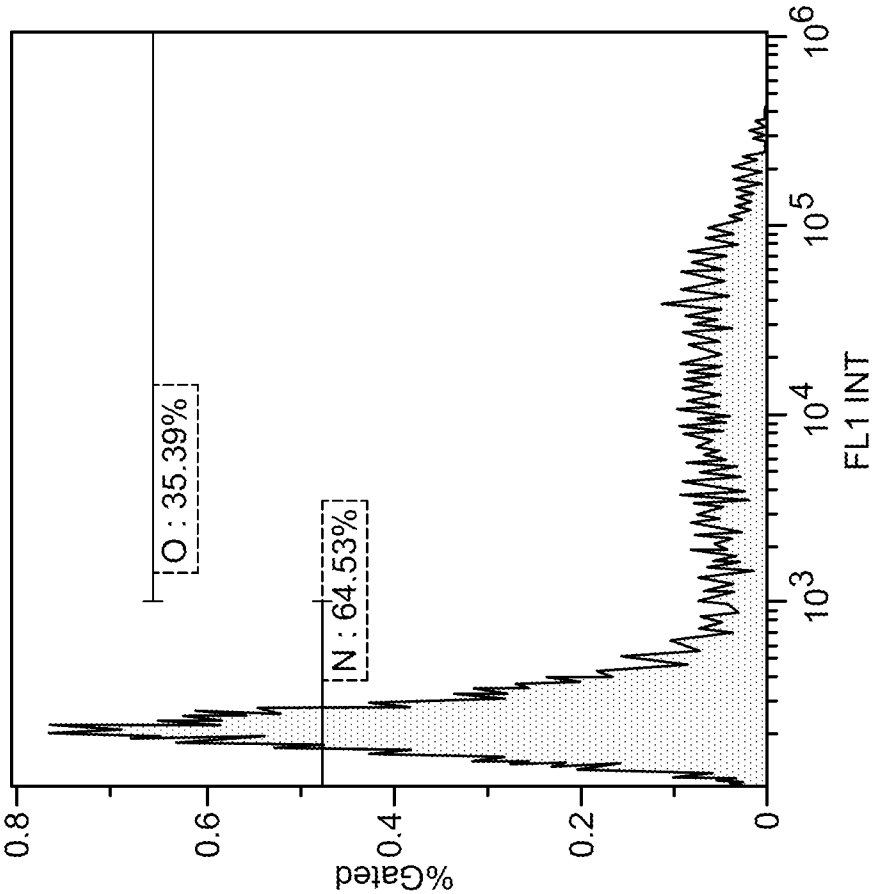
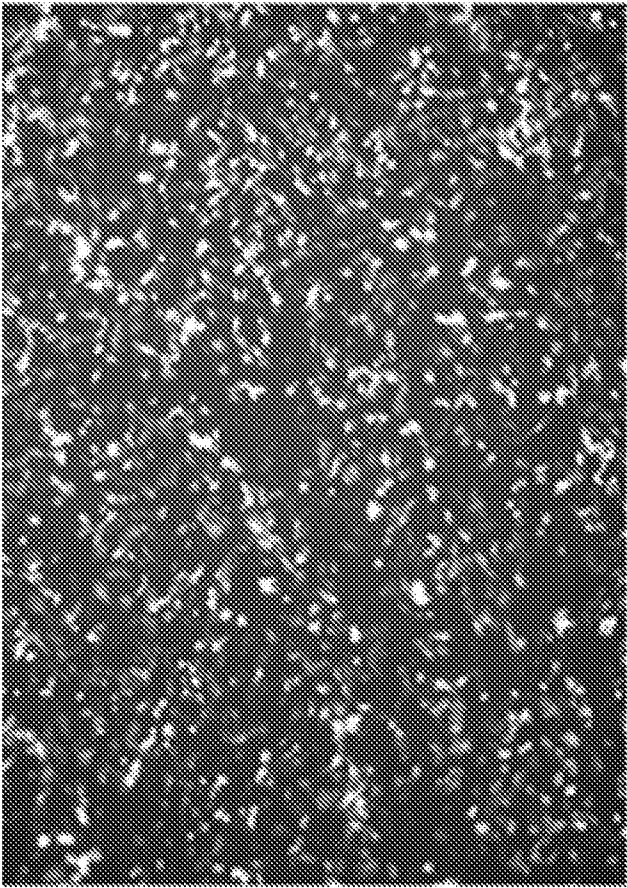


Figure 12A

SKOV-3



% Transfection: 35

Figure 12B

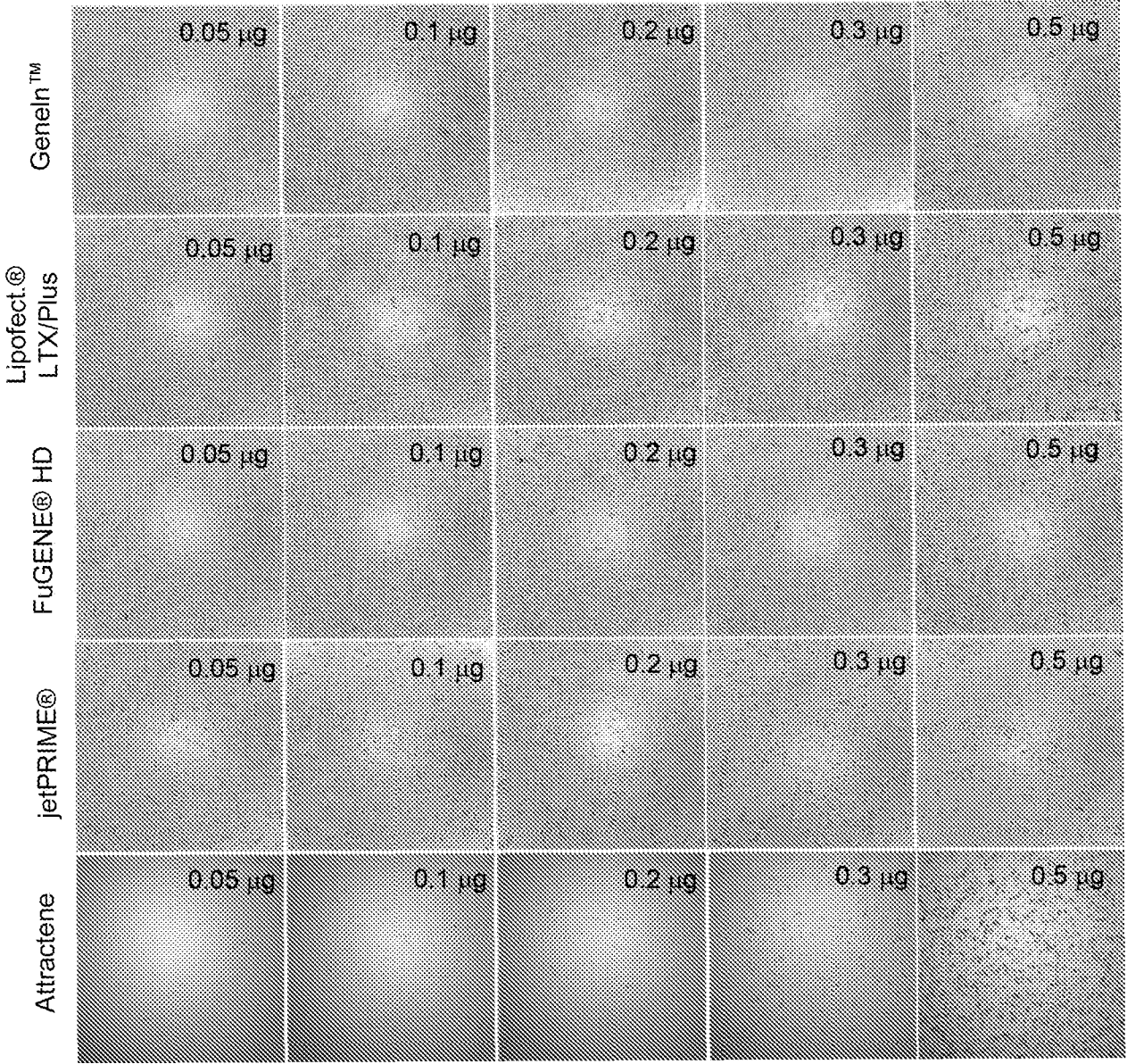


Figure 13

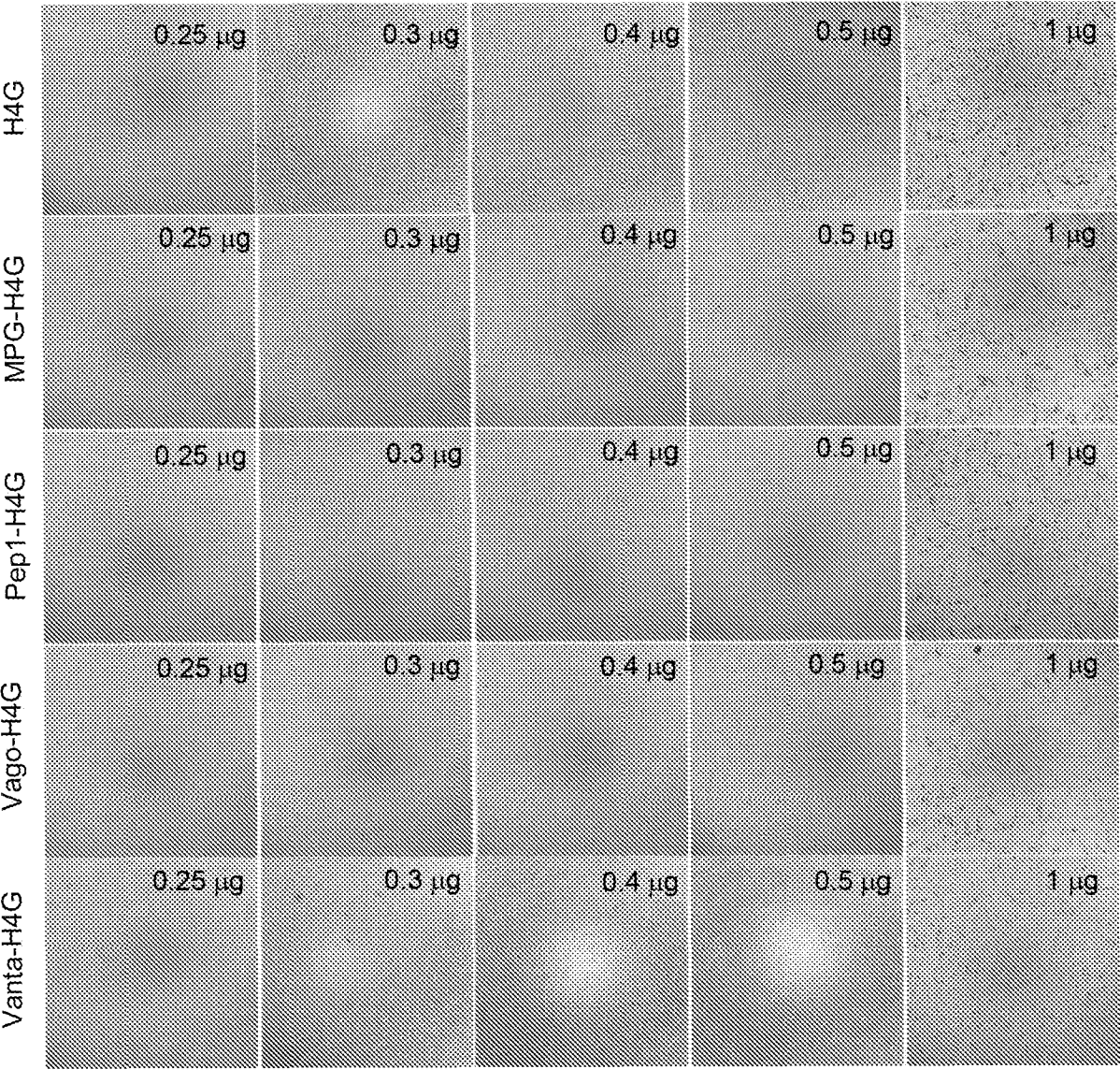


Figure 14

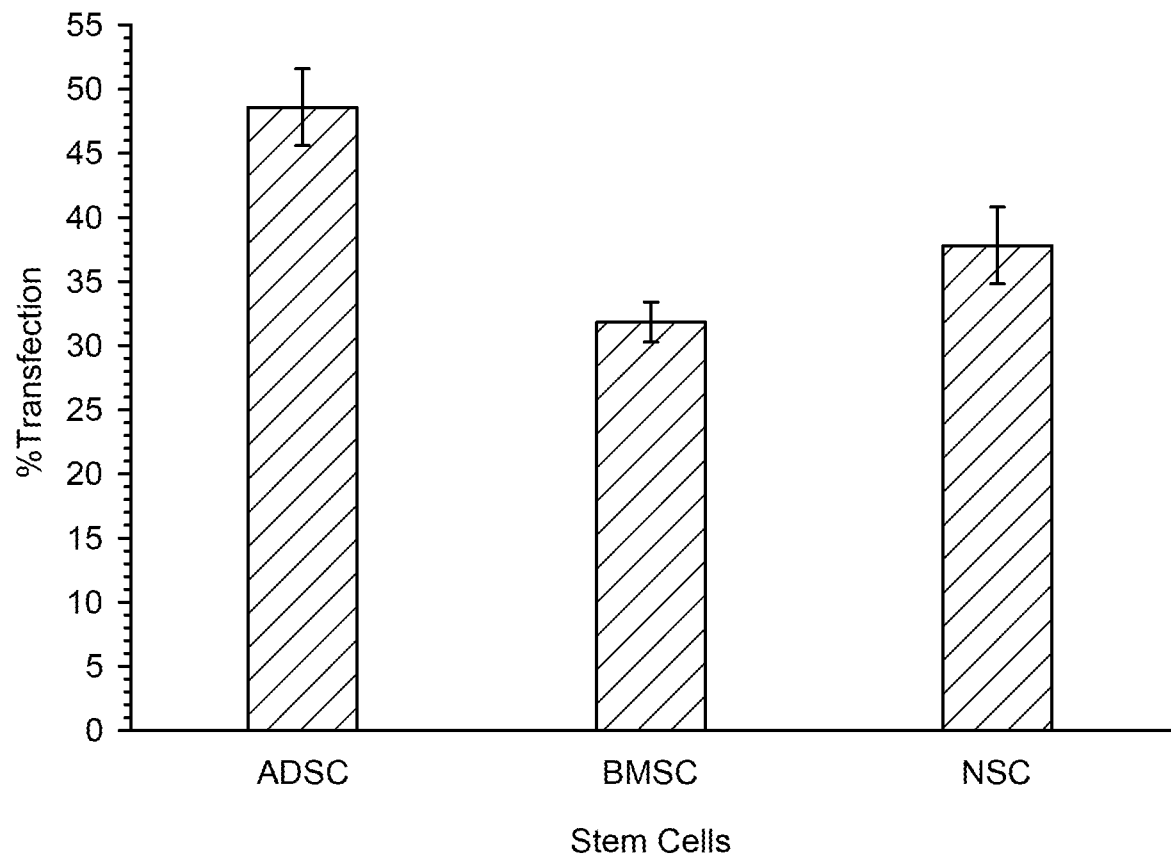


Figure 15

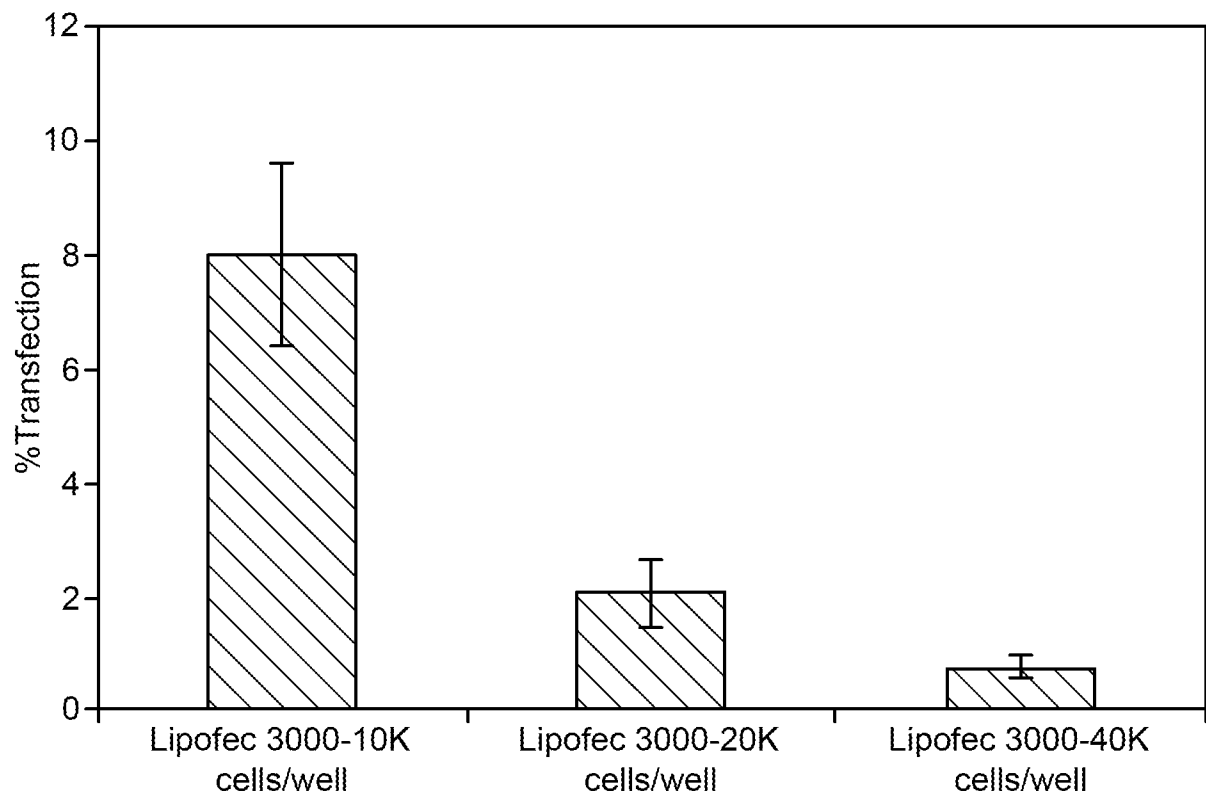


Figure 16A

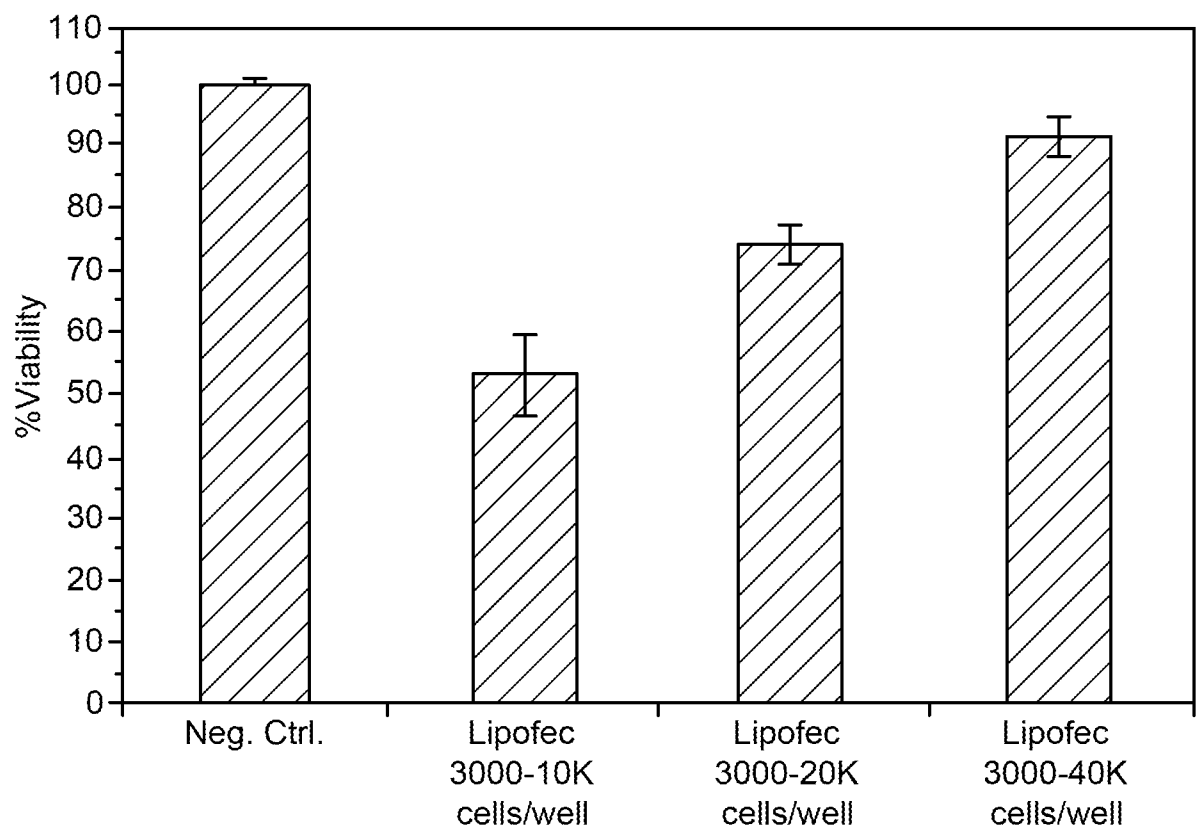


Figure 16B

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2018/042909

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - A61K 38/00; A61K 48/00; C07K 14/435; C07K 19/00; C12N 15/62; C12N 15/63 (2018.01)

CPC - A61K 38/00; A61K 48/00; C07K 14/00; C07K 14/47; C07K 19/00; C07K 2319/00; C07K 2319/01; C07K 2319/02; C12N 15/62 (2018.08)

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

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

See Search History document

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

USPC - 424/192.1; 435/455; 435/69.7; 435/320.1; 514/12; 514/1.1; 536/23.4 (keyword delimited)

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

See Search History document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2007/0098702 A1 (MEGEED et al) 03 May 2007 (03.05.2007) entire document	1, 9, 11, 21, 23-26, 47, 53-55, 57-59
--		
Y		2-8, 10, 12-20, 48-52, 56
X	WANG et al. "Incorporation of histone derived recombinant protein for enhanced disassembly of core-membrane structured liposomal nanoparticles for efficient siRNA delivery," J Control Release, 23 August 2013 (23.08.2013), Vol. 172, Pgs. 179-189. entire document	30, 35-39, 41-44
--		
Y		17-20, 31-34
Y	US 2013/0101628 A1 (WEBBER et al) 25 April 2013 (25.04.2013) entire document	2-6
Y	US 2004/0266694 A1 (TCHISTIAKOVA et al) 30 December 2004 (30.12.2004) entire document	3, 6
Y	US 7,465,784 B2 (WANG) 16 December 2008 (16.12.2008) entire document	7, 8
Y	US 2008/0207502 A1 (RASTELLI et al) 28 August 2008 (28.08.2008) entire document	10
Y	US 2011/0268660 A1 (DANIKAS et al) 03 November 2011 (03.11.2011) entire document	12
Y	WO 2013/132094 A1 (UNIVERSITÄTSKLINIKUM HEIDELBERG et al) 12 September 2013 (12.09.2013) entire document	13, 14
Y	US 2011/0082074 A1 (NISHIMURA et al) 07 April 2011 (07.04.2011) entire document	15, 16
Y	US 2011/0076342 A1 (MALKAS et al) 31 March 2011 (31.03.2011) entire document	31-34



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	FERREIRA et al. "Optimization of a gene electrotransfer method for mesenchymal stem cell transfection," <i>Gene Ther</i> , 07 February 2008 (07.02.2008), Vol. 15, Pgs. 537-544. entire document	48-52, 56
A	CANINE et al. "Biosynthesis and characterization of a novel genetically engineered polymer for targeted gene transfer to cancer cells," <i>J Control Release</i> , 18 April 2009 (18.04.2009), Vol. 138, Pgs.188-196. entire document	1-59
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A	WANG et al. "329. A Genetically Engineered Multifunctional Vector for HER2 Targeted Cancer Suicide Gene Therapy," <i>Molecular Therapy</i> , 01 May 2010 (01.05.2010), Vol. 18, Supp. 1, Pg. S127, Abstract only. entire document	1-59