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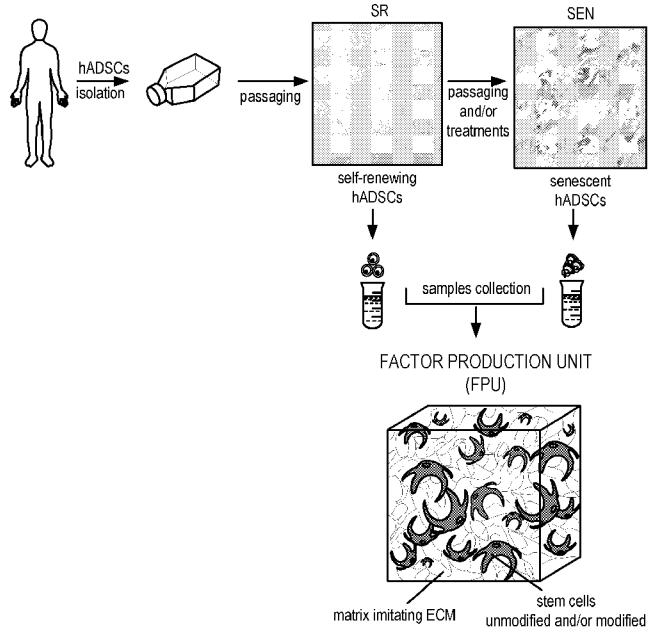
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(54) Title: METHODS AND DEVICES FOR THE PRODUCTION AND DELIVERY OF BENEFICIAL FACTORS FROM STEM CELLS

FIG. 1C



(57) Abstract: Provided herein are methods and devices related to inducing a population of self-renewing or senescent stem cells, to produce one or more beneficial factors for the treatment of a disease or disorder in an individual. Also provided are compositions and methods for inducing senescence, useful for inducing senescence in a population of stem cells, in order to produce one or more beneficial factors for the treatment of a disease or disorder in an individual. Methods and devices to control and customize the production of the beneficial factors for the requirements of a disease or disorder being treated are described. Also provided are factor production units for the production of the beneficial factors, and devices for the delivery of the beneficial factors to an individual in need.

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METHODS AND DEVICES FOR THE PRODUCTION AND DELIVERY OF BENEFICIAL FACTORS FROM STEM CELLS

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Application Serial No. 62/170,604, filed June 3, 2015, U.S. Provisional Application Serial No. 62/170,619, filed June 3, 2015, and U.S. Provisional Application Serial No. 62/175,203, filed June 12, 2015, each of which are incorporated herein by reference in their entirety.

BACKGROUND OF THE INVENTION

[0002] Adult stem cells, for example, adult mesenchymal stem cells (MSCs), generate differentiated cell types within many organs throughout the lifespan of an organism and are thus ultimately responsible for the longevity of multicellular organisms. Stem cells possess three important properties: (1) they self-renew, allowing the maintenance of the original stem cell population; (2) they differentiate into multiple types of mature cells in order to replace the mature cells that turn over in adult tissues; and (3) they maintain the stability stem cell pool through the life (Tollervey and Lunyak, 2011). Utilizing these properties in the clinical setting, stem cell transplantation-based therapies have, for example, been shown to: restore neuronal integrity by stimulating the release of neurotrophic factors by neighboring cells, prevent cognitive decline caused by aging, facilitate nerve recovery after injury both in the CNS and in the periphery; stimulate remyelination processes and glial regenerative support to neurons; prevent retinal damage and maintain retinal barrier properties; impede oxidative insults, produce strong suppression of inflammation and autoimmune response, provide immunomodulation, guide angiogenesis and create microenvironment conducive to regeneration or organ and tissue repair.

[0003] Human adipose derived mesenchymal stem cells (hADSCs or hAMSCs) are currently one of the primary sources of stem cells with direct clinical relevance. Transplanted mesenchymal stem cells, however, pose problems such as oncogenic potential, and poor retention upon implantation.

[0004] While it is known that stem cells possess signaling capabilities and are able to produce and secrete factors, such production cannot be controlled with transplantation. Thus there

remains a need to control and customize the production of, produce, and deliver therapeutic factors from stem cells to individuals in need. Provided herein are methods and devices that address this need.

BRIEF SUMMARY OF THE INVENTION

[0005] Provided herein are methods and devices related to inducing a population of self-renewing (SR) or senescent (SEN) stem cells, to produce one or more beneficial factors for the treatment of a disease or disorder in an individual. Also provided are compositions and methods for inducing senescence, useful for inducing senescence in a population of stem cells, in order to produce one or more beneficial factors for the treatment of a disease or disorder in an individual. Methods and devices to customize the production of the beneficial factors for the requirements of the disease or disorder being treated are also described. Also provided are factor production units (FPUs) for the production of the beneficial factors, and delivery of the beneficial factors to individual in need.

[0006] In one aspect of the invention, provided herein is a method of treating a disease or disorder in an individual comprising delivering one or more factors produced by a population of stem cells to the individual or to a biological fluid from the individual. In one variation, the stem cells comprise mesenchymal stem cells (MSCs). In some variations, the stem cells comprise SR and SEN cells. In some particular variations, the population of stem cells comprises at least 50% SR cells, or comprises at least 50% SEN cells. In some variations, the stem cells have been induced to produce the factors upon exposure to an inducing agent. In a particular variation, the exposure of the population of cells to the inducing agent is for about 24 hours. In some variations, the inducing agent comprises IL-2. In some variations, the stem cells comprise at least 50% SR cells, whereas in other variations, the stem cells comprise at least 50% SEN cells. In some variations, the factors are secreted from the cells. As the invention also contemplates delivery, in some variations, the factors are delivered 24, 48 or 72 hours post-induction. In some variations, the delivery comprises use of a transdermal patch, a plasmapheresis system, a microneedle-based system, a cream, or a dermaroller. In some variations, the disease or disorder is cancer, an autoimmune disease, a cardiovascular disease, diabetes, a skin disease, a neurodegenerative disease, osteoporosis, osteoarthritis, a spinal cord injury, a disease of the liver, a disease of the kidney, an age-related pathology, hair loss, a burn, a condition in need of a skin graft, or a skin lesion. In some variations, the stem cells are adipose derived stem cells

(ADSCs). In some variations, the stem cells are from a vesicular stromal fraction. In some variations, the factors are autologous to the individual, whereas in other variations, the factors are allogeneic to the individual. In some variations, the factors are produced in a factor production unit. In some variations, the factors comprise Interleukin 1 beta (IL1b), Interleukin 3 (IL3), Interleukin-13 Receptor subunit alpha-2 (IL13Rα2), Interleukin 1 receptor alpha (IL1Rα), Probetacellulin (BTC), Colony stimulating factor (CSF1), Fibroblast growth factor 6 (FGF6), Glial cell line-derived neurotrophic factor (GDNF), insulin-like growth factor 1 (IGF-1), Leptin, platelet-derived growth factor B beta (PDGF BB), Brain-derived neurotrophic factor (BDNF), Bone morphogenetic protein 4 (BMP4), Bone morphogenetic protein 6 (BMP6), Ciliary neurotrophic factor (CNTF), Epidermal growth factor (EGF), Fibroblast growth factor 7 (FGF7), insulin-like growth factor-binding protein-4 (IGFBP4), Stem cell factor/c-kit ligand (SCF), Stromal Cell-Derived Factor-1 alpha (SDF1a), Stromal Cell-Derived Factor-1 beta (SDF1b), Angiotensin (ANG), colony stimulating factor 2 (CSF2), Transforming growth factor beta 1 (TGFb1), Transforming growth factor beta 3 (TGFb3), tumor necrosis factor superfamily member 14 (TNFSF14), Chemokine (C-C motif) ligand 2 (CCL2), Chemokine (C-C motif) ligand 5 (CCL5), Chemokine (C-C motif) ligand 7 (CCL7), Chemokine (C-C motif) ligand 8 (CCL8), Chemokine (C-C motif) ligand 11 (CCL11), Chemokine (C-C motif) ligand 13 (CCL13), Chemokine (C-C motif) ligand 22 (CCL22), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C motif) ligand 24 (CCL24), CXC Chemokine ligand 10 (CXCL10), Chemokine (C-X-C motif) ligand 13 (BLC), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C motif) ligand 28 (CCL28), chemokine (C-C motif) ligand 11 (Eotaxin 1), Chemokine (C-X-C motif) ligand 6 (GCP-2), FLT3LG (Fms-Related Tyrosine Kinase 3 Ligand), and Fractalkine (CX3CL1). In some variations, the factors are delivered to a biological fluid from the individual. In some variations, the factors are delivered to plasma from the individual. In some variations, the delivery of the factors to the plasma induces production of regulatory T cells in the blood. In some variations, the delivery of the factors further comprises introducing the blood back into the individual.

[0007] In another aspect of the invention, provided herein is a method of producing one or more factors in a factor production unit comprising adding an inducing agent to a population of stem cells in the factor production unit to induce the production of factors, whereby producing the one or more factors. The factors can be isolated from the factor production unit. In one variation, the stem cells in the factor production unit comprise mesenchymal stem cells (MSCs).

In another variation, the stem cells in the factor production unit comprise adipose derived stem cells (ADSCs). In another variation, the stem cells in the factor production unit are from a vesicular stromal fraction. The stem cells in the factor production unit can comprise SR and SEN cells. In one variation, the population of stem cells comprises at least 50% SR cells; in another variation, population of stem cells comprise at least 50% SEN cells. In some variations, the stem cells in the factor production unit have been induced to produce the factors upon exposure to an inducing agent. The inducing agent can be protein, a small molecule, or a gene-based inducing agent. In one variation, the inducing agent comprises IL-2. In some variations, the factors are secreted from the cells. In some variations, the factors are obtained, and can be obtained 24, 48 or 72 hours post-induction. In some variations, the population of stem cells is from a single individual; in other variations, the population of stem cells is from a plurality of individuals. In a particular variations, a collection of factors is produced and comprises Interleukin 1 beta (IL1b), Interleukin 3 (IL3), Interleukin-13 Receptor subunit alpha-2 (IL13Rα2), Interleukin 1 receptor alpha (IL1Rα), Probetacellulin (BTC), Colony stimulating factor (CSF1), Fibroblast growth factor 6 (FGF6), Glial cell line-derived neurotrophic factor (GDNF), insulin-like growth factor 1 (IGF-1), Leptin, platelet-derived growth factor B beta (PDGF BB), Brain-derived neurotrophic factor (BDNF), Bone morphogenetic protein 4 (BMP4), Bone morphogenetic protein 6 (BMP6), Ciliary neurotrophic factor (CNTF), Epidermal growth factor (EGF), Fibroblast growth factor 7 (FGF7), insulin-like growth factor-binding protein-4 (IGFBP4), Stem cell factor/c-kit ligand (SCF), Stromal Cell-Derived Factor-1 alpha (SDF1a), Stromal Cell-Derived Factor-1 beta (SDF1b), Angiotensin (ANG), colony stimulating factor 2 (CSF2), Transforming growth factor beta 1 (TGFb1), Transforming growth factor beta 3 (TGFb3), tumor necrosis factor superfamily member 14 (TNFSF14), Chemokine (C-C motif) ligand 2 (CCL2), Chemokine (C-C motif) ligand 5 (CCL5), Chemokine (C-C motif) ligand 7 (CCL7), Chemokine (C-C motif) ligand 8 (CCL8), Chemokine (C-C motif) ligand 11 (CCL11), Chemokine (C-C motif) ligand 13 (CCL13), Chemokine (C-C motif) ligand 22 (CCL22), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C motif) ligand 24 (CCL24), CXC Chemokine ligand 10 (CXCL10), Chemokine (C-X-C motif) ligand 13 (BLC), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C motif) ligand 28 (CCL28), chemokine (C-C motif) ligand 11 (Eotaxin 1), Chemokine (C-X-C motif) ligand 6 (GCP-2), FLT3LG (Fms-Related Tyrosine Kinase 3 Ligand), and Fractalkine (CX3CL1). In several variations, the factors are useful for the treatment of cancer, an autoimmune disease, a cardiovascular disease, diabetes, a

skin disease, a neurodegenerative disease, osteoporosis, osteoarthritis, a spinal cord injury, a disease of the liver, a disease of the kidney, an age-related pathology, hair loss, a burn, a condition in need of a skin graft, or a skin lesion. In a particular variation, the factors are useful for derma-cosmetic applications.

[0008] In another aspect of the invention, provided herein is a method of producing one or more factors suitable for derma-cosmetic applications comprising, incubating a population of stem cells with 10% PRP, whereby producing one or more factors suitable for derma-cosmetic applications.

[0009] In another aspect of the invention, provided herein is a method of increasing the number of regulatory T cells in a sample, the method comprising contacting a sample comprising T cells with a factor composition, wherein the factor composition comprises factors collected from SR-hADSCs 72 hours following incubation with IL-2. In some variations, the sample contacted with the factor composition is blood. In other variations, the sample contacted with the factor composition is plasma.

[0010] In another aspect of the invention, provided herein is a factor production unit comprising a substrate and a population of input stem cells. In some variations of the invention, the substrate is a 3-dimensional substrate. The substrate of the factor production unit can comprises a polymer material, for example in some variations the polymer material comprises a biodegradable polymer; whereas in other variations, the polymer material comprises a non-biodegradable polymer. In some variations, the polymer material comprises a polyethylene terephthalate, a polyester, a polymethylmethacrylate, polyacrylonitrile, a silicone, a polyurethane, a polycarbonate, a polyether ketone ketone, a polyether ether ketone, a polyether imide, a polyamide, a polystyrene, a polyether sulfone, a polysulfone, a polycaprolactone (PCL), a polylactic acid (PLA), a polyglycolic acid (PGA), a polyglycerol sebacic, a polydiol citrate, a polyhydroxy butyrate, a polyether amide, a polydiaxanone, fibronectin, collagen, gelatin, hyaluronic acid, chitosan, and combinations, blends, or copolymers thereof. In other variations, the substrate comprises a plurality of electrospun nanofibers or 3-D printed nanofibers. In a particular variation, the nanofibers are electrospun with the stem cells. In some variations, the plurality of electrospun fibers are configured as an artificial extracellular matrix. In some variations, the population of stem cells is disposed on a surface of the substrate, whereas in some variations, the population of stem cells is disposed within a polymer material of the substrate. In

some variations, the stem cells SR and SEN stem cells, for example SR-MSCs and SEN-MSCs. In some variations, the population of stem cells comprise at least 50% SR cells – in some variations the SR cells are induced SR cells. In some variations, the population of stem cells comprises at least 50% SEN cells – in some variations the SEN cells are induced SEN cells. In some variations, the factor production unit is part of an aphereisis system. In a particular variation, the apheresis system is a plasmapheresis system. In some variations, the factors are produced from the factor production unit and the factors are used for modulation of immune cells. In some variations, the factors are produced and used to increase production of regulatory T cells. In some variations, the factors are produced and the factors are used for treatment of autoimmune diseases , cancer, diabetes, a skin disease, a neurodegenerative disease, osteoporosis, osteoarthritis, a disease of the liver, a disease of the kidney, an age-related pathology, a condition in need of a skin graft, or a skin lesion.

[0011] In another aspect of the invention, provided herein are particular factor compositions for use in the treatment of various diseases and disorders. In one variation, a factor composition of the invention comprises factors collected from SR-hADSCs 72 hours following incubation with IL-2. In another variation, a factor composition of the invention comprises Interleukin 1 beta (IL1b), Interleukin 3 (IL3), Interleukin-13 Receptor subunit alpha-2 (IL13Rα2), Interleukin 1 receptor alpha (IL1Rα), Probetacellulin (BTC), Colony stimulating factor (CSF1), Fibroblast growth factor 6 (FGF6), Glial cell line-derived neurotrophic factor (GDNF), insulin-like growth factor 1 (IGF-1), Leptin, platelet-derived growth factor B beta (PDGF BB), Brain-derived neurotrophic factor (BDNF), Bone morphogenetic protein 4 (BMP4), Bone morphogenetic protein 6 (BMP6), Ciliary neurotrophic factor (CNTF), Epidermal growth factor (EGF), Fibroblast growth factor 7 (FGF7), insulin-like growth factor-binding protein-4 (IGFBP4), Stem cell factor/c-kit ligand (SCF), Stromal Cell-Derived Factor-1 alpha (SDF1a), Stromal Cell-Derived Factor-1 beta (SDF1b), Angiotensin (ANG), colony stimulating factor 2 (CSF2), Transforming growth factor beta 1 (TGFb1), Transforming growth factor beta 3 (TGFb3), tumor necrosis factor superfamily member 14 (TNFSF14), Chemokine (C-C motif) ligand 2 (CCL2), Chemokine (C-C motif) ligand 5 (CCL5), Chemokine (C-C motif) ligand 7 (CCL7), Chemokine (C-C motif) ligand 8 (CCL8), Chemokine (C-C motif) ligand 11 (CCL11), Chemokine (C-C motif) ligand 13 (CCL13), Chemokine (C-C motif) ligand 22 (CCL22), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C motif) ligand 24 (CCL24), CXC Chemokine ligand 10 (CXCL10), Chemokine (C-X-C motif) ligand 13 (BLC), Chemokine (C-C motif) ligand 23

(CCL23), Chemokine (C-C motif) ligand 28 (CCL28), chemokine (C-C motif) ligand 11 (Eotaxin 1), Chemokine (C-X-C motif) ligand 6 (GCP-2), FLT3LG (Fms-Related Tyrosine Kinase 3 Ligand), and Fractalkine (CX3CL1). In some variations, the factor compositions of the invention can be further formulated in the form of a cream or lotion. In other variations, a factor composition of the invention is further formulated on a patch comprising microneedles. In other variations, the factor compositions of the invention are further formulated to be combined with a dermaroller-based delivery system. In another aspect of the invention, provided herein are kits comprising any one of the factor compositions of the invention.

[0012] In another aspect of the invention, provided herein is a method of inducing senescence in a SR-stem cell, for example for the purpose of inducing a certain group of factors, the method comprising transfecting into the cell one or microRNAs (miRNAs) selected from the group consisting of miR-17-5p, miR-18a-5p, miR-20a-5p, mir-92a1-5p, mir-19a-3p, mir-125b1-5p, mir100-5p, and mir-let7a-2-3p. In one variation, the SR-stem cell is a SR-hADSC.

[0013] It is to be understood that one, some, or all of the properties of the various variations described herein may be combined to form other variations of the present invention. These and other aspects of the invention will become apparent to one of skill in the art.

BRIEF DESCRIPTION OF THE DRAWINGS

[0014] FIG. 1A illustrates an exemplary method for practicing an aspect of the invention described herein.

[0015] FIG. 1B illustrates an exemplary method of treating an individual using a composition of hADSCs (interchangeably referred to herein as hADMCs as described herein).

[0016] FIG. 1C illustrates an exemplary method of the invention starting from the isolation of hADSCs from an individual, to placement in an exemplary factor production unit described herein.

[0017] FIGS. 2A and 2B show exemplary methods for producing factors and factor compositions, and practicing an aspect of the invention as described herein.

[0018] FIG. 2C illustrates one exemplary method for practicing an aspect of the invention as described herein, for exemplary use of the factors for immunomodulation to influence regulatory T-cell (Treg) production.

[0019] FIG. 2D pictorially illustrates hADSCs in a factor production unit of the invention, as described herein.

[0020] FIGS. 3A-3D illustrate how replicative senescence (SEN) impairs the migratory properties of the human adipose derived mesenchymal stem cells (hADSCs, also referred to herein interchangeably hADSCs). FIG. 3A shows a growth curve of hADSCs and is represented as cumulative population doubling over day in culture. FIG. 3B shows detection of senescence-associated β-galactosidase. FIG. 3C shows *ex vivo* migration assays for SR (left) and SEN (right) hADSCs. FIG. 3D shows the migration of SR-hADSCs (left) and SEN-hADSCs (right).

[0021] FIGS. 4A-4C illustrate the gene expression of IL-2 receptor isoforms and their association with membrane in SR-hADSCs and SEN-hADSCs induced with IL-2. FIG. 4A shows a schematic representation of IL-2 receptor composition. FIG. 4B shows IL-2 receptors α, β, and γ assessed by quantitative PCR (qPCR) SR and SEN-hADSC, either, in the presence or absence of IL-2. FIG. 4C shows the cellular membrane-associated protein levels of IL-2Ra and IL-2Rβ.

[0022] FIG. 5 illustrates the effect of stimulation of the SR and SEN-hADSCs with IL-2. STAT5A, STAT5B and VEGFA mRNA expression was assessed by quantitative RT-PCR.

[0023] FIGS. 6A-6D show a comparison of gene expression levels between SR and SEN cells upon IL-2 treatment.

[0024] FIGS. 7A-7D illustrate gene expression levels for SR and SEN cells upon IL-2 treatment among functionally coherent sets of genes.

[0025] FIGS. 8A-8D illustrate the analysis for RNA-seq profiling of SR and SEN-hADSCs subjected to IL-2 treatment. FIG. 8A provides a schematic representation of the RNA-seq analysis design. FIG. 8B shows the distributions of the gene-specific RNA-seq read counts for each condition prior to ACTB normalization. FIG. 8C shows the condition-specific RNA-seq

read counts for ACTB that were used for normalization. FIG. 8D shows distributions of the gene specific RNA-seq read counts for each condition after ACTB normalization.

[0026] FIG. 9 shows External RNA Controls Consortium (ERCC, a common set of external RNA controls) dose response used for quality control of RNA-seq experiments.

[0027] FIGS. 10A-10B represent tables of the genes differentially expressed upon IL-2 treatment in SEN-hADSCs (senescent hADSCs) and SR-hADSCs (self-renewing hADSCs). FIG. 10A shows biological pathways enriched for genes up-regulated upon IL-2 treatment in SR and SEN-hADSCs. FIG. 10B shows biological pathways enriched for genes down- regulated upon IL-2 treatment in SR and SEN-hADSCs.

[0028] FIGS. 11-90 illustrate the increase in secretion of the named proteins (factors) from SR-hADSCs or SEN-hADSCs maintained in a factor production unit, following incubation media alone (no IL-2 stimulation) or following stimulation with IL-2.

[0029] FIGS. 91-96 illustrate the presence of the particular named factors basally present in the 10% platelet rich plasma (PRP) used as culturing media for hADCSs.

[0030] FIG. 97 illustrates a FACS analysis gating strategy to identify T cells (Tregs).

[0031] FIG. 98 illustrates that factors produced in an exemplary factor production unit of the invention influences production of Tregs.

[0032] FIG. 99 illustrates an exemplary gating strategy, for the identification of Treg populations as described in FIG. 98.

[0033] FIG. 100 shows a schematic diagram of an exemplary factor production unit.

[0034] FIG. 101 shows an exemplary factor production unit in schematic form.

[0035] FIG. 102 shows an exemplary factor production unit in schematic form comprising a plurality of hollow fibers.

[0036] FIG. 103 is a cross-sectional view of the factor production unit provided in FIG. 102 taken at line A-A.

[0037] FIG. 104 shows another exemplary factor production unit in schematic form comprising a fluid treatment compartment and a cell compartment.

[0038] FIG. 105 depicts another exemplary factor production unit comprising electrospun polymer fibers formed as a membrane or fiber mat.

[0039] FIGS. 106A-B show an exemplary factor production unit that can be part of a reverse dialysis system or apheresis system. Specifically, FIG. 106A shows the factor production unit comprising a cartridge formed by a plurality of hollow polymeric fibers (tubes). FIG. 106B provides a cross-sectional view of one of the hollow polymeric tubes in FIG. 106A showing stem cells entrapped within the fiber walls.

[0040] FIG. 107 shows an exemplary factor production unit within an enclosed system.

[0041] FIG. 108 illustrates that senescence associated-miRNAs (SA-miRNAs) function to establish the hADSC senescent phenotype.

[0042] FIG. 109 illustrates a field depicting SA-β-Gal positivity and conversion of SR-hADSCs into SEN-hADSCs.

[0043] FIG. 110 demonstrates the direct influence of SA-miRNAs on gene transcription (on SA-miRNA target genes).

[0044] FIG. 111 demonstrates the indirect influence of SA-RNAs on gene transcription.

[0045] FIG. 112 shows the mean normalized protein expression levels in SR-hADSCs and SEN- hADSCs transfected with SA-miRNAs.

[0046] FIG. 113 illustrates the novel genes that are the targets of SA-miRNA in replicative senescence, and their functional relationships and enrichment.

DETAILED DESCRIPTION OF THE INVENTION

[0047] Described herein are methods and compositions related to inducing a population of stem cells (SCs), for example mesenchymal stem cells (MSCs), to produce one or more beneficial factors for the treatment of a disease or disorder in an individual, where such production is customized for the requirements of the disease or disorder being treated. Also

provided are compositions and methods for inducing senescence, useful for inducing senescence in a population of stem cells, in order to produce one or more beneficial factors for the treatment of a disease or disorder in an individual. Also provided is a factor production unit for the production of the beneficial factors along with methods of making and using thereof.

I. Production of Factors

A. Background and Overall System

[0048] The invention described herein provides compositions, apparatuses, and methods for: the production of one or more beneficial factors by induced stem cells, and for the delivery and administration of such factors to an individual in need. The production system is customizable, tailored to produce factors beneficial for the particular clinical need. The factors can be produced using an individual's own cells (an autologous system) or using cells from another individual (an allogeneic system). Delivery can entail acute or chronic administration paradigms, and virtually any delivery system can be utilized.

[0049] Beneficial factors as provided herein can be polypeptides (full length proteins and peptides) and include wound healing factors, apoptotic factors, anti-apoptotic factors, anti-inflammatory factors, immunomodulatory factors, angiogenic factors, chemokines factors, cytokines factors, interleukins, interleukin receptors, growth factors, growth factor receptors, hormones, adhesion promoting factors, proliferation inducing factors, signal-transduction stimulators and their receptors, neurotrophic factors, regenerative factors, and repair triggering factors. Beneficial factors are not limited to proteins, however, and also include small molecules and metabolites.

B. Input Cells

[0050] As provided herein, populations of mammalian cells comprising stem cells are induced to produce one or more desired beneficial factors. The cell populations used for production (i.e. the input cells) need not be comprised purely of stem cells. One or more cell types can be included in the input cell populations as long as the input cells comprise a suitable type of stem cell that can be induced or generically modified to secrete a factor. Exemplary stem cells include without limitation, embryonic stem (ES) cells, adult stem cells, induced pluripotent stem cells (iPSCs), and SEN cells induced to be SR using a variety of methods. More particularly the

adult stem cells include without limitation hematopoietic stem cells (HSCs) and mesenchymal stem cells (MSCs). Other types of cells that may be employed are stromal vesicular fraction, plasma cells, cord blood cells, placental cells, bone marrow derived cells, epithelial cells, endothelial cells, immune cells, fibroblasts, chondrocytes, hepatocytes, antigen presenting cells, mast cells, muscular cells, antibody producing cells, neurons, and glial cells.

[0051] In one exemplary variation, MSCs are induced for the production of one or more beneficial factors. The use of MSCs in the cell population may be beneficial. MSCs are a subset of non-hematopoietic adult stem cells that originate from the mesoderm and typically possess self-renewal ability and multilineage differentiation into not only mesoderm lineages, such as chondrocytes, osteocytes, adipocytes, and muscle cells, but also ectodermic cells and endodermic cells. MSCs exist in almost all tissues.

[0052] MSCs may be derived from any suitable tissue. In one variation, the MSCs are derived from adipose tissue (ADSCs), and in particular, the stromal vascular fraction (SVF) obtained from digested or mechanically separated adipose tissue. As used herein, the term "adipose" refers to any fat tissue and the adipose tissue may be from any organism having fat tissue. The adipose tissue may be brown or white adipose tissue, derived from subcutaneous, omental/visceral, mammary, gonadal, or other adipose tissue sites in a mammal. In certain variations, the adipose is subcutaneous white adipose tissue, visceral adipose tissue, or a lipoaspirate sample. A convenient source of adipose tissue is from liposuction surgery, however, the source of adipose tissue need not be so limited. The adipose tissue may be digested with any suitable enzyme (e.g. collagenase) to yield MSCs or may be mechanically separated. In some variations, the MSCs human are adipose derived MSCs (hADMCs or hADSCs or hADMSCs). In other variations, the MSCs are from non-human mammalian adipose tissue.

[0053] The input cells may be autologous (cells from the individual who receives the factors) or allogeneic (cells not from the individual who receives the factors). The input cells may comprise cells from a single individual, or alternatively comprise a mixture of cells from more than one individual. The cells may be purely ADSCs, or may be a heterogeneous mix of cells. It is understood that a skilled artisan will have the ability to customize the input cells in order to control the subsequent factor production.

[0054] In some variations, the input cell comprise stem cells, wherein the stem cells are at least 20%, 30%, 40%, 50%, 60%, 70%, 80%, or even 90% SR stem cells (e.g. SR-ADSCs, or SR-hADSCs). In an exemplary variation the input cells are MSCs and comprise at least 50% SR MSCs. The SR stem cells can be defined in regards their morphology, proliferation index and one or many markers.

[0055] In some variations, the input cell comprise stem cells, wherein the stem cells are at least 20%, 30%, 40%, 50%, 60%, 70%, 80%, or even 90% SEN stem cells (e.g. SEN-ADSCs, or SEN-hADSCs). In an exemplary variation the input cells are MSCs and comprise at least 50% SEN MSCs. The SEN stem cells can be defined in regards their morphology, proliferation index and one or many markers.

1. Induction of Senescence

[0056] In some variations, to achieve the production of a particular set of desired factors, it is desirable to utilize stem cells that are senescent or are nearing senescence (collectively referred to as SEN). As used herein SEN stem cells are those cells that are replicatively senescent. Replicative senescence is characterized by growth arrest, apoptosis resistance, high levels of metabolic activities, morphological and cell-size changes, high levels of expression of the tumor suppressors P16, P21, P53 and/or RB, increased activity of senescence associated beta galactosidase (SA-β-gal) and the loss of the ability to synthesize and repair DNA. The replicative aging of stem cells can influence their biological properties.

[0057] In particular variations, the stem cells are SEN-ADSCs, for example SEN-hADSCs. Stem cells may be naturally SEN or they may be induced to undergo senescence. When referring to SEN cells throughout, it is to be understood that this term encompasses both naturally occurring SEN stem cells as well as those stem cells induced to be SEN. Exemplary methods to induce stem cells to undergo senescence include, but are not limited to, delivery of noncoding miRNAs (described below), delivery of senescence-inducers such as those described in WO2013/078392, including, but not limited to exposure to a genotoxin, radiation, ultraviolet light, a tumor suppressor inducer, a mitotic inhibitor, a nucleic acid damaging agent, an antitumor antibiotic, a topoisomerase inhibitor, a hormone inhibitor, a growth factor inhibitor, or a PARP inhibitor.

[0058] In one variation, a method of inducing senescence comprises transfection of senescence-associated miRNA mimics into a population of SR cells or a population of stem cells comprising at least some SR cells in need of induction to achieve a SEN state. In this variation, SR-ADSCs are transfected with a miRNA selected from miR-17-5p, miR-18a-5p, miR-20a-5p, mir-92a1-5p, mir-19a-3p, mir-125b1-5p, mir100-5p, and mir-let7a-2-3p, as described in Example 10 and FIGS. 108-112.

2. Induction of Stemness (Rejuvenation)

[0059] In other variations, to achieve the production of a particular set of desired factors, it is desirable to utilize stem cells that are SR and exhibit a high degree of stemness. In particular variations, the stem cells are SR-ADSCs, for example SR -hADSCs. The stem cells can be naturally SR, or they may rejuvenated to be SR. When referring to SR cells throughout, it is to be understood that this term encompasses both naturally occurring SR stem cells as well as those stem cells induced to be SR. Exemplary methods to induce stem cells to undergo rejuvenation include, but are not limited to those described in WO2012058097 and WO2013126565 (reducing the level or activity of SINE/ALU retrotransposon transcripts in a population of stem cells).

[0060] In one variation, an exemplary method comprises isolation of a sample comprising stem cells. The sample is assayed to determine if it is SEN or SR, by looking at particular characteristics as described above. If SEN, cells may be rejuvenated to be SR as provided above. The factors released by rejuvenated SEN stem cells may be the same or different from SR stem cells.

[0061] In one variation, rejuvenating a SEN stem cell involves reducing the level or activity of SINE/ALU retrotransposon. Reduction may include introducing into said cell any construct that comprises or encodes a small interfering RNA (siRNA or shRNA) molecule that targets SINE/ALU retrotransposon transcripts. For example, a small interfering RNA can comprise a molecule selected from the group consisting of a single strand RNA, a paired double strand RNA (dsRNA), a small hairpin RNA (shRNA), and a PIWI RNA (piRNA). The construct may produce a stable down-regulation of SINE/ALU transcripts, or in some variations a temporary down-regulation. For example, the construct may comprise a vector, such as a plasmid vector or

a viral vector. For example, a viral vector may be selected from the group consisting of a retroviral vector, a lentiviral vector, an adenoviral vector, and an adeno-associated vector.

[0062] Any appropriate mechanism for introducing the construct may be used, for example, transformation, transduction, transfection, or infection. In some variations, the method may include via a lipid or liposome. In addition, the delivery of the Synthetic piRNA that targets SINE/ALU retrotransposons can be accomplished by use of any type of biolistic device that provides a physical method of transfecting cells with DNA and is not dependent on specific ligand-receptors or any biochemical features (see, e.g., US20040033589).

[0063] In one variation, rejuvenation may be achieved by those methods described in Wang et al. (Nature. 2014 Dec 18;516(7531):405-9), with delivery of HERVH to drive HERVH-based transcription; or to drive LBP9 transcription factor-driven rejuvenation of adult stem cells.

[0064] In some variations, the step of reducing the level or activity of SINE/ALU retrotransposon transcripts in a population of input stem cells in an amount sufficient to induce or restore proliferative capacity is performed only in cells first identified as SEN. For example, cells (fresh or cryopreserved) may be screened by quality control (QC) techniques as described herein to identify SEN cells, and these cells may be targeted for rejuvenation. Thus, any of the methods described herein may include a QC step to identify the senescent state of the cells prior to rejuvenation and/or induction. Alternatively, in some variations all of the cells in a mixed population of SEN and SR stem cells may be treated for rejuvenation using any of the methods described herein for rejuvenation. Once rejuvenated, the factors of a population of just formerly SEN rejuvenated cells, or a mixed population of SR/rejuvenated SEN may be used directly from these cells (e.g., without induction). Alternatively or additionally a population of rejuvenated SEN cells, a mixed population of rejuvenated SEN and SR cells, or a population of just SR cells may be induced to produce factors, and their resulting factors used as described herein. In some variations, factors (and/or the cells themselves) from induced and non-induced populations may be combined, or used separately. In some variations, extracts from induced or non-induced populations are administered. This is schematically described in FIG. 1A.

[0065] The use of rejuvenated stem cells may be particularly important in situations where cryopreserved or other storage methods are used. Prolonged passage or revival of the stem cells

from cryopreservation generally reduces the capacity of stem cells to divide, when compared to freshly isolated stem cells, which may be in a SR state.

C. Induction of Stem Cells and the Production of Factors

[0066] As provided herein, the production of factors from SEN and SR stem cells is customizable for the treatment of a broad range of diseases and disorders. In response to inducing agents, under particularized sets of conditions, stem cells can be induced to produce or secrete particular combinations of factors. Contributing to the particular combinations of factors produced include which type of stem cells are induced, characterization of the stem cell population as SR or SEN, the inducing agent selected for use, the duration of induction, and the time interval post-induction.

[0067] In variations provided herein, collections of factors can be characterized generally to be, for example, collections of a plurality of factors, where one or more of the factors are wound healing factors, apoptotic factors, anti-apoptotic factors, anti-inflammatory factors, immunomodulatory factors, angiogenic factors, chemokines factors, cytokines factors, interleukins, interleukin receptors, growth factors, growth factor receptors, hormones, adhesion promoting factors, proliferation inducing factors, signal-transduction stimulators and their receptors, neurotrophic factors, regenerative factors, and repair triggering factors.

1. Inducing Agents and Conditions

[0068] The stem cells of the invention are placed in contact with (e.g. combined with) an inducing agent of the invention. As used herein, an inducing agent can be any molecule or genetic modification capable of interacting with or influencing a stem cell (e.g. bind a receptor, specifically or non-specifically; induce transcription and translation), produce inducing factors by integrating into the genome of stem cells or express them ectopically, influencing or inducing a stem cell's gene expression, influencing a stem cell's signal transduction, and/or influencing a stem cell's transcriptional, translational, or post-translational machinery to induce the production and secretion of one or more factors.

[0069] Non-limiting examples of inducing agents include small molecules, proteins, peptides, antibodies, oligonucleotides, aptamers, factors encoded by a nucleic acid molecule, as well as RNAi, miRNA, or long ncRNA.

[0070] Representative examples of virus vectors used for gene introduction include an adenovirus vector, an adeno-associated virus vector, and a retrovirus vector. A target gene may be introduced into a cell by introducing a target gene into a DNA or RNA virus, such as a detoxicated retrovirus, herpes virus, vaccinia virus, poxvirus, poliovirus, Sindbis virus, Sendai virus, SV40, or human immunodeficiency virus (HIV), and infecting the cell with such recombinant virus, or with the use of CRISPR technology.

[0071] In one variation, the inducing agent comprises a cytokine, for example IL-2, retinoid acid and its derivatives, chemotactic factors, chemokines, hormones, growth factors, leukotrienes, prostaglandins, thromboxanes and platelet activating factor (PAF), and mediators secreted by cells exemplified but not limited to Mast cell secreted mediators.

[0072] In one exemplary variation, the inducing agent is IL-2, or an isoform of IL-2.

[0073] Induction factors may be combined with the cells in any type of media, or delivered by the means of genetic engineering (e.g. if the inducing factor is encoded by a nucleic acid molecule), as well as delivered as RNAi, miRNA, long ncRNA.

[0074] The media comprising the factors produced/secreted upon induction may be referred to herein as "conditioned media."

[0075] In one exemplary variation, the cells are cultured in a media comprising platelet rich plasma (PRP, for example 10% PRP) and the inducing agent is mixed with the media.

[0076] In another variation the cell are cultured in plasma, serum, umbilical cord blood serum, and platelet derivatives like platelet lysate. In one variation, the SVF is cultured using human platelet lysate. In other variations, platelet-rich plasma is included in the SVF culture medium

[0077] In another exemplary variation, when a stromal vesicular fraction is used for factor production, fetal bovine serum (FBS) and fibroblast growth factor (FGF)-2 are substances that can be used in the culture medium.

[0078] In another variation, the cells are cultured in a serum free media. The serum free media may comprise components such as the elements provided in standard serum-free media formulations, including an energy source such as glucose, inorganic salts, fat soluble components, a nitrogen source and vitamins or lipid compositions.

[0079] In general, inducing the stem cells include exposing the stem cells to the inducing agent (interchangeably referred to herein throughout as exposing the stem cells to an inducing agent/priming with an inducing agent/contacting with an inducing agent/inducing with an inducing agent/incubating with an inducing agent/stimulating with an inducing agent), for a predetermined amount of time, such as longer than 5 minutes, 1 hour, 2 hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 11 hours, 12 hours, 13 hours, 14 hours, 15 hours, 16 hours, 17 hours, 18 hours, 19 hours, 20 hours, 21 hours, 22 hours, 23 hours, 24 hours, 30 hours, 36 hours, 42 hours, 48 hours, 3 days, 4 days, or even longer than 5 days. The cells may be exposed to a constant level of the inducing agent or to a varying level (e.g., initial higher, then followed with lower-levels, increasing levels over the time of exposure, decreasing levels over the time of exposure, random levels over the time of exposure, etc.). Following exposure, the cells may be washed or otherwise treated to remove the inducing agent, prior to using the factors produced by the cells. Varying incubation times influence the production of the factors and thus can be varied in order to customize the production for a particular downstream clinical application. In some variations, factors are collected immediately after the removal of the inducing agent; in some variations, the factors are collected/removed/delivered/used 5 minutes, 1 hour, 2 hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 11 hours, 12 hours, 13 hours, 14 hours, 15 hours, 16 hours, 17 hours, 18 hours, 19 hours, 20 hours, 21 hours, 22 hours, 23 hours, 24 hours, 30 hours, 36 hours, 42 hours, 48 hours, 3 days, 4 days, or even longer than 5 days after removal of the induction agent. In some exemplary variations, the factors are collected/removed/delivered/used 24, 48, or 72 hours following removal of the inducing agent. In other exemplary variations, the cells are combined with the induction agent for a prescribed period of time as above, the induction agent is removed (e.g. media is replaced) and the cells are allowed to recover for a predetermined time period post-induction ranging from one (1) hour, six (6) hours, 12 hours, 24 hours, 36 hours, 48 hours, 60 hours, or 72 hours, or any combination of these time periods post-induction.

2. Induction of Factor Production

[0080] The induction and production can be tailored to produce specific factors. This may be achieved in various ways, e.g., by selecting a certain cell population, by adjusting the composition of the cell culturing media, or by selecting a particular induction agent. As provided herein, and described below, the production of factors take place in any one of the

factor production units provided herein. A factor production unit comprises a population of input stem cells and a substrate that provides support for the cell population.

[0081] The duration of culturing (e.g., post induction) may be adjusted or controlled to customize factor production by the factor production unit. Factors can be collected at predetermined times ranging from 5 minutes to 5 days post induction, and is described above.

[0082] Factors which may beneficial in the methods described herein include without limitation, interleukins that are involved in skin regeneration/rejuvenation pathways, interleukin receptors and binding proteins, growth factors, growth factor receptors, chemokines, cytokines , chemotactic factors, molecules that provide cell adhesion, factors that may promote cell proliferation, neurotrophic factors, factors that may promote skin regeneration, factors that may promote or suppress wound healing, factors that may promote hyaluronic acid synthesis, factors that may promote skin elasticity, factors that suppress malignancy formation, factors related to inhibition of UV-induced skin damage and pigmentation, and factors that stimulate hair growth, factors that stimulate metabolism, endocrine functions and improve insulin sensitivity, factors that promote nitric oxide production, anti-apoptotic factors, pro-apoptotic factors, anti-necrotic, anti-inflammatory factors and factors useful to suppress asthma and allergic reactions , immunomodulatory, angiogenic, immunomodulators, signal transduction ligands and receptors, neurotrophic factors suppressing brain inflammation, brain trauma and neuromuscular disease aspects , factors suppressing abnormalities in neurocrest development, factors potentiating reversal of degeneration of spinal cord motor neurons axons, and stimulating neurogenesis and neuronal survival, factors promoting restoration of extacellular matrix (ECM) by production of collagen, elastin and hyaluronan, bactericidal, anti-microbial, anti-fungal activities, and factors promoting cell survival, tissue repair, regeneration and cell differentiation.

[0083] FIGS. 11-17 show the increase in secretion of the below named proteins (factors) from SR-hADSCs maintained in a factor production unit of the invention, 24 hours post incubation with media containing 10% PRP (platelet-rich plasma) alone (no IL-2 stimulation). Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support. The factors produced from the factor production unit are beneficial and can provide therapeutic benefits for: stimulation of immunoresponse in burns and diseases leading to inflammation upon tissue damage, such as wound healing, Inflammatory Bowel Disease (IBD) such as Crohn's disease (CD) and ulcerative

colitis, Rheumatoid arthritis (RA), Sjogren's syndrome, polymyositis, dermatomyositis and scleroderma, derma-cosmetic applications related to aged and photo-damaged skin, and for treatments required antimicrobial protein with bactericidal and antifungal activity,

[0084] FIG. 11 shows the increase in secretion of Interleukin 5 (IL5) and Interleukin 6 (IL6). Controlled production and delivery of IL-6 may be desirable for delivery for anti-inflammatory conditions, osteoporosis, and for improvement of sleep-associate conditions. Controlled production and delivery of IL-5 may be desirable for enhancing immunity, such as increase in production of Th1 cells, macrophages, IFN-gamma, and dendritic cells.

[0085] FIG. 12 shows the increase in secretion of Interleukin 1 receptor 4 (IL1R4). FIG. 13 shows the increase in secretion of Neurotrophin 3 (NT3), platelet derived growth factor A alpha (PDGF AA), platelet derived growth factor A beta (PDGF AB), and pro-platelet basic protein (PPBP). FIG. 14 shows the increase in secretion of Chemokine (C-C motif) ligand 18 (CCL18), Chemokine (C-Cmotif) ligand 25 (CCL25), Chemokine (C-C motif) ligand 27 (CCL27), and CXC chemokine ligand 11 (CXCL11). FIG. 15 shows the increase in secretion of Intercellular Adhesion Molecule 1 (ICAM-1) and Metalloproteinase inhibitor 2 (TIMP-2). FIG. 16 shows the increase in secretion of Metalloproteinase inhibitor 1 (TIMP-1). FIG. 17 shows the increase in secretion of vascular epithelium (VE) Cadherin (calcium dependent cell adhesion protein).

[0086] FIGS. 18-19 show the increase in secretion of the below named proteins (factors) from SR-hADSCs, 24 hours post incubation with 10% PRP alone (no IL-2 stimulation). These proteins were found to not be present in PRP. FIG. 18 shows the increase in secretion of Interleukin 4 (IL4). FIG. 19 shows the increase in secretion of insulin-like growth factor-binding protein-1 (IGFBP1).

[0087] The factors produced by this factor production unit (FIGS. 18-19) can provide therapeutic benefits for stimulation of activated B-cell and T-cell proliferation, and the differentiation of B cells into plasma cells. IL-4 induces B-cell class switching to IgE, and up-regulates MHC class II production. IL-4 decreases the production of Th1 cells, macrophages, IFN-gamma, and dendritic cell. The presence of IL-4 in extravascular tissues promotes alternative activation of macrophages into M2 cells and inhibits classical activation of macrophages into M1 cells. IGFBP1 and 2 and their proteolytic fragments have been shown to

improve tissue repair under inflammatory conditions, through effects on proliferation and migration of human gingival fibroblasts.

[0088] FIGS. 20-31 show an increase in the below named proteins (factors) from SR-hADSCs maintained in a factor production unit of the invention, 48 hours post incubation with 10% PRP alone (no IL-2 stimulation). Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support.

[0089] The factors produced from the factor production unit under these conditions may provide therapeutic benefits for: hair growth and morphogenesis, cutaneous wound, a dermatologic disorder, a dermatological lesion, dermatitis, psoriasis, condyloma, verruca, hemangioma, keloid, skin cancer, atopic dermatitis, Behcet disease, chronic granulomatous disease, cutaneous T cell lymphoma, ulceration, a pathological condition characterized by initial injury inducing inflammation and immune dysregulation leading to chronic tissue remodeling including fibrosis and loss of function, skin defense against infection, new synthesis of collagen, elastin and hyaluronan, inhibition of melanoma growth, diabetic ulcers, myocardial infraction, atherosclerosis, Celiac Disease, rheumatoid arthritis (RA), Inflammatory Bowel Disease (IBD), asthma, encephalitis, chronic obstructive pulmonary disease (COPD), inflammatory osteolysis, allergic disorders, septic shock, pulmonary fibrosis (e.g. , idiopathic pulmonary fibrosis), inflammatory vacultides (e.g. , polyarteritis nodosa, Wegner's granulomatosis, Takayasu's arteritis, temporal arteritis, and lymphomatoid granulomatosus), post-traumatic vascular angioplasty (e.g. restenosis after angioplasty), undifferentiated spondyloarthropathy, undifferentiated arthropathy, arthritis, inflammatory osteolysis, chronic hepatitis, and chronic inflammation resulting from chronic viral or bacterial infections, chronic liver fibrosis, cirrhosis, fulminant hepatic failure, allergic airway inflammation, acute lung injuries, myocardial infarction, fetal maternal tolerance, osteoarthritis, GVHD, treatment of neurodegenerative pathologies, such as for example Parkinson's disease, Alzheimer's disease, progressive supranuclear palsy, multiple system atrophy, amyotrophic lateral sclerosis, Huntington's chorea or following trauma such as stroke and cerebral or spinal traumas.

[0090] FIG. 20 shows the increase in secretion of Interleukin 9 (IL9) and Interleukin 18 binding protein alpha (IL18BPa). FIG. 21 shows the increase in secretion of Interleukin 1 receptor type II (IL1R2), Interleukin 2 receptor beta (IL-2Rb), Interleukin 2 receptor gamma (IL-

2Rg), Interleukin 5 receptor alpha (IL5Ra), Interleukin 10 receptor beta (IL10Rb), Interleukin 18 receptor accessory protein (IL18Rb), and Interleukin 21 receptor (IL-21R). FIG. 22 shows the increase in secretion of Insulin-like growth factor 2 (IGF2), Transforming growth factor alpha (TGFa), Transforming growth factor beta 1/latency-associated peptide (LAP) (TGFb1), and Transforming growth factor beta 2 (TGFb2). FIG. 23 shows the increase in secretion of Receptor tyrosine-protein kinase ErbB-3 (ErbB3), Fas ligand (Fas LG), Leukemia inhibitory factor (LIF), Prolactin (PRL) factor, platelet-derived growth factor receptor alpha (PDGFRa), platelet-derived growth factor receptor beta (PDGFRb), Stem cell factor kit receptor (SCFR), and Sialic acid-binding Ig-like Lectin 5 (Siglec 5). FIG. 24 shows the increase in secretion of CXC chemokine ligand 16 (CXCL16). FIG. 25 shows the increase in secretion of activated leukocyte cell adhesion molecule (ALCAM), E selectin (cell surface glycoprotein in immune-adhesion), Intercellular adhesion molecule 2 (ICAM2), L selectin (Lymphocyte adhesion molecule), and Platelet endothelial cell adhesion molecule (PECAM 1). FIG. 26 shows the increase in secretion of Activin A (INHBA), Insulin-like growth factor 2 (IGF-2), and Leptin Receptor (LEPR). FIG. 27 shows the increase in secretion of Bone morphogenetic protein 5 (BMP5), Bone morphogenetic protein 7 (BMP7), Macrophage colony-stimulating factor 1 receptor (MCSFR), matrix metalloproteinase 1 (MMP1), matrix metalloproteinase 3 (MMP3), matrix metalloproteinase 9 (MMP9), and matrix metalloproteinase 13 (MMP13). FIG. 28 shows the increase in secretion of monocyte differentiation antigen (CD14), cell differentiation antigen (CD80), Cardiotrophin-1 (CT-1), and Leukemia inhibitory factor (LIF). FIG. 29 shows the increase in secretion of Endoglin (ENG). FIG. 30 shows the increase in secretion of Tyrosine kinase with immunoglobulin-like and EGF-like domains 1 (TIE1) and Tyrosine kinase with immunoglobulin-like and EGF-like domains 2 (TIE2). FIG. 31 shows the increase in secretion of Activin A (Inhibin beta A, INHBA), Leptin Receptor (Leptin R), and Transforming growth factor beta 1 (TGFb1).

[0091] FIG. 32 shows the increase in secretion of Nerve growth factor receptor (NGFR) from SR-MSCs maintained in a factor production unit of the invention, 48 hours post incubation with 10% PRP alone (no IL-2 stimulation). NGFR was found to not be present in in PRP. The factors produced from the factor production unit under these conditions can provide therapeutic benefits for treatment of neurodegenerative pathologies, such as for example Parkinson's disease, Alzheimer's disease, progressive supranuclear palsy, multiple system atrophy, amyotrophic lateral sclerosis, Huntington's chorea or following trauma such as stroke and cerebral or spinal

traumas and stand alone or combinational treatments for conditions requiring musculoskeletal and cardiac repair.

[0092] FIGS. 33-39 show the increase in secretion of the below named proteins (factors) from SR-hADSCs maintained in a factor production unit of the invention, 72 hours post incubation with 10% PRP alone (no IL-2 stimulation). The factors produced from the factor production unit may provide therapeutic benefits for treatment of neurodegenerative pathologies, such as for example Parkinson's disease, Alzheimer's disease, progressive supranuclear palsy, multiple system atrophy, amyotrophic lateral sclerosis, Huntington's chorea or following trauma such as stroke and cerebral or spinal traumas and stand alone or combinational treatments for conditions requiring musculoskeletal and cardiac repair. cutaneous wound, a dermatologic disorder, a dermatological lesion, dermatitis, psoriasis, condyloma, verruca, hemangioma, keloid, skin cancer, atopic dermatitis, Behcet disease, chronic granulomatous disease, cutaneous T cell lymphoma, ulceration, a pathological condition characterized by initial injury inducing inflammation and immune dysregulation leading to chronic tissue remodeling including fibrosis and loss of function, skin defense against infection, new synthesis of collagen, elastin and hyaluronan, inhibition of melanoma growth, diabetic ulcers, myocardial infraction, atherosclerosis, Celiac Disease, rheumatoid arthritis (RA), Inflammatory Bowel Disease (IBD), asthma, encephalitis, chronic obstructive pulmonary disease (COPD), inflammatory osteolysis, allergic disorders, septic shock, pulmonary fibrosis (e.g. , idiopathic pulmonary fibrosis), inflammatory vacultides (e.g. , polyarteritis nodosa, Wegner's granulomatosis, Takayasu's arteritis, temporal arteritis, and lymphomatoid granulomatosus), post-traumatic vascular angioplasty (e.g. restenosis after angioplasty), undifferentiated spondyloarthropathy, undifferentiated arthropathy, arthritis, inflammatory osteolysis, chronic hepatitis, and chronic inflammation resulting from chronic viral or bacteria infections, chronic liver fibrosis, cirrhosis, fulminant hepatic failure, allergic airway inflammation, acute lung injuries, myocardial infarction, fetal maternal tolerance, osteoarthritis, GVHD.

[0093] In FIGS. 33-39, secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support. FIG. 33 shows the increase in secretion of Interleukin 1 beta (IL1b), Interleukin 3 (IL3), Interleukin-13 Receptor subunit alpha-2 (IL13Rα2), and Interleukin 1 receptor alpha (IL1Rα). FIG. 34 shows the increase in secretion of Probetacellulin (BTC), Colony stimulating factor (CSF1),

Fibroblast growth factor 6 (FGF6), Glial cell line-derived neurotrophic factor (GDNF), insulin-like growth factor 1 (IGF-1), Leptin, and platelet-derived growth factor B beta (PDGF BB). FIG. 35 shows the increase in secretion of stem cell factor/c-kit ligand (SCF), Stromal Cell-Derived Factor-1 alpha (SDF1a), Stromal Cell-Derived Factor-1 beta (SDF1b), Transforming growth factor beta 1 (TGFb1), Transforming growth factor beta 3 (TGFb3), and tumor necrosis factor superfamily member 14 (TNFSF14). FIG. 36 shows the increase in secretion of Insulin-like growth factor 1 (IGF1). FIG. 37 shows the increase in secretion of Transforming growth factor beta 1 (TGFb1) and platelet-derived growth factor B beta (PDGF BB). FIG. 38 shows the increase in secretion of Chemokine (C-C motif) ligand 2 (CCL2), Chemokine (C-C motif) ligand 5 (CCL5), Chemokine (C-C motif) ligand 7 (CCL7), Chemokine (C-C motif) ligand 8 (CCL8), and Chemokine (C-C motif) ligand 11 (CCL11). FIG. 39 shows the increase in secretion of Chemokine (C-C motif) ligand 13 (CCL13), Chemokine (C-C motif) ligand 22 (CCL22), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C motif) ligand 24 (CCL24), and CXC Chemokine ligand 10 (CXCL10).

[0094] FIGS. 40-42 show the increase in secretion of the below named proteins (factors) from SR-hADSCs maintained in a factor production unit of the invention, 72 hours post incubation with 10% PRP alone (no IL-2 stimulation). These factors were found to not be present in PRP. FIGS. 40-42 show the increase in secretion of the below named proteins (factors) from SR-hADSCs maintained in a factor production unit of the invention, 72 hours post incubation with 10% PRP alone (no IL-2 stimulation). These factors were found to not be present in PRP. The factors produced from the factor production unit under these conditions may provide therapeutic benefits for treatment of neurodegenerative pathologies, such as for example Parkinson's disease, Alzheimer's disease, progressive supranuclear palsy, multiple system atrophy, amyotrophic lateral sclerosis, Huntington's chorea or following trauma such as stroke and cerebral or spinal traumas, condyloma, verruca, hemangioma, keloid, skin cancer, retinoditis pigmentosa, idiopathic pulmonary fibrosis, chronic liver fibrosis, cirrhosis, fulminant hepatic failure, allergic airway inflammation, acute lung injuries atopic dermatitis, Behcet disease, chronic granulomatous disease, cutaneous T cell lymphoma, ulceration, a pathological condition characterized by initial injury inducing inflammation and immune dysregulation leading to chronic tissue remodeling including fibrosis and loss of function, renal ischemic injury, cystic fibrosis, sinusitis and rhinitis or an orthopaedic disease, autoimmune hepatitis and stand alone or combinational treatments for conditions requiring musculoskeletal and cardiac repair.

[0095] FIG. 40 shows the increase in secretion of Brain-derived neurotrophic factor (BDNF), Bone morphogenetic protein 4 (BMP4), Bone morphogenetic protein 6 (BMP6), Ciliary neurotrophic factor (CNTF), Epidermal growth factor (EGF), Fibroblast growth factor 7 (FGF7), and insulin-like growth factor-binding protein-4 (IGFBP4). FIG. 41 shows the increase in secretion of chemokine (C-X-C motif) ligand 13 (BLC), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C motif) ligand 28 (CCL28), chemokine (C-C motif) ligand 11 (Eotaxin 1), Chemokine (C-X-C motif) ligand 6 (GCP-2), FLT3LG (Fms-Related Tyrosine Kinase 3 Ligand), and Fractalkine (CX3CL1). FIG. 42 shows the increase in secretion of Angiotensin (ANG) and colony stimulating factor 2 (CSF2). Eotaxin 1 works as a drug against asthma and allergic reactions. Flt3 LG stimulates proliferation and differentiation of hematopoietic cells progenitors, Fractalkine modulates cytotoxic effector T cells, induced migration T & B cell lymphocytes, NK cells and monocytes, BLC controls organization of B-cells in lymphoid tissue. CCL23 is associated with immunomodulation in lung and liver tissue, ANG signaling is associated with protective effects in cardiovascular diseases, CSF2 is used as a potential to therapy for rheumatoid arthritis and stimulates macrophages. In addition, stimulates production of white blood cells and prevents neutropenia post chemotherapy. It is approved for treatment in Non-Hodgkins lymphoma, acute lymphocutic leukemia, fungal infection and Hodgkins disease.

[0096] FIG. 43 shows the increase in secretion of Chemokine (C-C motif) ligand 27 (CCL27) and TNFRSF1B (Tumor Necrosis Factor Receptor Superfamily, Member 1B) from SR-hADSCs maintained in a factor production unit of the invention, 24 hours post stimulation with IL-2. Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support.

[0097] FIGS. 44-53 show the increase of the below named proteins (factors) from SR-hADSCs maintained in a factor production unit of the invention, 48 hours post stimulation with IL-2. Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support.

[0098] FIGS. 44-53 show the increase of the below named proteins (factors) from SR-hADSCs maintained in a factor production unit of the invention, 48 hours post stimulation with IL-2. Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support. The factors produced

from the factor production unit under these conditions may provide therapeutic benefits for treatment of autoimmune diseases. As referred to herein, "autoimmune diseases" refer to a condition in a subject characterized by cellular, tissue and/or organ injury caused by an immunological reaction of the subject to its own cells, tissues and/or organs. Illustrative, non-limiting examples of autoimmune diseases which can be treated with the immunomodulatory cells of the invention include alopecia areata, ankylosing spondylitis, antiphospholipid syndrome, autoimmune Addison's disease, autoimmune diseases of the adrenal gland, autoimmune hemolytic anemia, autoimmune hepatitis, autoimmune oophoritis and orchitis, autoimmune thrombocytopenia, Behcet's disease, bullous pemphigoid, cardiomyopathy, celiac sprue- dermatitis, chronic fatigue immune dysfunction syndrome (CFIDS), chronic inflammatory demyelinating polyneuropathy, Churg-Strauss syndrome, cicatrical pemphigoid, CREST syndrome, cold agglutinin disease, discoid lupus, essential mixed cryoglobulinemia, fibromyalgia-fibromyositis, glomerulonephritis, Graves' disease, Guillain-Barre, Hashimoto's thyroiditis, idiopathic pulmonary fibrosis, idiopathic thrombocytopenia purpura (ITP), IgA neuropathy, juvenile arthritis, lichen planus, Meniere's disease, mixed connective tissue disease, multiple sclerosis, type I or immune- mediated diabetes mellitus, myasthenia gravis, pemphigus vulgaris, pernicious anemia, polyarteritis nodosa, polychondritis, polyglandular syndromes, polymyalgia rheumatica, polymyositis and dermatomyositis, primary agammaglobulinemia, primary biliary cirrhosis, psoriasis, psoriatic arthritis, Raynauld's phenomenon, Reiter's syndrome, sarcoidosis, scleroderma, progressive systemic sclerosis, Sjogren's syndrome, Good pasture's syndrome, stiff-man syndrome, systemic lupus erythematosus, lupus erythematosus, takayasu arteritis, temporal arteristis/giant cell arteritis, ulcerative colitis, uveitis, vasculitides such as dermatitis herpetiformis vasculitis, vitiligo, Wegener's granulomatosis, Anti-Glomerular Basement Membrane Disease, Antiphospholipid Syndrome, Autoimmune Diseases of the Nervous System , Familial Mediterranean Fever, Lambert-Eaton Myasthenic Syndrome, Sympathetic Ophthalmia, Polyendocrinopathies, Psoriasis, etc. as well diseases and conditions required enhancing of angiogenesis.

[0099] FIGS. 44 shows the increase in secretion of Interleukin 9 (IL9), Interleukin 11 (IL11), Interleukin 12 alpha (IL12a), Interleukin 12 beta (IL12b), and Interleukin 18 binding protein alpha (IL18BPa). FIG. 45 shows the increase in secretion of Interleukin 1 receptor type I (IL1R1), Interleukin 1 receptor type II (IL1R2), Interleukin 1 receptor type IV (IL1R4), Interleukin 2 receptor beta (IL-2Rb), Interleukin 2 receptor gamma (IL-2Rg), Interleukin 5

receptor alpha (IL5Ra) Interleukin 10 receptor beta (IL10Rb), Interleukin 18 receptor beta (IL18Rb), and Interleukin 21 receptor (IL-21R). FIG. 46 shows the increase in secretion of Fibroblast growth factor 4 (FGF4), FGF9, MSP alpha/HGF like factor (HGF like), Insulin-like growth factor 1 (IGF1), IGF2, insulin-like growth factor-binding protein-6 (IGFBP6), LAP (TGF beta family), and platelet derived growth factor A alpha (PDGFAA). FIG. 47 shows the increase in secretion of platelet derived growth factor A beta (PDGFAB), platelet derived growth factor B beta (PDGFBB), Stromal Cell-Derived Factor-1 alpha (SDF1a), Sialic acid-binding Ig-like Lectin 5 (Siglec 5), Transforming growth factor alpha (TGFa), Transforming growth factor beta 2 (TGFb2), Vascular endothelial growth factor (VEGF), and Vascular endothelial growth factor D (VEGFD). FIG. 47 also shows the increase in secretion of DR6, Dtk, EGFR, Endoglin, ErbB3, Fas, Fas LG, and IGF1 sR. FIG. 48 shows the increase in secretion of Leptin (LEP), Leptin Receptor (LEPR), Macrophage colony-stimulating factor 1 receptor (MCSFR), Neurotrophin 4 (NT4), Osteoprotegerin (OPG), platelet-derived growth factor receptor alpha (PDGFRa), platelet-derived growth factor receptor beta (PDGFRb), and Prolactin (PRL). FIG. 49 shows the increase in secretion of Stem cell factor receptor (SCFR), Angiopoietin 1 receptor (TIE1), Angiopoietin 1 receptor (TIE2), TNF superfamily member 10C (TNFSF10C), TNF superfamily member 10D (TNFSF10D), TNF superfamily member 14 (TNFSF14), urokinase plasminogen activator receptor (uPAR), and Vascular endothelial growth factor receptor-2 (VEGFR2). FIG. 50 shows the increase in secretion of Chemokine (C-C motif) ligand 2 (CCL2), CCL3, CCL5, CCL8, CCL17, CCL20, CCL25, CXC chemokine ligand 5 (CXCL5), CXCL11, and CXCL16. FIG. 51 shows the increase in secretion of activated leukocyte cell adhesion molecule (ALCAM), Bone morphogenetic protein 5 (BMP5), BMP7, E selectin (endothelial cell adhesion molecule), Intercellular adhesion molecule 2 (ICAM2), ICAM3, L selectin (Lymphocyte adhesion molecule), and matrix metalloproteinase 1 (MMP1). FIG. 52 shows the increase in secretion of matrix metalloproteinase 13 (MMP13), MMP3, MMP9, Platelet endothelial cell adhesion molecule (PECAM 1), Metalloproteinase inhibitors TIMP 1, TIMP 2, TIMP 4, and vascular epithelium (VE) Cadherin (calcium dependent cell adhesion protein). FIG. 53 shows the increase in secretion of monocyte differentiation antigen (CD14), cell differentiation antigen (CD80), Cardiotrophin-1 (CT-1), Leukemia inhibitory factor (LIF), Macrophage migration inhibitory factor (MIF), Thrombopoietin (THPO), and Lymphotactin (XCL1).

[0100] As shown in FIG. 44, certain factors are increased. IL18BPa can block interleukins IL18 induced interferon gamma production and is associated with suppression of inflammatory responses initiated by infections, trauma and allergies. IL9 prevents apoptosis and inhibition of melanoma. IL11 is associated with adipogenesis inhibitory factor, improves platelet recovery after chemotherapy and modulates Ag/Ab responses. IL9 participates in bone-cell proliferation differentiation. IL12 induces interferon gamma, stimulates differentiation of Th1 and Th2, potent immunomodulators.

[0101] FIG. 54 shows the increase in secretion of Nerve growth factor receptor (NGFR) from SR-hADSCs maintained in a factor production unit of the invention, 48 hours post stimulation with IL-2. FIG. 54 also shows increase in the secretion of IL8 and TNFRSF1A with IL-2 at 24h post-IL-2 stimulation. NGFR, IL8 and TNFRSF1A were found to not be present in PRP.

[0102] FIGS. 55-57 show the increase in the secretion of the below named proteins (factors) from SR-hADSCs maintained in a factor production unit of the invention, 72 hours post stimulation with IL-2. Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support. FIG. 55 shows the increase in secretion of Interleukin 1 receptor alpha (IL1Ra), Interleukin 6 (IL6), and Interleukin-13 receptor subunit alpha-2 (IL13Ra2). FIG. 56 shows the increase in secretion of Fibroblast growth factor 6 (FGF6), pro-platelet basic protein (PPBP), stem cell factor (SCF), and Vascular endothelial growth factor receptor-3 (VEGFR3). FIG. 57 shows the increase in secretion of Chemokine (C-C motif) ligand 22 (CCL22), CCL23, CCL24, CCL26, and CXC chemokine ligand 10 (CXCL10).

[0103] FIG. 58 shows the increase in secretion of Angiotensin (ANG), Brain-derived neurotrophic factor (BDNF), Bone morphogenetic protein 4 (BMP4), colony stimulating factor 2 (CSF2), Epidermal growth factor (EGF), Fibroblast growth factor 7 (FGF-7), Interferon gamma (IFNγ), insulin-like growth factor-binding protein-1 (IGFBP 1), and IGFBP 2 from SR-hADSCs maintained in a factor production unit of the invention, 72 hours post stimulation with IL-2. These factors were found to not be present in PRP.

[0104] FIG. 59 shows the increase in secretion of Fibroblast growth factor 6 (FGF6), CXC chemokine ligand 16 (CXCL16), and Stromal Cell-Derived Factor-1 alpha (SDF1a) from SEN-hADSCs maintained in a factor production unit of the invention, 24 hours post incubation with

10% PRP alone (no IL-2 stimulation). Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support.

[0105] FIG. 60 shows the increase in secretion of Brain-derived neurotrophic factor (BDNF), B lymphocyte chemokine (CXCL13; BLC), Chemokine (C-C motif) ligand 1 (CCL1), Flt-3 LG (Fms-Related Tyrosine Kinase 3 Ligand), Fractalkine (T-cell chemokine CX3CL1), granulocyte chemotactic protein 2 (GCP-2)/CXCL6, Interleukin 1 alpha (IL1a), Interleukin 4 (IL4), IL15, and Interferon gamma (IFNγ) from SEN-hADSCs maintained in a factor production unit of the invention, 24 hours post incubation with 10% PRP alone (no IL-2 stimulation). These factors were found to not be present in PRP.

[0106] FIGS. 61-70 show the increase in the secretion of the below named proteins (factors) from SEN-hADSCs maintained in a factor production unit of the invention, 48 hours post incubation with 10% PRP alone (no IL-2 stimulation). Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support. FIG. 61 shows the increase in secretion of Interleukin 2 beta (IL-2b), IL3, IL5, and IL6. FIG. 62 shows the increase in secretion of Interleukin 1 receptor type II (IL1R2), Interleukin 2 receptor gamma (IL-2Rg), Interleukin 5 receptor alpha (IL5Ra), Interleukin 10 receptor beta (IL10Rb), Interleukin 18 receptor binding protein alpha (IL18BPa), Interleukin 18 receptor beta (IL18Rb), and Interleukin 21 receptor (IL-21R). FIG. 63 shows the increase in secretion of Insulin-like growth factor 1 (IGF1), IGF2, LAP (TGF beta family), Leptin (LEP), Leptin Receptor (LEPR), platelet derived growth factor A alpha (PDGFAA), platelet derived growth factor A beta (PDGFAB), and platelet derived growth factor B beta (PDGFBB).FIG. 64 shows the increase in secretion of platelet-derived growth factor receptor alpha (PDGFRa), Stem cell factor (SCF), Stem cell factor receptor (SCFR), Transforming growth factor beta 1 (TGF b1), Transforming growth factor beta 2 (TGF b2), Transforming growth factor alpha (TGFa), Vascular endothelial growth factor receptor-2 (VEGFR2), and VEGFR3.FIG. 65 shows the increase in secretion of Death receptor 6 (DR6; TNF receptor superfamily member 21), Glial cell line-derived neurotrophic factor (GDNF), Neurotrophin 3 (NT3), Tyrosine kinase with immunoglobulin-like and EGF-like domains 1 (TIE1), TIE2, and TNF superfamily member 14 (TNFSF14).FIG. 66 shows the increase in secretion of Chemokine (C-C motif) ligand 2 (CCL2), CCL5, CCL8, CCL17, CCL18, and CCL23.FIG. 67

shows the increase in secretion of Chemokine (C-C motif) ligand 24 (CCL24), CCL25, CCL26, CCL27, CXC Chemokine ligand 10 (CXCL10), and CXCL11.FIG. 68 shows the increase in secretion of activated leukocyte cell adhesion molecule (ALCAM), Bone morphogenetic protein 5 (BMP5), BMP7, E selectin (endothelial cell adhesion molecule), Intercellular adhesion molecule 1 (ICAM1), ICAM2, L selectin (Lymphocyte adhesion molecule), and matrix metalloproteinase 1 (MMP1).FIG. 69 shows the increase in secretion of matrix metalloproteinase 3 (MMP3), MMP9, MMP13, Platelet endothelial cell adhesion molecule (PECAM 1), Metalloproteinase inhibitors TIMP 1, TIMP 2, and TIMP 4.FIG. 70 shows the increase in secretion of monocyte differentiation antigen (CD14), monocyte differentiation antigen (CD80), Cardiotrophin-1 (CT-1), and Leukemia inhibitory factor (LIF). CT-1 has a broad spectrum of biological activities *in vivo* such; it can reduce nephrotoxicity, can prevent neuronal death upon injury and imposes protection on neuromuscular degeneration in amyotrophic lateral sclerosis (ALS).

[0107] FIGS. 71-72 show the increase in the secretion the below named proteins (factors) from SEN-hADSCs maintained in a factor production unit of the invention, 48 hours post incubation with 10% PRP alone (no IL-2 stimulation). These factors were found to not be present in PRP. FIG. 71 shows the increase in secretion of Bone morphogenetic protein 4 (BMP4), Chemokine (C-C motif) ligand 11 (CCL11), CCL23, Ciliary neurotrophic factor (CNTF), Epidermal growth factor (EGF), Fibroblast growth factor 7 (FGF7), insulin-like growth factor-binding protein-1 (IGFBP1), IGFBP2, IGFBP4, and Nerve growth factor receptor (NGFR). FIG. 72 shows the increase in secretion of Interleukin 7 (IL7), IL10, IL13, and IL16.

[0108] FIG. 73 shows the increase in secretion of Probetacellulin (BTC), Interleukin-13 receptor subunit alpha-2 (IL13Ra2), and Stromal Cell-Derived Factor-1 beta (SDF1b) from SEN-hADSCs maintained in a factor production unit of the invention, 72 hours post incubation with 10% PRP alone (no IL-2 stimulation). Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support.

[0109] FIG. 74 shows the increase in secretion of Hepatocyte growth factor (HGF), Interleukin 8 (IL8), and TNFRSF1A (Tumor Necrosis Factor Receptor Superfamily, member 1A) from SEN-hADSCs maintained in a factor production unit of the invention, 72 hours post

incubation with 10% PRP alone (no IL-2 stimulation). These factors were found to not be present in PRP.

[0110] FIG. 75 shows the increase in secretion of Chemokine (C-C motif) ligand 23 (CCL23), Ciliary neurotrophic factor (CNTF), Epidermal growth factor (EGF), CCL11 (Eotaxin 1), IL4, and Nerve growth factor receptor (NGFR) from SEN-hADSCs maintained in a factor production unit of the invention, 24 hours post stimulation with IL-2. These factors were found to not be present in PRP.

[0111] FIG. 75 also shows the increase in secretion of CXCL16, HCC4, sgp130, and TNFRSF1B at 24h post IL-2 stimulation. Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media.

[0112] FIGS. 76-86 show the increase in the secretion of the below named proteins (factors) from SEN-hADSCs, 48 hours post stimulation with IL-2. Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support. FIG. 76 shows the increase in secretion of Interleukin 1 beta (IL1b), IL3, IL5, IL6, IL9, IL10, IL12b, and Interleukin 18 binding protein alpha (IL18BPa). FIG. 77 shows the increase in secretion of Interleukin 1 receptor alpha (IL1Ra), IL1R4, IL10Rb, IL18Rb, IL1R2, IL-21R, IL-2Rb, IL-2Rg, and IL5Ra. FIG. 78 shows the increase in secretion of Fibroblast growth factor 6 (FGF6), insulin-like growth factors IGF1 and IGF2, LAP (TGF beta family), Neurotrophin 3 (NT3), platelet derived growth factor A alpha (PDGFAA), platelet derived growth factor A beta (PDGFAB), and platelet-derived growth factor receptor alpha (PDGFRa). FIG. 79 shows the increase in secretion of Stem cell factor (SCF), Transforming growth factor 2 (TGF2), TGFa, TGFb1, TGFb3, Tumor necrosis factor beta (TNFb), Vascular endothelial growth factor receptor-2 (VEGF R2), and VEGF R3. FIG. 80 shows the increase in secretion of DR6 (TNF receptor superfamily member 21), Endoglin (ENG), Receptor tyrosine-protein kinase erbB-3 (ErbB3), Fas ligand (Fas LG), Glial cell line-derived neurotrophic factor (GDNF), GITR ligand (GITR LG), and Leptin receptor (LEPR). FIG. 81 shows the increase in secretion of Prolactin (PRL), Stem cell factor receptor (SCFR), Sialic acid-binding Ig-like Lectin 5 (Siglec 5), Angiopoietin 1 receptor (TIE1), and Angiopoietin 1 receptor (TIE2). FIG. 82 shows the increase in secretion of Chemokine (C-C motif) ligand 8 (CCL8), CCL13, CCL15, CCL17, CCL18, and CCL20. FIG. 83 shows the increase in secretion of Chemokine (C-C motif) ligand 22 (CCL22), CCL24, CCL26, CXC chemokine ligand 9

(CXCL9), and CXCL11. FIG. 84 shows the increase in secretion of Activin A (INHBA), Bone morphogenetic protein 5 (BMP5), E selectin (endothelial cell adhesion molecule), Intercellular adhesion molecule 1 (ICAM 1), ICAM 2, L selectin (Lymphocyte adhesion molecule), and Macrophage colony-stimulating factor (MCSF). FIG. 85 shows the increase in secretion of matrix metalloproteinase 1 (MMP1), MMP13, MMP3, MMP9, Platelet endothelial cell adhesion molecule (PECAM 1), and Metalloproteinase inhibitor 4 (TIMP-4). FIG. 86 shows the increase in secretion of monocyte differentiation antigen (CD14), Lymphotactin (XCL1), Cardiotrophin-1 (CT-1), Leukemia inhibitory factor (LIF), Macrophage Migration Inhibitory Factor (MIF), and pro-platelet basic protein (PPBP).

[0113] FIG. 87 shows the increase in secretion of Brain-derived neurotrophic factor (BDNF), Bone morphogenetic protein 4 (BMP4), Fibroblast growth factor 7 (FGF7), insulin-like growth factor-binding protein-2 (IGFBP2), IL-2, IL16, and Interferon gamma (INF gamma) from SEN-hADSCs maintained in a factor production unit of the invention, 48 hours post stimulation with IL-2. These factors were found to not be present in PRP.

[0114] FIGS. 88-89 show the increase in secretion of the below named proteins (factors) from SEN-hADSCs maintained in a factor production unit of the invention, 72 hours post stimulation with IL-2. Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support. FIG. 88 shows the increase in secretion of Adiponectin (Acrp30), Agouti-related protein (AgRP), ANGPT2 (Angiopoietin 2), basic-Fibroblast Growth Factor (bFGF), Probetacellulin (BTC), Interleukin-13 receptor subunit alpha-2 (IL13Ra2), Leptin (LEP), Neurotrophin 4 (NT4), and Stromal Cell-Derived Factor-1 alpha (SDF1a). FIG. 89 shows the increase in secretion of Chemokine (C-C motif) ligand 2 (CCL2), CCL4, CCL5, CCL23, CCL25, CCL27, CXC Chemokine ligand 10 (CXCL10), Stromal Cell-Derived Factor-1 beta (SDF1b), Metalloproteinase inhibitors 1 (TIMP1), TIMP2, and tumor necrosis factor superfamily member 14 (TNFSF14).

[0115] FIG. 90 shows the increase in secretion of Granulocyte-macrophage colony-stimulating factor (GM-CSF) and IL13 from SEN-hADSCs maintained in a factor production unit of the invention, 72 hours post stimulation with IL-2. These factors were found to not be present in PRP.

[0116] In general, the input cells and systems provided herein can produce factors including, but not limited to, HB-EGF; FGFs 1, 2, and 4; PDGF; IGF-1; TGF-ß1 and ß2; TGF- ß3; IL-1α and -ß; IL-10; IL-4; IL-2, IL-12; IL-6, IL-8, IL-17a; LEP and LEPR; Endoglin; Adipoq; IGFBP1, IGFPB3; CSF1, CSF3 and receptor CSFR1; PPBP/NAP-2; HGF; NGRF; EGF; TNF-α; and combinations thereof.

[0117] Exemplary interleukins produced using the input cells and systems provided herein involved in skin regeneration pathways include without limitation, IL 1b (interleukin 1ß), IL 2b (interleukin 2ß), IL 3 (interleukin 3), IL 6 (interleukin 6), IL6ST (interleukin 6ST), IL 9 (interleukin 9), IL 11 (interleukin 11), IL12a (interleukin 12α), IL 12b (interleukin 12ß), IL 13 (interleukin 13), and IL 17 (interleukin 17).

[0118] Exemplary interleukin receptors and binding proteins produced using the input cells and systems provided herein include without limitation, IL1Ra (interleukin 1 receptor α), IL 1R1 (interleukin 1 receptor type 1), IL 1R2 (interleukin 1 receptor type 2), IL 1R4 (interleukin 1 receptor 4), IL 2Ra (interleukin 2 receptor α), IL 2Rg (interleukin 2 receptor γ), , IL 5Ra (interleukin 5 receptor α), IL 6R (interleukin 6 receptor), IL 10Rb (interleukin 10 receptor ß), IL 13Ra (interleukin 13 receptor α), IL 18 Rb (interleukin receptor ß), IL 18 BP (interleukin 18 binding protein), IL 21 R (interleukin 21 receptor).

[0119] Exemplary growth factors produced using the input cells and systems provided herein include without limitation, bFGF2 (basic fibroblast growth factor 2), bNGF (beta-nerve growth factor), FGF4 (fibroblast growth factor 4), FGF6 (fibroblast growth factor 6), FGF 9 (fibroblast growth factor 9), Fas ligand, IGFBP1 (insulin growth factor binding protein 1), IGFBP3 (insulin growth factor binding protein 3), IGFBP6 (insulin growth factor binding protein 6), LAP (transforming growth factor like), IGF-1 (insulin-like growth factor 1), IGF-2 (insulin-like growth factor 2), PDGF (platelet-derived growth factor), PDGFAA (platelet-derived growth factor Aα), PDGFAB (platelet-derived growth factor Aß), PDGFBB (platelet-derived growth factor Bß), TGFB1 (transforming growth factor ß1), ANG (angiogenin), BDNF (brain-derived neurotrophic factor), BMP4 (bone morphogenic protein 4), BMP 6 (bone morphogenic protein 6), bNGF (beta-nerve growth factor), BTC (probetacellulin), CNTF (ciliary neurotrophic factor), EGF (epidermal growth factor), HGF (hepatocyte growth factor), hepatocyte-like growth factor, NT3 (neurotrophin 3), NT4 (neurotrophin 4), OPG (osteoprotegerin), Siglec5 (sialic acid binding If-like lectin 5), and TGF A (transforming growth factor alpha), TGF b1 (transforming

growth factor beta 1), TGF b 2 (transforming growth factor beta 3), VEGF (vascular endothelial growth factor), VEGFD (vascular endothelial growth factor D), and PLGF (placental growth factor).

[0120] Exemplary growth factors receptors produced using the input cells and systems provided herein include without limitation, PDGFRA (platelet-derived growth factor receptor α), VEGFR2 (vascular endothelial growth factor receptor 2), VEGFR3 (vascular endothelial growth factor receptor 3), NGFR (nerve growth factor receptor), EGFR (epithelial growth factor receptor), and TNFRSF 10D (tumor necrosis factor receptor 10D).

[0121] Exemplary chemokines produced using the input cells and systems provided herein include without limitation, CCL 2 (chemokine ligand 2), CCL 3 (chemokine ligand 3), CCL 4 (chemokine ligand 4), CCL 5 (chemokine ligand 5), CCL 7 (chemokine ligand 7), CCL 8 (chemokine ligand 8), CCL 13 (chemokine ligand 13), CCL 15 (chemokine ligand 16), CCL 17 (chemokine ligand 17), CCL 18 (chemokine ligand 18), CCL 19 (chemokine ligand 19), CCL 20 (chemokine ligand 20), CCL 22 (chemokine ligand 22), CCL 23 (chemokine ligand 23), CCL 24 (chemokine ligand 24), CCL25 (chemokine ligand 25), CCL 26 (chemokine ligand 26), CCL 27 (chemokine ligand 27), CCL 28 (chemokine ligand 28), CXC L1 (chemokine ligand 1), CXCL1/2/3 (chemokine ligand 1/2/3), CXCL5 (CX chemokine ligand 5), CXCL9 (CX chemokine ligand 9), CXCL 10 (CX chemokine ligand 10), CXCL 13 (CX chemokine ligand 13), and CXCL 16 (CX chemokine ligand 16).

[0122] Exemplary molecules that provide cell adhesion signaling produced using the input cells and systems provided herein include without limitation, ALCAM (cell adhesion molecule), E-selectin, and VE cadherin.

[0123] Exemplary factors that may promote cell proliferation produced using the input cells and systems provided herein include without limitation, BMP4 (bone morphogenic protein 4), BMP5 (bone morphogenic protein 5), BMP6 (bone morphogenic protein 6), BMP7 (bone morphogenic protein 7), CSF 1R (colony stimulating factor 1 receptor), ICAM2 (intercellular adhesion molecule 2), MMP 1 (matrix metallopeptidase 1), MMP3 (matrix metallopeptidase 3), MMP 9 (matrix metallopeptidase 9), and TIMP4 (metalloproteinase inhibitor 4).

[0124] Dermatological aging and the physiological changes associated with aging of the skin include xerosis, loss of barrier function, loss elasticity due to damage to collagen and elastin fibers, modification of rhytides, and loss of efficient turnover of epidermal cells, ultimately resulting in thinning of the skin, malar fat atrophy, and pigmentary changes. Although aging is inevitable, in some variations of the compositions described herein may be used to combat these physiological and anatomic changes. Exemplary factor that may promote skin regeneration produced using the input cells and systems provided herein include without limitation, CXCL 16 (chemokine ligand 16), IGF-2 (insulin-like growth factor 2), and TIE2 (tyrosine kinase with immunoglobin/EGF like domain).

[0125] Exemplary factors that may promote wound healing produced using the input cells and systems provided herein include without limitation, Activin A, IGF-2 (insulin-like growth factor 2), and LEPR (leptin receptor).

[0126] Exemplary factors that may promote hyaluronic acid synthesis in the skin produced using the input cells and systems provided herein include without limitation, Activin A, LEPR (leptin receptor, TGFB1 (transforming growth factor ß1), EGF (epidermal growth factor), HGF (hepatocyte growth factor), and PDGF (platelet-derived growth factor).

[0127] Exemplary factors that may promote skin elasticity produced using the input cells and systems provided herein include without limitation, IGFBP1 (insulin-like growth factor binding protein 1), IGFBP2 (insulin-like growth factor binding protein 2), IGFBP4 (insulin-like growth factor binding protein 4), TIMP1 (metalloproteinase inhibitor 1), and TIMP2 (metalloproteinase inhibitor 2).

[0128] Exemplary factors for suppression of malignancies and UV-induced skin aging produced using the input cells and systems provided herein include without limitation, endoglin and SCFR (c-KIT stem cell factor receptor.

[0129] Exemplary factors for suppressing wound healing or the inflammatory response produced using the input cells and systems provided herein include without limitation, CD 14 (cell differentiation antigen 14), CD 80 (cell differentiation antigen 80), IFNγ (interferon gamma), and LIF (leukemia inhibitory factor).

[0130] In an exemplary variation, NGF (nerve growth factor receptor) is produced using the input cells and systems provided herein may be a beneficial factor for the treatment of hair loss.

[0131] Other factors capable of being produced using the input cells and systems provided herein include without limitation, Adipoq (adiponectin), AgRP (agouti related protein), ANGPT2 (Angiopoietin 2), AREG (amphiregulin), Ax1 (tyrosine-protein kinase receptor UFO), BTC (betacellulin), CD 14 (cell differentiation antigen 14), CD 80 (cell differentiation antigen 80), CT-1 (cardiotropin-1), Dtk (tyrosine-protein kinase receptor TYRO3), ErbB3 (receptor tyrosine-protein kinase erB-3), OPG (osteoprotegerin), OSM (oncostatin M), PPBP (platelet basic protein), PRL (prolactin), THPO (thrombopoietin), and TIE-1 (angiopoietin 1 receptor).

[0132] In one exemplary variation, SR-hADSCs are stimulated with an IL-2 induction agent for 24 hours, and allowed to produce factors for 24 hours. FIG. 43 shows the collection of factors produced 24 hours post induction with IL-2.

[0133] In another exemplary variation, SR-hADSCs are stimulated with an IL-2 induction agent for 24 hours, and allowed to produce factors for 48 hours. FIGS. 43-57 show the collection of factors produced 48 hours post induction with IL-2.

[0134] In another exemplary variation, SR-hADSCs are stimulated with an IL-2 induction agent for 24 hours, and allowed to produce factors for 72 hours. FIGS. 43-58 show the collection of factors produced 72 hours post induction with IL-2.

[0135] In another exemplary variation, SR-hADSCs are media alone for 24 hours, and allowed to produce factors for 24 hours. FIGS. 11-19 show the collection of factors produced 24 hours post induction with media alone.

[0136] In another exemplary variation, SR-hADSCs are media alone for 24 hours, and allowed to produce factors for 48 hours FIGS. 11-42 show the collection of factors produced 48 hours post induction with media alone.

[0137] In another exemplary variation, SR-hADSCs are media alone for 24 hours, and allowed to produce factors for 72 hours. FIGS. 20-42 show the collection of factors produced 72 hours post induction with media alone.

[0138] In one exemplary variation, SEN-hADSCs are stimulated with an IL-2 induction agent for 24 hours, and allowed to produce factors for 24 hours. FIG. 75 show the collection of factors produced 24 hours post induction with IL-2.

[0139] In another exemplary variation, SEN-hADSCs are stimulated with an IL-2 induction agent for 24 hours, and allowed to produce factors for 48 hours. FIGS. 75-90 show the collection of factors produced 48 hours post induction with IL-2.

[0140] In another exemplary variation, SEN-hADSCs are stimulated with an IL-2 induction agent for 24 hours, and allowed to produce factors for 72 hours. FIGS. 75-90 show the collection of factors produced 72 hours post induction with IL-2.

[0141] In another exemplary variation, SEN-hADSCs are stimulated with media alone for 24 hours, and allowed to produce factors for 24 hours. FIGS. 59-60 show the collection of factors produced 24 hours post induction with media alone.

[0142] In another exemplary variation, SEN-hADSCs are stimulated with media alone for 24 hours, and allowed to produce factors for 48 hours. FIGS. 59-74 show the collection of factors produced 48 hours post induction with media alone.

[0143] In another exemplary variation, SEN-hADSCs are stimulated with media alone for 24 hours, and allowed to produce factors for 72 hours. FIGS. 59-74 show the collection of factors produced 72 hours post induction with media alone.

[0144] In an exemplary variation, the method for producing one or more factors in a factor production unit, the method comprises using input cells that comprise at least 50% SEN-hADSCs, adding an IL-2 inducing agent to the population of cells to promote production of the factors; and collecting the factors.

3. Exemplary Methods of Induction

[0145] FIG. 1A depicts an exemplary method for practicing an aspect of the invention described herein.

[0146] In general there may be multiple classes of stem cells and sub-combinations of them that are used as described herein, based on the SEN state of the cells. Each population and sub-

combination may produce different trophic factors. For example, a population of cells may be complete SR, completely SEN or (more likely) a mixed population of SR and SEN cells. A population of completely SR cells may be induced to produce particular factors, as described herein, and may produce a first profile of trophic factors (FIG. 1A "phenotype 3"). A population of just SEN cells may be rejuvenated as described herein and may produce factors either without induction ("phenotype 1") or with induction ("phenotype 2"). A fourth phenotype could be isolated SR cells that are not induced to produce factors ("phenotype 4"). These different populations (rejuvenated, formerly SEN cells, induced and not induced, and induced/induced SR cells) may be used alone or in various subcombinations to treat any of the diseases/disorders described herein.

[0147] FIG. 1A generically illustrates a method for modifying the properties of an exemplary input cell of the invention, a human adipose-derived mesenchymal stem cell (hADSC) to produce any of the phenotypes 1-3 just mentioned. As shown in FIG. 1A, an extract of mesenchymal stem cells (MSC) may be taken adipose tissue or a sample of cryopreserved cells may be used 101. The adipose tissue (and thus the MSC) may be derived from an autologous or heterologous source (e.g., from the same patient to be treated with the rejuvenated and/or induced hADSC and/or extract, or from a donor MSC). Adipose tissue may be harvested according to any appropriate procedure. The MSCs may be amplified and/or isolated from the adipose tissue, but in general the MSC is cultured 103. Optionally, either as a separate step of as part of the culturing step, the cells may be examined (QC) to determine the presence and/or identity of SEN cells. Thereafter, any SEN-hADSCs may be rejuvenated as described herein, so that all of the cells are in a SR state (which includes the formerly SEN cells, now rejuvenated), and not in a SEN state.

[0148] In some variations, only the identified SEN cells are rejuvenated either in a population of just SEN cells or in a mixed population of SEN and SR cells. For example, if rejuvenating only SEN cells, the SEN cells may first be isolated from the SR cells. Alternatively, all of the cells of a mixed population that may include both SEN and SR cells are rejuvenated.

[0149] For example, in FIG. 1A, the QC step may identify a population of just SEN cells 113, a mixed population of SEN/SR cells 115, and a population of just SR cells 117, or the method may include a cell sorting step for separating SEN and SR cells during the procedure. Thereafter, the cells may be allowed to produce trophic factors either with or without induction. For

example, all or some of the cells can be "induced" (e.g., made ready to reliably and effectively produce a desired sub-set of factors) by exposing them to, in this example, IL-2 107, 107', 107". Cells can be induced with IL-2 with or without rejuvenation for therapeutic end-points, as illustrated in FIG. 1. As shown in FIG. 1A, each subpopulation (rejuvenated SEN only 113, SR-only 117, and mixed rejuvenated SEN and SR 115, may be optionally induced, and may produce different sets of trophic factors. These different populations may be combined in any subcombination (including with un-induced SR cells or trophic factors from them) for use in any of the therapeutic methods described and indicateed herein. For example, rejuvenated SEN cells that are not induced may produce a beneficial set of trophic factors (phenotype 1), and induced rejuvenated SEN cells may produce a beneficial set of trophic factors (phenotype 2), and induced SR cells may produce a beneficial set of trophic factors (phenotype 3). As already described, any combination of these may be combined to form a set of therapeutic cells (hADSCs) and/or extracts therefrom.

[0150] In another variation, as illustrated in FIGS. 1A, 1B, 2A, and 2B, the production of one or more factors (or factor compositions as in FIG. 2A) using a factor production unit can be controlled or tailored. Upon induction/stimulation of the cell population, e.g., with IL-2, one or more factors is produced by the cell population. The one or more factors can then be collected at predetermined time points, e.g., at 24 hours, 48 hours, or 72 hours, as shown in the figures, depending on the factor desired to be collected. For example, if interleukins are produced at 24 hours, growth factors at 48 hours, and chemokines at 72 hours post induction, and growth factors are needed for formulation into a skin rejuvenation cream, the factor production unit can be cultured and factors collected at 48 hours post induction. Control of factor production can also be controlled by the type of cells and type of substrate included in the factor production unit. It is understood that time points for factor collection can be earlier than 24 hours and later than 72 hours.

[0151] FIG. 2B is a schematic showing five exemplary factor production units (A-E) populated with an individual's hADSCs for controlled production of factors. In this exemplary aspect, each factor production unit contains an ECM-like 3-D scaffold that mimics the natural growth environment for the stem cells. All five factor production units contain stem cells in a suitable media, e.g. 10% PRP containing StemPro MSC SFM Xeno-free medium (except for factor production unit A which represents a no cell control factor production unit. The factor

production units are populated with SR or SEN cells, and either stimulated, or not stimulated with IL-2 for 24 hours.

D. Factor Compositions

[0152] The factors produced, as described herein, may be formulated into any suitable composition. The compositions can be tailored to the particular indication of use, for any of the diseases and disorders described herein.

[0153] The factors may be formulated with any suitable carrier and/or excipient(s) into a topical composition, an oral dosage form, an implant, an injectable composition, or an intravenous composition. In some instances, additional agents are included to enhance skin penetration or bioavailability of the factors, or other ingredients that enhance skin appearance. One or more factors may be included in the compositions. The compositions may be formulated for immediate, sustained, or controlled release of the one or more factors.

[0154] The amount of factor incorporated into the compositions will typically be in a range that constitutes an effective amount of the desired amount of factor, to induce the desired biological response.

[0155] In one variation the composition comprises factors produced from SR stem cells (e.g. SR-hADSCs) induced with IL-2 for 24 hours, wherein the factors are collected 24 hours post completion of the induction.

[0156] In one variation the composition comprises factors produced from SR stem cells (e.g. SR-hADSCs) induced with IL-2 for 24 hours, wherein the factors are collected 48 hours post completion of the induction.

[0157] In one variation the composition comprises factors produced from SR stem cells (e.g. SR-hADSCs) induced with IL-2 for 24 hours, wherein the factors are collected 72 hours post completion of the induction.

[0158] In one variation the composition comprises factors produced from SEN stem cells (e.g. SEN -hADSCs) induced with IL-2 for 24 hours, wherein the factors are collected 24 hours post completion of the induction.

[0159] In one variation the composition comprises factors produced from SEN stem cells (e.g. SEN -hADSCs) induced with IL-2 for 24 hours, wherein the factors are collected 48 hours post completion of the induction.

[0160] In one variation the composition comprises factors produced from SEN stem cells (e.g. SEN -hADSCs) induced with IL-2 for 24 hours, wherein the factors are collected 72 hours post completion of the induction.

[0161] In one variation the composition comprises factors produced from SR stem cells (e.g. SR-hADSCs) not induced with any inducing agent.

[0162] In one variation the composition comprises factors produced from SEN stem cells (e.g. SEN -hADSCs) not induced with any inducing agent.

E. Treatment of Diseases and Disorders

[0163] One or more induced factors, the conditioned media comprising the one or more induced factors, or compositions comprising the one or more factors, as provided herein, may be used for the treatment of a variety of diseases and disorders.

[0164] A non-limited list of diseases and disorders that can be treated comprise cancer, an autoimmune disease, a cardiovascular disease, diabetes, a skin disease, a neurodegenerative disease, osteoporosis, osteoarthritis, a spinal cord injury, a disease of the liver, a disease of the kidney, an age-related pathology, hair loss, a burn, a condition in need of a skin graft, and a skin lesion.

[0165] A beneficial aspect of the factor production methods is that therapy can be customized according to the particular disease, disorder, or condition to be treated. The population of cells and substrate can be selected depending on the desired factors to be produced. Furthermore, the produced factors can be collected at predetermined times. Factors produced by the selected cell population at a particular time point may be more beneficial in treating certain diseases, disorders, or conditions than others.

[0166] Particular modes of use and delivery of factors, for treatment, are discussed in more detail below.

[0167] As described in greater detail herein, factors may be produced and directly delivered to an individual in need using any appropriate method (e.g. a cream composition, injected, implanted, via plasmapheresis, etc.).

[0168] Alternatively factors may be produced using an exemplary factor production unit of the invention and may be used for modulation of immune cells from the individual. In this variation, the factors can come in contact with immune cells in a sample (e.g. blood or plasma) from the individual, effect modulation (immunomodulation) of the immune cells (e.g. induce production/differentiation of Tregs), after which the sample is delivered back to the individual. In this variation, the factors themselves are only optionally delivered. Rather, their use takes place *ex vivo*. In one variation, contemplated herein is a combination therapy using the immunomodulated cells produced herein (e.g. the Tregs produced as described) in combination with other factor compositions produced using the methods described herein, other active agents or treatment modalities. These other agents or treatments may include known drugs and therapies for the treatment of such disorders such as but not limited to corticosteroids and non-steroidal anti-inflammatory compounds and stimulatory drugs.

[0169] Factors used to treat other diseases or disorders described herein may be accomplished according to a treatment schedule, at home or at a doctor's office.

[0170] FIG. 1B illustrates a general method for treating a subject with, for example rejuvenated and induced hADSCs. In this exemplary method, the method may include an initial step (e.g., when performing an autologous procedure) of extracting adipose tissue from the subject 201 to be treated, and then culturing the MSCs from this adipose tissue 203 (as shown and described above in FIG. 1A). The use of the subject's own cells is optional (as indicated by the dashed lines around 201, 203), as heterologous cells may be used (e.g., from a donor) instead or in addition, which may be particularly useful when using extracts of the treated hADSC that do not include intact hADSC.

[0171] The cultured MSCs (e.g., hADSC) may then be treated as described above in FIG. 1A to rejuvenate them by reducing or suppressing activity (and/or level) of the SINE/ALU retrotransposon 205, and/or then inducing them (e.g., by exposing them to IL-2) 207. When inducing the cells by exposure to an inducing agent such as IL-2, the concentration and duration

of the exposure may be selected to evoke a robust induction response. Examples of such treatment are described in examples below.

[0172] Once rejuvenated and induced, factors or extracts from the hADSC may be used to treat the patient, as described in 209 of FIG. 1B. In this example, extracts from the MSCs may be administered by any appropriate mechanism, including locally or systemically, e.g., by injection. As used herein administering the rejuvenated and induced MSC/hADSC may include administering the actual cells, and/or an extract of the cells.

1. Derma-Cosmetic and Skin Applications

[0173] In some variations, the induced factors, the conditioned media comprising the one or more induced factors, or compositions comprising the one or more factors may be used in compositions for application to the skin, e.g., cosmetic applications, for skin regeneration, for skin rejuvenation, for wound healing, or for aesthetic treatments. The factors can be used to treat cosmetic conditions such as, but not limited to, wrinkles, fine lines, scars (including acne scars), skin discoloration, age spots, decreased skin elasticity, sun damage, and hair loss. These cosmetic conditions can be treated by factors secreted from a factor production unit containing ADSCs in 10% PRP alone (no inducing agent). In some variations, the factors can be used in combination with microneedling applications to imitate light wounding to facilitate delivery of factors and physiological benefits.

[0174] Factors produced by a factor production unit in the presence of 10% PRP alone, collected at different time points (e.g. 24, 48, 72 hrs) may be used to effectively combat dermal aging on cellular level, to address both extrinsic and intrinsic aging.

[0175] In one variation, factors are produced by a factor production unit containing SR ADSCs in 10% PRP alone after 24 hours, and a composition comprising these factors may be used to achieve a balance between development of inflammation and its rapid resolution (a derma-cosmetic composition for a stage 1 dermal rejuvenation therapy). In this variation, an exemplary composition of factors, collected at 24 hours, comprises Interleukin 5 (IL5), Interleukin 6 (IL6), Interleukin 4 (IL4), Interleukin 1 receptor 4 (IL1R4), Neurotrophin 3 (NT3), platelet derived growth factor A alpha (PDGF AA), platelet derived growth factor A beta (PDGF AB), and pro-platelet basic protein (PPBP) Chemokine (C-C motif) ligand 18 (CCL18),

Chemokine (C-Cmotif) ligand 25 (CCL25), Chemokine (C-C motif) ligand 27 (CCL27), and CXC chemokine ligand 11 (CXCL11), (ICAM-1), Metalloproteinase inhibitor 2 (TIMP-2), Metalloproteinase inhibitor 1 (TIMP-1), Vascular epithelium (VE) Cadherin (calcium dependent cell adhesion protein), and insulin-like growth factor-binding protein-1 (IGFBP1).

[0176] In another variation, factors are produced by a factor production unit containing SR ADSCs in 10% PRP alone after 48 hours, and a composition comprising these factors (a derma-cosmetic composition for a stage 2 dermal rejuvenation therapy) may be used to facilitate the transition from an inflammatory phase of wound healing to a granulation phase (proliferative). In this variation, an exemplary composition of factors, collected at 48 hours, comprises Interleukin 9 (IL9), Interleukin 18 binding protein alpha (IL18BPa), Interleukin 1 receptor type II (IL1R2), Interleukin 2 receptor beta (IL-2Rb), Interleukin 2 receptor gamma (IL-2Rg), Interleukin 5 receptor alpha (IL5Ra), Interleukin 10 receptor beta (IL10Rb), Interleukin 18 receptor accessory protein (IL18Rb), and Interleukin 21 receptor (IL-21R), Insulin-like growth factor 2 (IGF2), Transforming growth factor alpha (TGFa), Transforming growth factor beta 1/latency-associated peptide (LAP), Transforming growth factor beta 1 (TGFb1), Transforming growth factor beta 2 (TGFb2), Receptor tyrosine-protein kinase ErbB-3 (ErbB3), Fas ligand (Fas LG), Leukemia inhibitory factor (LIF), Prolactin (PRL) factor, platelet-derived growth factor receptor alpha (PDGFRa), platelet-derived growth factor receptor beta (PDGFRb), Stem cell factor kit receptor (SCFR), and Sialic acid-binding Ig-like Lectin 5 (Siglec 5), CXC chemokine ligand 16 (CXCL16), Activated leukocyte cell adhesion molecule (ALCAM), E selectin (cell surface glycoprotein in immune-adhesion), Intercellular adhesion molecule 2 (ICAM2), L selectin (Lymphocyte adhesion molecule), Platelet endothelial cell adhesion molecule (PECAM 1), Activin A (INHBA), Insulin-like growth factor 2 (IGF-2), and Leptin Receptor (LEPR), Bone morphogenetic protein 5 (BMP5), Bone morphogenetic protein 7 (BMP7), Macrophage colony-stimulating factor 1 receptor (MCSFR), matrix metalloproteinase 1 (MMP1), matrix metalloproteinase 3 (MMP3), matrix metalloproteinase 9 (MMP9), and matrix metalloproteinase 13 (MMP13), monocyte differentiation antigen (CD14), cell differentiation antigen (CD80), Cardiotrophin-1 (CT-1), and Leukemia inhibitory factor (LIF), Endoglin (ENG), Tyrosine kinase with immunoglobulin-like and EGF-like domains 1 (TIE1) and Tyrosine kinase with immunoglobulin-like and EGF-like domains 2 (TIE2), Leptin Receptor (Leptin R), and Nerve growth factor receptor (NGFR).

[0177] In another variation, factors are produced by a factor production unit containing SR ADSCs in 10% PRP alone after 72 hours, and a composition comprising these factors (a derma-cosmetic composition for a stage 3 dermal rejuvenation therapy) may be used to facilitate the transition from granulation to wound re-epithelialization (peeling of skin, which is the beginning of dermal tissue remodeling). During this stage low strength, unorganized type III collagen and elastin structures produced during the ECM production phase are replaced by stronger type III collagen and structured elastin fibers to provide strength and resiliency to the dermis. In this variation, an exemplary composition of factors, collected at 72 hours, comprises such as Interleukin 1 beta (IL1b), Interleukin 3 (IL3), Interleukin-13 Receptor subunit alpha-2 (IL13Rα2), Interleukin 1 receptor alpha (IL1Rα), Probetacellulin (BTC), Colony stimulating factor (CSF1), Fibroblast growth factor 6 (FGF6), Glial cell line-derived neurotrophic factor (GDNF), insulin-like growth factor 1 (IGF-1), Leptin, platelet-derived growth factor B beta (PDGF BB), Brain-derived neurotrophic factor (BDNF), Bone morphogenetic protein 4 (BMP4), Bone morphogenetic protein 6 (BMP6), Ciliary neurotrophic factor (CNTF), Epidermal growth factor (EGF), Fibroblast growth factor 7 (FGF7), insulin-like growth factor-binding protein-4 (IGFBP4), Stem cell factor/c-kit ligand (SCF), Stromal Cell-Derived Factor-1 alpha (SDF1a), Stromal Cell-Derived Factor-1 beta (SDF1b), Angiotensin (ANG), colony stimulating factor 2 (CSF2), Transforming growth factor beta 1 (TGFb1), Transforming growth factor beta 3 (TGFb3), tumor necrosis factor superfamily member 14 (TNFSF14), Chemokine (C-C motif) ligand 2 (CCL2), Chemokine (C-C motif) ligand 5 (CCL5), Chemokine (C-C motif) ligand 7 (CCL7), Chemokine (C-C motif) ligand 8 (CCL8), Chemokine (C-C motif) ligand 11 (CCL11), Chemokine (C-C motif) ligand 13 (CCL13), Chemokine (C-C motif) ligand 22 (CCL22), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C motif) ligand 24 (CCL24), CXC Chemokine ligand 10 (CXCL10), Chemokine (C-X-C motif) ligand 13 (BLC), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C motif) ligand 28 (CCL28), chemokine (C-C motif) ligand 11 (Eotaxin 1), Chemokine (C-X-C motif) ligand 6 (GCP-2), FLT3LG (Fms-Related Tyrosine Kinase 3 Ligand), and Fractalkine (CX3CL1).

[0178] In another variation, combinations of derma-cosmetic compositions described above can be used to promote wound healing, e.g., healing of cuts and scrapes, burns, skin grafts, and pressure ulcers.

[0179] In another variation, any skin disorder may be treated by a composition of factors produced by the factor production units of the invention. Examples of skin disorders include psoriasis, psoriatic arthritis, dermatitis (eczema), for example, exfoliative dermatitis or atopic dermatitis, pityriasis rubra pilaris, pityriasis rosacea, parapsoriasis, pityriasis lichenoiders, lichen planus, lichen nitidus, ichthyosiform dermatosis, keratodermas, dermatosis, alopecia areata, pyoderma gangrenosum, vitiligo, pemphigoid (e.g., ocular cicatricial pemphigoid or bullous pemphigoid), urticaria, prokeratosis, rheumatoid arthritis that involves hyperproliferation and inflammation of epithelial-related cells lining the joint capsule; dermatitises such as seborrheic dermatitis and solar dermatitis; keratoses such as seborrheic keratosis, senile keratosis, actinic keratosis. photo-induced keratosis, and keratosis follicularis; acne vulgaris; keloids and prophylaxis against keloid formation; nevi; warts including verruca, condyloma or condyloma acuminatum, and human papilloma viral (HPV) infections such as venereal warts; leukoplakia; lichen planus; and keratitis. The skin disorder can be dermatitis, e.g., atopic dermatitis or allergic dermatitis, or psoriasis. In one variation, any of these conditions can be treated by factors produced by a factor production unit using SR hADSCs, for 72 hours. In this variation, the composition comprises Interleukin 1 beta (IL1b), Interleukin 3 (IL3), Interleukin-13 Receptor subunit alpha-2 (IL13Rα2), Interleukin 1 receptor alpha (IL1Rα), Probetacellulin (BTC), Colony stimulating factor (CSF1), Fibroblast growth factor 6 (FGF6), Glial cell line-derived neurotrophic factor (GDNF), insulin-like growth factor 1 (IGF-1), Leptin, platelet-derived growth factor B beta (PDGF BB), Brain-derived neurotrophic factor (BDNF), Bone morphogenetic protein 4 (BMP4), Bone morphogenetic protein 6 (BMP6), Ciliary neurotrophic factor (CNTF), Epidermal growth factor (EGF), Fibroblast growth factor 7 (FGF7), insulin-like growth factor-binding protein-4 (IGFBP4), Stem cell factor/c-kit ligand (SCF), Stromal Cell-Derived Factor-1 alpha (SDF1a), Stromal Cell-Derived Factor-1 beta (SDF1b), Angiotensin (ANG), colony stimulating factor 2 (CSF2), Transforming growth factor beta 1 (TGFb1), Transforming growth factor beta 3 (TGFb3), tumor necrosis factor superfamily member 14 (TNFSF14), Chemokine (C-C motif) ligand 2 (CCL2), Chemokine (C-C motif) ligand 5 (CCL5), Chemokine (C-C motif) ligand 7 (CCL7), Chemokine (C-C motif) ligand 8 (CCL8), Chemokine (C-C motif) ligand 11 (CCL11), Chemokine (C-C motif) ligand 13 (CCL13), Chemokine (C-C motif) ligand 22 (CCL22), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C motif) ligand 24 (CCL24), CXC Chemokine ligand 10 (CXCL10), Chemokine (C-X-C motif) ligand 13 (BLC), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C

motif) ligand 28 (CCL28), chemokine (C-C motif) ligand 11 (Eotaxin 1), Chemokine (C-X-C motif) ligand 6 (GCP-2), FLT3LG (Fms-Related Tyrosine Kinase 3 Ligand), and Fractalkine (CX3CL1).

[0180] These factors can be delivered alone, or in combination with factors produced at different time points, for example factors produced by SR cells in 10% PRP (24, 48, or 72 hours post incubation with PRP alone) can be combined with factors produced by SR cells + with IL-2 (72 hours post induction).

[0181] In some variations, step-wise doses of factors can be delivered for the treatment of a skin related condition.

[0182] In some variations step-wise doses of factors can be delivered in combination with immunomodulatory compositions described below.

[0183] Exemplary factors that may promote skin regeneration produced using the input cells and systems provided herein include without limitation, CXCL 16 (chemokine ligand 16), IGF-2 (insulin-like growth factor 2), and TIE2 (tyrosine kinase with immunoglobin/EGF like domain).

[0184] Exemplary factors that may promote wound healing produced using the input cells and systems provided herein include without limitation, Activin A, IGF-2 (insulin-like growth factor 2), and LEPR (leptin receptor).

[0185] Exemplary factors that may promote hyaluronic acid synthesis in the skin produced using the input cells and systems provided herein include without limitation, Activin A, LEPR (leptin receptor, TGFB1 (transforming growth factor ß1), EGF (epidermal growth factor), HGF (hepatocyte growth factor), and PDGF (platelet-derived growth factor).

[0186] Exemplary factors that may promote skin elasticity produced using the input cells and systems provided herein include without limitation, IGFBP1 (insulin-like growth factor binding protein 1), IGFBP2 (insulin-like growth factor binding protein 2), IGFBP4 (insulin-like growth factor binding protein 4), TIMP1 (metalloproteinase inhibitor 1), and TIMP2 (metalloproteinase inhibitor 2).

[0187] Exemplary factors for suppression of malignancies and UV-induced skin aging produced using the input cells and systems provided herein include without limitation, endoglin and SCFR (c-KIT stem cell factor receptor.

[0188] Exemplary factors for suppressing wound healing or the inflammatory response produced using the input cells and systems provided herein include without limitation, CD 14 (cell differentiation antigen 14), CD 80 (cell differentiation antigen 80), IFNγ (interferon gamma), and LIF (leukemia inhibitory factor).

[0189] When used as a cosmetic product (to treat a cosmetic or skin condition), the factors may be delivered according to a treatment schedule. Depending on the mode of factor delivery, treatments may be completed at home or at a doctor's office. Delivery of factors after a microneedling (described below) procedure or other skin surface procedure may be part of the treatment schedule.

2. Oncology Applications

[0190] In some variations, the produced/secreted factors, the conditioned media comprising the one or more factors, compositions comprising the one or more factors, or the immunomodulated immune cells (e.g the Tregs produced herein) can be used to treat a disease or disorder related to abnormal cell differentiation such as cancer. Examples of cellular proliferative and/or differentiation disorders include any type of cancer (e.g., carcinoma, sarcoma, metastatic disorders or hematopoietic neoplastic disorders, e.g., leukemias). As contemplated herein, the cancer may be cancer of the lung, breast, thyroid, lymph glands and lymphoid tissue, gastrointestinal organs, and the genitourinary tract. The cancer may be an adenocarcinoma which is generally considered to include malignancies such as most colon cancers, renal-cell carcinoma, prostate cancer and/or testicular tumors, non-small cell carcinoma of the lung, cancer of the small intestine and cancer of the esophagus.

[0191] In one variation of the invention, a composition of factors produced by SR cells, stimulated with IL-2, and collected 72 hours post stimulation, can be administered to an individual for treatment of cancer. Use of the factors for adoptive T cell therapy is also contemplated herein, when *ex vivo* immunomodulated T cells are produced using factors

produced by SR cells, stimulated with IL-2, and collected 72 hours post stimulation and contacted with blood or plasma.

3. Autoimmune Diseases

[0192] In some variations, the produced/secreted factors, the conditioned media comprising the one or more factors, compositions comprising the one or more factors, or the immunomodulated immune cells (e.g the Tregs produced herein) may be used for the treatment of, or for the reduction of signs and symptoms of autoimmune diseases.

[0193] In one variation of the invention, a composition of factors produced by SR cells, stimulated with IL-2, and collected 72 hours post stimulation, can be administered to an individual for treatment of an autoimmune disease. Such compositions comprise cytokines and prostaglandins and with the use of the devices described in this invention, such factors upon delivery to an individual can be released into the blood or affected tissues.

[0194] In one variation, provided herein are factors, which upon administration may be used to reset the effector T cell/Treg cell balance to treat T cell–dependent inflammatory autoimmune diseases, where there is often an imbalance between effector T cells (increase in number in certain autoimmune diseases) and functional Treg (decrease in number in certain autoimmune diseases) cells. Thus provided herein are methods and factor production units useful to reset the effector T cell/Treg balance without delivery of IL-2 drug itself. This approach is suitable for any autoimmune disease listed herein, including, but not limited to, autoimmune vasculitis, alopecia areata, diabetes, chronic graft-versus-host disease, Alzheimer's disease and age-related neurodegeneration, encephalomyelitis, multiple sclerosis, ALS, periodontal infections, rheumatoid arthritis, autoimmune inflammation of variable severity associated with cancer immunotherapies such as CAR-T, lupus, and ankylosing spondylitis *(Smigiel et al, Immunol Rev. 2014:40–59).* Such production may also be useful for wound healing and wound repair.

[0195] In one variation, the factors for the production of Tregs are produced in SR cells (or SEN cells rejuvenated to be SR), wherein the SR cells are induced to produce factors with IL-2 (combined with IL-2 for a period of about 24 hours). Factors produced under these conditions can boost Treg production (e.g. increase Tregs that are CD4+CD25+FoxP3+ and/or CD4+CD25-FoxP3+). In one variation, the SR cells are incubated with IL-2 for about 24 hours,

following which the conditioned media from the SR cells is brought into contact with blood, plasma, or peripheral blood mononuclear cells (PBMCs) of the blood for a period of about 72 hours, thus immunomodulating the naïve T cells in the blood, plasma, or PBMCs.

[0196] FIG. 2C shows an exemplary aspect of the invention which includes production and testing of factors useful for immunomodulation and exemplifies the production of Tregs.

4. Neurodegenerative Diseases and Stroke

[0197] In some variations, the produced/secreted factors, the conditioned media comprising the one or more factors, compositions comprising the one or more factors, or the immunomodulated immune cells (e.g the Tregs produced herein) may be used for the treatment of, or for the reduction of signs and symptoms of, neurodegenerative diseases, including but not limited to Alzheimer's disease, multiple sclerosis, Parkinson's disease, amyolateral sclerosis (ALS), and Huntington's disease as well to prevent neuronal death upon injury. Exemplary factors that may aid in the treatment of neurodegenerative diseases using the input cells and systems provided herein include factors produced by SEN hADSCs + IL-2, collected at 24-72 hrs post induction; or factors produced by SR hADSCs +IL-2 at 48hrs post induction. The factors obtained from a factor production unit using SEN ADSCs+IL-2 collected 48 hours after stimulation can be delivered to achieve therapeutic effects for cellular migration and enhancement of enhancement of revascularization and prevention of apoptosis as required. In some variations factors from these two conditions are combined and delivered to an individual in need.

5. Age-Related Diseases

[0198] In some variations, the produced/secreted factors, the conditioned media comprising the one or more factors, compositions comprising the one or more factors, or the immunomodulated immune cells (e.g the Tregs produced herein) may be used for the treatment of, or for the reduction of signs and symptoms of age-related diseases. Such age-related diseases include, without limitation, osteoporosis, osteoarthritis, and arthritis. Exemplary factors that may aid in the treatment of age-related diseases using the input cells and systems provided herein include without limitation Interleukin 9 (IL9) ,Interleukin 18 binding protein alpha (IL18BPa), Interleukin 1 receptor type II (IL1R2), Interleukin 2 receptor beta (IL-2Rb),

Interleukin 2 receptor gamma (IL-2Rg), Interleukin 5 receptor alpha (IL5Ra), Interleukin 10 receptor beta (IL10Rb), Interleukin 18 receptor accessory protein (IL18Rb), and Interleukin 21 receptor (IL-21R), Insulin-like growth factor 2 (IGF2), Transforming growth factor alpha (TGFa), Transforming growth factor beta 1/latency-associated peptide (LAP), Transforming growth factor beta 1 (TGFb1), Transforming growth factor beta 2 (TGFb2), Receptor tyrosine-protein kinase ErbB-3 (ErbB3), Fas ligand (Fas LG), Leukemia inhibitory factor (LIF), Prolactin (PRL) factor, platelet-derived growth factor receptor alpha (PDGFRa), platelet-derived growth factor receptor beta (PDGFRb), Stem cell factor kit receptor (SCFR), and Sialic acid-binding Ig-like Lectin 5 (Siglec 5), CXC chemokine ligand 16 (CXCL16), Activated leukocyte cell adhesion molecule (ALCAM), E selectin (cell surface glycoprotein in immune-adhesion), Intercellular adhesion molecule 2 (ICAM2), L selectin (Lymphocyte adhesion molecule), and Platelet endothelial cell adhesion molecule (PECAM 1), Activin A (INHBA), Insulin-like growth factor 2 (IGF-2), Leptin Receptor (LEPR), Bone morphogenetic protein 5 (BMP5), Bone morphogenetic protein 7 (BMP7), Macrophage colony-stimulating factor 1 receptor (MCSFR), matrix metalloproteinase 1 (MMP1), matrix metalloproteinase 3 (MMP3), matrix metalloproteinase 9 (MMP9), and matrix metalloproteinase 13 (MMP13), monocyte differentiation antigen (CD14), cell differentiation antigen (CD80), Cardiotrophin-1 (CT-1), and Leukemia inhibitory factor (LIF), Endoglin (ENG), Tyrosine kinase with immunoglobulin-like and EGF-like domains 1 (TIE1) and Tyrosine kinase with immunoglobulin-like and EGF-like domains 2 (TIE2), Leptin Receptor (Leptin R), and Nerve growth factor receptor (NGFR).

[0199] In an exemplary variation, when factors for the treatment of age-related diseases is desired, a population of SR stem cells (e.g. hADSCs) can be placed in a factor production unit in media containing 10% PRP and factors can be collected at 48 hrs.

6. Cardiovascular Diseases

[0200] In some variations, the produced/secreted factors, the conditioned media comprising the one or more factors, compositions comprising the one or more factors, or the immunomodulated immune cells (e.g the Tregs produced herein) may be used for the treatment of, or for the reduction of signs and symptoms of, cardiovascular diseases. Such cardiovascular diseases include, without limitation, myocardial infarction, and enhancement of stem cells related therapies. The factors obtained from the factor production unit comprising SR ADSCs at 48 hrs after placement in 10% PRP alone or in combination with factors obtained from a factor

production unit using SEN ADSCs+IL-2 collected 48hours after stimulation can be delivered to achieve therapeutic effects for myocyte differentiation, cellular migration and enhancement of angiogenesis. A similar composition of factors can be used for treatment of the conditions when enhancement of revascularization and prevention of apoptosis is required.

[0201] In some variations when enhanced cell survival and paracrine stimulation by HGF is required to promote cardioprotection in myocardial infarction, an factor production unit containing SEN ADSCs without IL-2 stimulation (in PRP alone) may be used to produce factors, with factors collected 72hrs after placement in the PRP.

7. Other Diseases

[0202] In some variations, the produced/secreted factors, the conditioned media comprising the one or more factors, compositions comprising the one or more factors, or the immunomodulated immune cells (e.g the Tregs produced herein) may be used for the treatment of, or for the reduction of signs and symptoms of, other diseases including without limitation diabetes, spinal cord injury, Crohn's disease, aplastic anemia, rheumatoid arthritis, brain injury, graft versus host disease (GVHD), kidney diseases, liver cirrhosis, , and stroke, diseases of the nervous system, and spinal cord injury.

II. Factor Production Units

[0203] Described herein are systems for producing various factors, beneficial for a variety of diseases and disorders as discussed above. The systems may include a factor production unit comprising a population of input stem cells and a substrate that provides support for the cell population. Upon contact with an appropriate induction agent, the cell population of the factor production units is stimulated to produce/secrete one or more factors. The production of a particular type of factor may be tailored by the choice of induction agent, choice of cell, choice of substrate, and/or duration of cell culture post-stimulation/induction.

[0204] FIG. 2D pictorially illustrates hADSCs in an exemplary factor production unit of the invention, as described herein. The factor production unit illustrate contains 3-D scaffolds made from polymeric matrix/fibers that mimic the 3-D extracellular matrix (ECM) in which stem cells (e.g. MSCs) naturally reside. The factor production unit allows the cells to be maintained in their natural environment thereby maintaining the morphology and secretory properties of the

stem cells. The stem cells produce growth factors, cytokines and other trophic factors important in the maintenance and regulation of local environment of the factor production unit, as well as secretion of bioactive molecules outside of the factor production unit space. The bottom left two panels are shown with the 3-D scaffolds without the cells the bottom right two panels show GFP-expressing hADSCs cells from a healthy 49 year old patient at 10x and 40X magnification (PD 8). GFP-expressing ADSCs were generated by lenti-viral transduction of the patient ADSCs for visualization of the cells in the matrix. GFP-expressing hADSCs were maintained in a factor production unit in 10% PRP in StemPro MSC SFM Xeno-free medium (ThermoFisher Scientific) for 12 days. GFP demonstrates the cell morphology and cell viability in the factor production unit.

A. Cells

[0205] As provided herein, the input cell populations may include any suitable type of stem cell that can be induced to produce/secrete a factor. The factors that are produced may be used for the treatment of, or for the reduction in signs and symptoms of, a variety of diseases and disorders.

[0206] The factor production unit can comprise a population of input cells, which are induced to produce factors, for delivery to an individual. The input cells may be autologous (cells from the individual who receives the factors) or allogeneic (cells not from the individual who receives the factors).

[0207] The factor production unit can comprise SR cells (including SEN cells that are rejuvenated to be SR) SEN cells (including SR cells that are induced to be SEN), only SR cells, only SEN cells, a mixture of SR and SEN cells, and any variations thereof.

B. Substrates

[0208] In addition to the cell population, the factor production units also comprise a substrate that provides support for the cell population.

[0209] Any suitable structure capable of being a matrix or scaffold for the cell population, or that can hold or carry the cell population can be employed as a substrate. For example, cells of the population can be placed and supported upon the surface of substrates such as films,

membranes, sheets, meshes, discs, rods, fibers, nanofibers, etc., or can be disposed within the substrate material itself (e.g., encapsulated or embedded within the material).

[0210] Factor production units can hold cells within a volume, e.g., a multi-well plate, a tube, a chamber, or other container. In some variations, the factor production unit is an assembly that includes various compartments and/or filtering mechanisms. In further variations, the factor production unit is an implant that can be placed within a body tissue or lumen. Alternatively, the factor production unit may comprise a coating disposed upon or layered upon another structure, e.g., upon the well of a multi-well plate.

[0211] In some variations, the factor production unit is part of an apheresis system. The term "apheresis" is a general term given to a process or system that removes a component of blood. The process or system is more specifically defined by the particular blood component that is removed. For example, if plasma is removed, the process or system is referred to as "plasmapheresis" or a "plasmapheresis type system." Apheresis systems can be used to exchange cells types (e.g., erythrocytapheresis performed for sickle cell disease), treat plasma (e.g., to remove antibodies, paraproteins, cholesterol) or blood (to remove a component thought to contribute to a disease state), or modify blood components (e.g., photopheresis).

[0212] Polymers used to form the substrates are biocompatible, and can be biodegradable or non-biodegradable. Exemplary polymers include without limitation, polyamides, poly(siloxanes), poly(silicones), poly(ethylene), poly(vinyl pyrrolidone), poly(2-hydroxy ethyl methacrylate), poly(N-vinyl pyrrolidone), poly(methyl methacrylate), poly(vinyl alcohol) poly(acrylic acid), poly(vinyl acetate), polyacrylamide, poly(ethylene-co-vinyl acetate), poly(ethylene glycol), poly(methacrylic acid), polylactides, polyglycolides, poly(lactide-co-glycolides), polyanhydrides, polyorthoesters, poly(carbonate), poly(acrylo nitrile), poly(ethylene oxide), polyaniline, polyvinyl carbazole, polystyrene, poly(vinyl phenol), polyhydroxyacids, poly(caprolactone), polyanhydrides, polyhydroxyalkanoates, polyurethanes, collagen, albumin, alginate, chitosan, fibronectin, gelatin, starch, hyaluronic acid, and blends and copolymers thereof.

[0213] The substrate may comprise one or more fibers. Fibers may be in the millimeter, micrometer, or nanometer range. As used herein, "fiber" refers to a fiber having any diameter, including nanofibers (diameter less than 1000 nanometers (nm)) and microfibers (diameter less

than 50 micrometers (μm)). The diameter of the fibers used to make the substrates described herein may range from about 50 nm to about 20 μm. For example, the fiber diameter may be about 50 nm, about 100 nm, about 200 nm, about 300 nm, about 400 nm, about 500 nm, about 600 nm, about 700 nm, about 800 nm, about 900 nm, about 1 μm, about 2μm, about 5 μm, about 6 μm, about 7 μm, about 8 μm, about 9 μm, about 10 μm, about 15 μm, about 20 μm, about 25 μm, about 30 μm, about 35 μm, about 40 μm, about 45 μm, or about 50 μm.

[0214] It may be beneficial in some instances for the substrate to comprise one or more nanofibers. These nanofibers can be configured to form two-dimensional (2D) or three-dimensional (3D) substrates of various size, shape, and geometry. In one variation, the nanofibers are used to construct an artificial extracellular matrix (ECM). The nanofibers may or may not be hollow. Additionally, the nanofibers may include pores of various shape, diameter, and/or distribution on or within the nanofibers.

[0215] When used to construct an appropriate ECM environment, choosing a material that accurately mimics the mechanical properties of the native ECM may provide an optimal environment for the maintenance of the cell population and for the production of factors. Included materials may be non-biodegradable polymers or polymers designed to slowly degrade. Non-biodegradable polymers may comprise polyurethane, polycarbonate, or polyester terephthalate. Biodegradable polymers may comprise polycaprolactone, polylactic acid, polyglycolic acid, gelatin, collagen, or fibronectin.

C. Formation of Substrates

[0216] The substrates may be formed by any suitable process. For example, they may be formed by extrusion, injection molding, vacuum thermoforming, or embossing the polymer material. When composed of fibers, the fibers can be also be formed by extrusion and injection molding. However, the fabrication of nanofibers can be challenging due to their minute diameters. Traditional methods, such as formation in porous solids or at the step-edges of laminated crystals, are often ineffective and costly. An alternative method is electrostatic fiber formation or electrospinning or 3-D laser printing.

[0217] In electrospinning, a high voltage (e.g., about 0.3 to about 0.50 kV) is typically applied between a target (or collector) and a conducting capillary into which a polymer solution or melt

is injected. The high voltage can also be applied to the solution or melt through a wire if the capillary is a nonconductor such as a glass pipette. The collector may be a metal plate or screen, a rotating drum, or even a liquid bath if the capillary is vertical. Initially the solution at the open tip of the capillary is pulled into a conical shape (the so-called "Taylor cone") through the interplay of electrical force and surface tension. At a certain voltage range, a fine jet of polymer solution (or melt) forms at the tip of the Taylor cone and shoots toward the target. Forces from the electric field accelerate and stretch the jet. This stretching, together with evaporation of solvent molecules, causes the jet diameter to become smaller. As the jet diameter decreases, the charge density increases until electrostatic forces within the polymer overcome the cohesive forces holding the jet together (e.g., surface tension), causing the jet to split or "splay" into a multifilament of polymer fibers. The fibers continue to splay until they reach the collector, where they are collected as nonwoven fibers, and are optionally dried. A rapidly rotating collector collects aligned fibers while stationary collectors collect randomly oriented fiber mats. These fibers and mats can then be formed, shaped, etc. into various 2D or 3D structures. In one variation, the fibers are formed to resemble the structure of extracellular matrix.

[0218] Various parameters of the electrospinning process can be adjusted to modify fiber morphology. For example, solution parameters, processing parameters, and parameters such a temperature and humidity can affect fiber morphology, e.g., fiber diameter and/or porosity of the fiber. More specifically, solution parameters such as polymer concentration, polymer molecular weight, and solution viscosity; and processing parameters such as applied voltage, flow rate of the solution, and distance of between the collector and the nozzle can be adjusted.

[0219] In some variations, blends of different polymers may be electrospun together and one polymer preferentially dissolved to increase scaffold porosity.

[0220] Polymers that may be useful in making the polymer solutions for electrospinning may include without limitation, a polyethylene terephthalate, a polyester, a polymethylmethacrylate, polyacrylonitrile, a silicone, a polyurethane, a polycarbonate, a polyether ketone ketone, a polyether ether ketone, a polyether imide, a polyamide, a polystyrene, a polyether sulfone, a polysulfone, a polycaprolactone (PCL), a polylactic acid (PLA), a polyglycolic acid (PGA), a polyetherketoneketone (PEKK), a polyglycerol sebacic, a polydiol citrate, a polyhydroxy butyrate, a polyether amide, a polydiaxanone, and combinations, blends, or copolymers thereof. Alternative polymer solutions used for electrospinning may include natural polymers such as

fibronectin, collagen, gelatin, hyaluronic acid, chitosan, or combinations thereof. In an exemplary variation the polymer is polycaprolactone.

[0221] It is understood that electrospinning solutions may include any polymer or combination of polymers in any compositional ratio. The concentration range of polymer or polymers in solvent or solvents may be, without limitation, about 5 wt % to about 50 wt %. Some non-limiting examples of polymer concentration in solution may include about 5 wt %, about 10 wt %, about 15 wt %, about 20 wt %, about 25 wt %, about 30 wt %, about 35 wt %, about 40 wt %, about 45 wt %, or about 50 wt %, or concentrations between any two of these values.

[0222] In some non-limiting examples, the polymer solution may comprise a weight percent ratio of polyethylene terephthalate to polyurethane of about 10% to about 90%. For example, the weight percent ratios may be about 10%, about 25%, about 33%, about 50%, about 66%, about 75%, about 90%, or a weight percent ratio between any two of these values.

[0223] The polymer solutions may also include one or more solvents such as acetone, dimethylformamide, dimethylsulfoxide, N-methylpyrrolidone, acetonitrile, hexanes, ether, dioxane, ethyl acetate, pyridine, toluene, xylene, tetrahydrofuran, trifluoroacetic acid, hexafluoroisopropanol, acetic acid, dimethylacetamide, chloroform, dichloromethane, water, alcohols, ionic compounds, or combinations thereof.

[0224] The polymer solutions may also include additional materials. Non-limiting examples of such additional materials may include radiopaque materials, electrically conductive materials, fluorescent materials, luminescent materials, antibiotics, growth factors, vitamins, cytokines, steroids, anti-inflammatory drugs, small molecules, sugars, lipids, salts, peptides, proteins, cell factors, or any combination thereof.

[0225] Particles such as salt or sucrose may be included in the electrospinning process and deposited throughout the scaffold. These particles may later be dissolved for increasing scaffold porosity. The properties of the fibers can be controlled to optimize the fiber diameter, the fiber spacing or porosity, the morphology of each fiber such as the porosity of the fibers or the aspect ratio, varying the shape from round to ribbon-like. Solution parameters may be controlled to customize the modulus or other mechanical properties of each fiber, the fiber composition, and/or the degradation rate. The fibers may also be formed as drug eluting fibers, anti-bacterial

fibers, or radiopaque fibers to aid in positioning or locating the fibers in an x-ray, CT, or other scan.

[0226] An exemplary scaffold can be made by first preparing a polymer nanofiber precursor solution by dissolving 2-30 wt % polyethylene terephthalate (PET) in a mixture of 1,1,1,3,3,3-hexafluoroisopropanol (HFIP) and trifluoroacetic acid, and then heating the solution to 60° C followed by continuous stirring to dissolve the PET. The solution may be cooled to room temperature and the solution placed in a syringe (e.g., 60 cc) with a blunt tip needle (e.g., 20 gauge). The nanofibers can be formed by electrospinning using a high voltage DC power supply (Glassman High Voltage, Inc., High Bridge, N.J.) set to 1 kV-40 kV (e.g., +15 kV) positive or negative polarity, a 5-30 cm (e.g., 15 cm) tip-to-substrate distance, and a 1 μl/hr to 100 mL/hr (e.g., 10 ml/hr) flow rate. It is also possible to use a needle array including a large number of needles (e.g., >1000) to increase system output. Fiber diameter may be controlled by the viscosity of the precursor solution and the solvent used and suitable exemplary fibers are in the range of 100 nanometer 30 microns. Approximately 0.2-3 mm (e.g., 1 mm) thickness of randomly oriented and/or highly-aligned fibers may be deposited onto the form, and polymer rings added, followed by an additional approximately 0.2-3.0 mm (e.g., 2 mm) of fiber added while the form is rotated. The scaffold may be placed in a vacuum overnight to ensure removal of residual solvent (typically less than 10 ppm) and treated using a radiofrequency gas plasma for 1 minute to make the fibers more hydrophilic and promote cell attachment. Samples may be stored in re-closeable polyethylene bags, or the like.

[0227] Alternatively, the substrate fibers may be formed from a ceramic material. Exemplary ceramic materials include without limitation, titanium dioxide (TiO2), silicon dioxide (SiO2), zirconium dioxide (ZrO2), aluminum oxide ($Al2O_3$), lithium titanate ($Li_4Ti_5O_{12}$), titanium nitride (TiN), and platinum (Pt). In some variations, the nanofiber is made from a ceramic material provided as particles mixed with a polymer.

[0228] When the cell population is to be contained within the substrate material, e.g., in the material of the nanofiber, it can be added to the polymer solution which is then electrospun into nanofibers. Alternatively, the cell population can be sprayed (e.g., electrosprayed) via a separate nozzle (fiberization tip) while the nanofibers are electrospun so that the cells become embedded, encapsulated, or otherwise contained within the nanofibers before they dry.

[0229] Once made, the nanofibers can be configured to form two-dimensional (2D) or three-dimensional (3D) substrates of various size, shape, and geometry. For example, the nanofibers can be used to construct an artificial tissue such as ECM. The nanofibers can also be used to form meshes or fiber mats. The meshes, fiber mats, or collection of nanofibers may be incorporated into bandages, wound dressings, pads, wipes, etc. Alternatively, the nanofibers may be used to construct a filter or component of the factor production unit, as further described below.

[0230] In certain variations, the substrates are formed by electrospinning nanofibers onto a pre-shaped mandrel (preform) with the desired substrate shape. The mandrel may be coated with Teflon or similar material to facilitate removal of the substrate after deposition. In one variation, the mandrel shape is based on a native tissue or organ. The fibers are typically formed by extruding a polymer and/or ceramic solution from a fiberization tip, creating an electronic field proximate to the fiberization tip, and positioning a ground or opposite polarity within the mandrel. The mandrel may be rotated to align the fibers on the mandrel or a second ground or polarity may be placed in the mandrel so that rapid switching of the electric field can be done to align the fibers. The nanoscale polymer fibers may be randomly aligned or maybe substantially parallel or both.

[0231] The nanofiber structures, as well as other substrates described herein (e.g., films, membranes, meshes, sheets, implants, etc.), may be seeded with a cell population comprising one or more cell types to form a factor production unit. Seeding to apply the cells on the substrate surface may be accomplished by such known methods as spraying, electrospraying, pipetting, and printing. In some variations, the cells are electrosprayed onto the substrate. In other variations, electrospraying of cells occurs simultaneously with electrospinning of the nanofibers to seed the cells on the nanofiber or to encapsulate (or distribute) the cells within the nanofiber material. In yet further variations, the cells may be mixed with a polymer and/or ceramic material, and then extruded or injection molded into a substrate of desired size, shape, or geometry. The cells may be seeded or distributed on or within the substrate in any suitable manner. For example, the cells may be provided in a pattern on the substrate (e.g., symmetric or asymmetric pattern), or homogenously or heterogeneously distributed within the substrate material.

[0232] The substrates or nanofibers may also be coated or otherwise treated with at least one compound that is operative to promote cellular attachment to the substrate. The at least one compound may be selected from the group consisting of proteins, peptides, cytokines, growth factors, antibiotic compounds, lipids, anti-inflammatory compounds, and combinations thereof.

[0233] Hollow fibers/nanofibers can also be made by electrospinning. Here a single nozzle system may be used to electrospin two solutions, typically two different polymer solutions. The first polymer is considered the core of the fiber and the second polymer the shell of the fiber. The core material is generally a sacrificial polymer configured to be removed (e.g., by heating) after electrospinning to leave behind a hollow fiber.

D. Disposition of Cells on Substrates

[0234] The cell population may be disposed on a surface of the substrate or within the material of the substrate (e.g., the body of the substrate). In variations where the substrate comprises fibers or nanofibers, the cell population can be disposed on the surface of the fibers or nanofibers and/or a surface of the structure formed by the fibers or nanofibers, or within the material of the fiber or nanofiber itself. The cell populations can be placed on substrate surfaces by pipetting, spraying (including electrospraying), printing, or embossing the cells onto the substrate surface, or by extruding, injection molding, or thermoforming polymer-cell suspensions. Other ways of including a cell population on or within the substrate can be employed. In some variations, a cell population may be added to a polymer composition, and the resulting polymer-cell suspension electrospun so that the cells are disposed within the polymer material of the fiber. The type of substrate and/or fiber used, as well as the type of cell included on or within the substrate and/or fiber may be manipulated so that factor production by the factor production unit can be customized for the particular indication of use. For example, when the factors are to be used for cosmetic use, the substrate may comprise a plurality of nanofibers arranged as an artificial extracellular matrix, e.g., adipose extracellular matrix, and the cell population may comprise mesenchymal stem cells. In another variation, factors are produced by a factor production unit comprising a plurality of nanofibers arranged as an artificial extracellular matrix and hADSCs.

E. Exemplary Factor Production Units

[0235] In one exemplary variation, the factor production unit comprises a 3D substrate comprising nanofibers that are formed to substantially mimic the structure of extracellular matrix found within adipose tissue. A stromal vascular fraction containing MSCs, as well as endothelial cells, macrophages, monocytes, pericytes, fibroblasts, mast cells, and immune cells may be placed on this particular substrate and cultured and induced to produce one or more factors. The conditioned media containing the one or more factors may be used in any one or more of the applications provided herein (e.g. cosmetic compositions, e.g., for skin rejuvenation, wound healing, or for treating medical conditions such as an oncologic, cardiovascular, autoimmune, neurodegenerative, inflammatory or age-related diseases such as osteoporosis and arthritis).

[0236] The factor production units of the invention can be stand-alone, or can be a part of a larger system, for example part of any one of the apheresis or plasmapheresis systems described herein. Referring to FIG. 107, the factor production unit can be part of an enclosed system. In FIG. 107, the factor production unit (500) is configured to connect to an individual's circulatory system to expose the individual to factors released therefrom. Any suitable factor unit described herein may be included as part of the enclosed system. Here the enclosed system comprises a vessel (502), a factor production unit (500) within the vessel (502), a fluid oxygenation device (504), an oxygenated fluid inlet (506) for introducing fluid, e.g., blood or plasma, into the factor production unit (500), a fluid outlet (508) for removing fluid from the factor production unit (500), a temperature support chamber (512), a sample collection outlet (514), and an infusion pump (516) for administration of heparin or other drugs. Peristaltic pumps (510) drive fluid flow through the enclosed system. Fluid flow through the factor production unit (500) may range from about 50 ml/min to about 500 ml/min with a plasma viscosity of about 1.10-1.30 mPA at 37°C. In some instances, fluid flow through the enclosed system ranges from about 0.1 ml/min to about 50 ml/min. The factor production unit (500) is generally configured to tolerate temperatures between about 37°C to about 40°C. Temperature support chamber (512) generally maintains the temperature of the factor production unit (500) at 37°C.

[0237] Specifically, the enclosed system in FIG. 107 comprises a vessel (502) that accommodates a fluid volume of at least 6 ml. It is understood that the vessel can accommodate other fluid volumes. The factor production unit (500) is generally formed with a medical grade

polymer that is non-heparin binding (e.g., at a heparin concentration of about 41.5 U/ml) and that tolerates DMSO (e.g., about 7-13% by weight); and cells, e.g., mesenchymal stem cells. The factor production unit (500) may be configured to be permeable to factors with a molecular weight ranging from about 1-3 kD, ranging from about 3-6 kD, or ranging from 6-50 kD. The factor production unit may also be permeable to factors having molecular weights of 50kD and above. Fluid flowing through the fluid inlet (506) may first pass through an oxygenation device (504) that provides, e.g., about 21% O_2, about 5% CO_2, and about 74% N_2 to the factor production unit (500) to support cell viability. Factors that are collected at sample station (514) are typically collected at volumes of ranging from about 0.2 ml to about 1 ml.

[0238] In some variations, the factor production unit is a membrane or mat formed from electrospun polymer fibers, for example, as disclosed in PCT Publication No. WO 2015/153011. For example, and as shown in FIG. 105, the factor production unit can comprise electrospun polymer fibers (300) formed as a membrane or fiber mat (substrate) (302). The fibers contain stem cells (not shown) for the training of patient-specific immune cells (e.g., T-cells) via release of instructive cytokines, matrikines, trophic factors , mediators, hormones, and/or trans-membrane and immune-cell docking receptors, from the stem cells. This exemplary variation can be used for immunomodulation applications, for example to increase the production of Tregs, for example for the treatment of autoimmune diseases, as described above. For example, when the fiber mat (factor production unit) is part of an enclosed system such as a plasmapheresis system, the fiber mat may be contacted or placed in proximity to plasma containing immune cells. The cells within the fiber mat may secrete factors into the plasma useful for modulating the immune cells or effecting a change in the immune cells. The stem cells and/or immune cells may also produce factors for collection and later use.

[0239] Factor production units comprising fiber mats and stem cells may be useful immunomodulation treatments, as noted above. Here circulating cells, pooled by apheresis immune cell populations (e.g., T-cells, B-cells, macrophages, NK cells, dendritic cells, or antigen presenting cells, etc.), or cryopreserved or isolated cells, are placed within provided media and attached to the fiber mat or placed in close proximity to the fiber mat and exposed to factors secreted from the fiber mat *ex-vivo* to effect a change in the cells (effect immunomodulation in the cells). These enhanced immune cells can then be released from the mat into the plasma, and the plasma containing the changed cells, e.g., mature T-cells, activated

macrophages, dendritic cells, NK cells, etc., can be delivered back to the individual in a dose dependent manner. Delivery back to the individual can be by injection of the immunomodulatory cells, as well as in combination with medicaments and pharmaceutical compositions delivered into the blood circulation.

[0240] The immunomodulatory cells, as well as the factor-containing compositions described herein may be delivered into the lymphatics (intralymphatic administration), or by other routes, such as but not limited to, subcutaneous administration or sublingual administration, orally, transcutaneously (topical vaccination), intradermally, intramedullary, intrathecal, intraventricular, intranasally, conjunctival, intrabronchial, transdermally, intrarectally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, and intraocularly. The immunomodulatory cells and factor-containing compositions may also be delivered by an implantable device.

[0241] In some variations, a factor production unit may be used to deliver factors for the production of Tregs.

[0242] In other variations, the factor production unit can be part of a reverse dialysis type system comprising at least one cartridge formed by hollow polymeric fibers (tubes) that contain stem cells entrapped within the fiber walls. The stem cells may be autologous or allogeneic. Referring to FIG. 106A, an exemplary system includes a factor production unit (400) comprising a cartridge (402) that includes plurality of polymeric tubes (404) that run in parallel. In an exemplary variation, the system first takes a subject's blood and for circulation through a cartridge (402). As shown in FIG. 106B, which is a cross-sectional view of one of the polymeric tubes (404) in FIG. 106A, blood (406) passing through the hollow tubes (404) of the cartridge (402) permeate the tube wall (410) to contact the entrapped stem cells (408) therein, which enables the release of factors into the lumen (L) of the tube (404) and back into the blood (406). The blood with factors can then be given back to the patient. This cycle would be repeated until the desired factor dosage is achieved. These types of cartridges may also be used in plasmapheresis type systems, as further described below, where cells are removed from the blood to form plasma, and the plasma circulated through the cartridge. Factors released into the plasma can be recombined with the cells prior to introduction back into the patient. A similar type of hollow fiber cartridge is disclosed in U.S. 8,172,784. The hollow tubes can include pores within their walls that allow the release of factors from the stem cells. The pores may be

arranged in any suitable fashion in the tube walls, e.g., homogeneously throughout, or in a symmetric or asymmetric pattern. Any suitable pore diameter may also be used. In other instances, the hollow fiber walls are made from a material permeable to the factors. Similar to the pores, the entire tube wall could be permeable or only portions thereof. Instead of being entrapped within the fiber walls, the stem cells can also be seeded and/or adhered to the inner and/or outer surfaces of the fiber walls.

[0243] In some variations, the factor production unit can comprise a cartridge that includes a pleated cylindrical membrane, as disclosed in U.S. Patent 4,929,354. The factor production unit can include membranes having other suitable geometries.

[0244] Alternatively, the factor production unit may comprise a substrate, where the substrate is a single or multi-well plate having at least one layer of polymer fibers deposited on a surface of the well(s), as disclosed in U.S. 9,074,172. The polymer fibers may be conducive to the growth of biological cells thereon, and thus may be used for cell culture. The polymer fibers may be deposited on a surface of the well(s) by electrospinning, or 3D-printing.

[0245] In some variations, the factor production unit is a component of a plasmapheresis type system where blood is removed from an individual, separated into plasma and blood cells outside the body (extracorporeal), and one or more factors produced/secreted from the factor production unit into the plasma before return of the plasma and cells to the individual. Here the separated plasma can be circulated through various factor production units, e.g., filters comprising a plurality of fibers, to incorporate the one or more factors into the plasma for delivery back to the individual. Delivery of the factors may also be combined with drugs or genetically engineered biologics.

[0246] In one variation, the apparatus for extracorporeal circulation includes a factor production unit in the form of a cartridge or vessel comprising one or more compartments, and has at least a perfusion inlet and a perfusion outlet. A cell population can be supported on a matrix within a compartment of the cartridge, which provides a suitable environment for living cells while allowing perfusion of the cells with suitable media for maintaining the cells. Such cell compartments can be, e.g., hollow fibers, with circulation of blood or plasma outside the fibers, or flat plates; see, e.g., U.S. 6,759,245.

[0247] When the factor production unit is used for immunomodulation treatments, it may be disposed upstream to a cell collecting unit. In this variation, circulating cells or plasma, pooled by apheresis immune cell populations (e.g., T-cells, B-cells, macrophages, NK cells, dendritic cells, or antigen presenting cells, etc.), or cryopreserved or isolated cells, are exposed to factors secreted by the factor production unit *in vitro* to effect a change in the cells. These enhanced immune cells can then be collected and delivered back to the subject.

[0248] The factor production unit described herein may comprise any type of stem cell. In some variations, the factor production unit includes modified hADMSCs. Methods of treating an individual may be accomplished by connecting their circulatory system to these factor production units, thereby exposing the individual (through the blood) to factors produced by the input cells.

[0249] Apparatuses comprising factor production units may also continuously separate plasma from cellular components of blood using an ultrafiltrate generator. The ultrafiltrate (e.g., plasma) may be circulated through the cartridge containing cultured stem cells, e.g., hADSCs. Alternatively, whole blood can be treated in the factor production unit.

[0250] Factor production units may generally contain a semi-permeable barrier made of a material that allows the passage of macromolecules and other cell derived products to and from the individual's plasma. In many variations cells themselves do not leave the factor production unit, however the invention is not so limited. After circulation and one or multiple passes through the factor production unit, the treated blood or ultrafiltrate (e.g., plasma, which may be recombined with the cellular components of the individual's blood) may be returned to the individual via venous access. The individual's blood or plasma may be supplemented with heparin to prevent clotting. This circulation may be maintained continuously for, e.g., a 2 hour, 3 hour, 4 hour, 5 hour, 6 hour, 7 hour, 8 hour, 9 hour, 10 hour, etc. period of therapy. Blood or plasma may carry factors to the individual from the stem cells in the factor production unit.

[0251] The factor production units may also include a fluid treatment compartment and a cell compartment, and optionally a selectively permeable barrier separating the fluid treatment compartment and the cell compartment. The cell reservoir can be in fluid communication with the cell compartment of the factor production unit, wherein the cell reservoir comprises a population of stem cells, e.g., hADSCs. Blood or ultrafiltrate from an individual can be passed

into the fluid treatment compartment, where agents secreted by the stem cells pass into the blood or ultrafiltrate, either by direct contact between the stem cells and the blood or ultrafiltrate, or by passage of the agents across the optional selectively permeable barrier, when present.

[0252] FIG. 100 FIG. 100 illustrates a schematic diagram of an exemplary factor production unit. The factor production unit (1) which may have multiple cartridges and (2) contain modified (e.g., rejuvenated and induced) hADSCs as described herein. In this example, the factor production unit (1) includes an oxygenated fluid inlet (3) for introducing an oxygenated fluid from an oxygenated fluid supply (4), an oxygenated fluid outlet (3'), a liquid inlet (5) for introducing a biological liquid, supplied by pump (6) from immunoisolation unit (7), into the factor production unit and a liquid outlet (5') for removing the biological liquid containing one or more factors from the factor production unit for return to the immunoisolation unit (7). Blood from an individual (9) flows via pump (6') into a plasmapheresis unit (8), from which a portion of the plasma then flows into the immunoisolation unit (7), via pump (6''). Treated plasma (with the one or more factors) flows from the immunoisolation unit (7) and is mixed with blood from the plasmapheresis unit (8) prior to flowing back into the individual (9).

[0253] Referring to FIG. 101, another example of a factor production unit is shown in schematic form (see U.S. 7,160,719 and U.S. 8,172,784). System (10) is represented by and external factor production unit (FPU) (42) that includes modified hADSCs for the production of one or more factors. Blood or plasma can flow through the factor production unit (42) via biological fluid inlet pathway (32) and after the introduction of one or more factors, can exit via biological fluid outlet pathway (33). For example, a catheter can be used to place a mammal's bloodstream in fluid communication with EB (42) via biological fluid inlet path (32). In some variations, the apparatus includes an ultrafiltrate (UF) generator (41). In those cases, blood from the mammal (51) flows along blood path (31) into UF generator (41), where the cellular components are separated from plasma. The ultrafiltered plasma then flows along path (32) into EB (42), while the cellular components rejoin the treated UF via path (34). The biological fluid then returns to mammal (51) or to the biological fluid reservoir via path (35).

[0254] Although FIGS. 100 and 101 depict the various components of a factor production unit in a specific orientation and having similar dimensions, the components can be in any orientation, size, or shape.

[0255] The flow rate of an individual's plasma through a reverse dialysis system or plasmapheresis system can be adjusted as needed, e.g., to a rate of about 50-500 ml/minute, e.g., 50, 100, 200, 300, 400, and 500 ml/minute. In some variations, the flow rate will be adjusted to optimize passage of secreted factors from the stem cells (e.g., hADSCs) to the ultrafiltrate. In some variations, the target flow rate will be 175 ml/minute. Treatment of the individual (e.g., circulation of the individual's plasma through a factor production unit) can continue for a therapeutically effective time, e.g., between 1 hour and 72 hours, e.g., about 2, 3, 4, 5, 10, 12, 15, 18, 20, or 23 hours. Individuals can undergo multiple rounds of modified hADSC therapy with each round lasting for, e.g., between 1 hour and 24 hours. This therapy can be continued, e.g., until a desired therapeutic factor dose or effect has been achieved, as decided by the individual or the individual's healthcare provider.

[0256] The factors can be collected at other predetermined time points post induction. Alternatively, a predetermined duration of time for circulation of plasma or blood through a factor production unit, e.g., a hollow fiber cartridge, or the number of flow cycles through the factor production unit can be predetermined in order to customize the amount (dose) of factors received by an individual.

[0257] Factors generated by the cells can be released into the blood, plasma or culture media. The factors can be released into the blood, plasma or culture media flowing through the factor production unit, e.g., a hollow fiber cartridge or released into a media in which the factor production unit, e.g., an electrospun nanofiber extracellular matrix, is being cultured. Depending on the duration of factor production unit culturing or exposure of the factor production unit to flowing blood/plasma/media, and type of cell included in the factor production unit, different factors and/or different amounts (doses) of factors may be produced. Accordingly, the manufacture of factors can be controlled or tailored based upon the particular composition of the factor production unit and its duration of culturing or exposure to flowing plasma/media. When the factor production unit is exposed to flowing blood/plasma/media, the production and dosing of factors can also be tailored based on the number of flow cycles.

[0258] In other variations, the factor production unit may be integrated (e.g., with an integrated cell chamber) or may be configured to use one or more removable cartridges for holding/culturing the stem cells. The cartridges can be configured for single use (disposable) or repeated use. A number of suitable configurations of cartridges are known in the art, see, e.g.,

U.S. Pat. Nos. 5,270,192; 7,160,719; 6,858,146; 6,582,955; 6,759,245; 8,172,784; Dixit and Gitnick, Eur. J. Surg. Suppl. (582):71-6 (1998); and Legallais et al., J. Memb. Sci. 181:81-95 (2001). Such cartridges can include, e.g., hollow fibers or flat plates. A semi-permeable membrane can be used to separate the biological fluid to be treated from the cells, and such a membrane can form part of the cartridges, e.g., an exterior wall of the cartridge. The cartridges may be configured to be inserted into an factor production unit, e.g., as part of the factor production unit or as an entire factor production unit. Accordingly, the factor production unit may be part of a larger system.

[0259] FIG. 102 is a schematic illustration of an exemplary factor production unit represented by hollow fiber cartridge (100), containing a number of hollow fibers (140), and an inlet (110) and outlet (120). The hollow fibers are semi-permeable, allowing passage of the factors secreted by the stem cells, e.g., hADSCs, into the blood or plasma.

[0260] FIG. 103 is a cross-sectional view of a factor production unit (100) at line A-A in FIG. 102, illustrating the hollow fibers (140), which have an interior capillary lumen (130) surrounded by an extracapillary space (150). In hollow fiber factor production unit, the stem cells can be either in the lumen (130), while the blood or plasma flows through the extra-capillary space (150), or vice-versa.

[0261] FIG. 104 is a schematic illustration of another exemplary factor production unit, represented by a flat-plate or two-compartment factor production unit (200), including a fluid treatment compartment (210) and a cell compartment (220), separated by a semi-permeable membrane (230). Blood or plasma flows through fluid treatment compartment (210) along path (250). Cell compartment (220) includes stem cells, e.g., rejuvenated and induced hADSCs (240). A similar type of unit is described in further detail in U.S. 6,759,254.

[0262] In one exemplary variation, the factor production unit comprises an apparatus configured to deliver factors derived from modified hADSCs, the apparatus comprising: a first compartment; a second compartment; a selectively permeable barrier separating the first compartment and the second compartment; a population of hADSC within the second compartment, wherein the level or activity of SINE/ALU retrotransposon transcripts in the hADSCs is reduced to an amount sufficient to induce or restore proliferative capacity and/or pluripotency to said hADSCs, further wherein the hADSCs have been induced by exposing the

hADSCs to interleukin-2 (IL-2) so that the production of factors in the cells is enhanced; and a fluid inlet and a fluid outlet connected to the first compartment, wherein the fluid inlet and outlet permit fluid communication between the first compartment and the bloodstream of an individual.

[0263] The selectively permeable barrier may comprise a bundle of hollow fibers. Alternatively or additionally, the apparatus may include one or more filters for filtering the blood (or plasma) and/or for filtering fluid from the second compartment before it communicates with the first compartment. The second compartment may be configured as a cartridge that can be removably connected to the apparatus. The cartridge may be snap-connected to the rest of the apparatus, which may also include support for maintaining the hADSC alive and healthy before and during the treatments described herein.

[0264] Any of these apparatuses may also include fluidic handling components, including pumps, channels, filters, etc.; for example, any of these apparatuses may include a pump configured to circulate blood or plasma through the first compartment. Any of these apparatuses may include a filter in fluid communication with the first compartment.

[0265] Alternatively, the factor production unit may include a substrate comprising a plurality of polymer fibers contained within. These polymer fibers may be made by electrospinning. The fiber substrates of the present invention may be used with factor production units of different sizes and shapes, as well as those that are disposable or permanent (i.e., reusable). The polymer fibers in these substrates may also be randomly arranged relative to one another or may be aligned with one another. Depending on the factor production unit geometry, the fiber substrates may be adhered to the factor production unit walls or other surfaces or may be dispersed, individual fibers that are free-floating in the cell culture media contained in a factor production unit. To adhere polymer fibers to a factor production unit, the fiber may be deposited directly onto a surface by placing a negatively charged substrate behind the factor production unit. This technique permits uniform deposition of positively charged fibers onto the factor production unit surface. Alternatively, the fibers may be attached to the factor production unit walls with adhesives, heat, laser welding, ultrasonic welding, or other methods.

[0266] In an exemplary variation, methods of treatment include using hADSCs, using any of the factor production units described herein. For example, a method of treatment may include: reducing the level or activity of SINE/ Alu retrotransposon transcripts in extracted hADSC in an

amount sufficient to induce or restore proliferative capacity and/or pluripotency to said hADSC; and inducing the hADSC (either or both rejuvenated, formerly SEN-hADSC or SR-hADSC) by exposing the hADSC to interleukin-2 (IL-2) to enhance the production of factors; and induction the hADSC (either or both rejuvenated, formerly SEN-hADSC or SR-hADSC) by exposing the hADSC to interleukin-2 (IL-2) to enhance the production of factors; and connecting an factor production unit apparatus to the individual, wherein the factor production unit apparatus comprises a first compartment and a second compartment separated by a selectively permeable membrane, wherein the second compartment comprises the hADSC; and passing an individual's blood or plasma through the first compartment to expose the blood or plasma to factors produced by the hADSC in the second compartment. Connecting the apparatus to the individual may include connecting the apparatus to the individual's circulatory system through an inlet and an outlet of the factor production unit apparatus.

[0267] In yet further variations, the treatment method may include: connecting an factor production unit to the individual, wherein the factor production unit comprises a first compartment and a second compartment separated by a selectively permeable membrane, wherein the second compartment comprises a population of hADSC that have been rejuvenated by reducing the level or activity of SINE/ Alu retrotransposon transcripts in the hADSC in an amount sufficient to induce or restore proliferative capacity and/or pluripotency to said hADSC, and further wherein the hADSC have been induced by exposure to interleukin-2 (IL-2) to enhance the production of factors; and passing the individual's blood or plasma through the first compartment to expose the blood or plasma to the hADSC in the second compartment.

[0268] Any of these methods may include a extracting the hADSC from an individual or obtaining or reviving of the hADSC after cryopreservation. The individual may be the same individual that the hADSC or an extract of the hADSC are administered to (e.g., autologous treatment).

[0269] Other methods may include identifying an individual having a disease (e.g., any of the disease discussed above which may benefit from MSC treatment), and providing an factor production unit for treating blood or plasma from the individual that includes a fluid treatment compartment and a cell compartment, and a selectively permeable barrier separating the fluid treatment compartment and the cell compartment, wherein the cell compartment includes a

population of rejuvenated and induced hADSCs and exposing the individual's plasma or blood to the hADSCs in the factor production unit.

III. Use and Delivery of Factors

[0270] Methods of delivering the factors are also described herein. Once the factors are produced by the input cells, for example in the factor production units provided herein, they may be delivered to an individual in a variety of ways. The method of delivery is generally dependent on the type of composition that has been formulated with the factor. One or more factors may be delivered by conventional routes like sublingual administration, orally, intravenously, via injection, topically, transdermally, transcutaneously (topical vaccination), intradermally, intramedullary, intrathecal, intraventricular, intranasally, conjunctival, intrabronchial, transdermally, intrarectally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly or through the CSF or intralymphatic administration. .

[0271] In an exemplary variation, one or more factors are delivered using an apheresis-type delivery such as plasmapheresis. When plasmapheresis is performed, blood is removed from an individual, separated into plasma and blood cells outside the body (extracorporeal), and one or more factors are added into the plasma before return of the plasma and cells to the individual. Here, the separated plasma can be circulated through the factor production unit as described herein to incorporate the one or more factors into the plasma for delivery back to the individual. Delivery of the factors may also be combined with drugs or biologics.

[0272] When the factors are formulated into oral dosage forms, they may be delivered orally as a tablet, capsule, or as a coating thereon; as a dissolvable film; as an oral spray; etc.

[0273] When the factors are formulated into an intravenous dosage form, the factors can be delivered intravenously as a solution. Injectable compositions may be delivered via a syringe, image-guided needle, or other needled device (e.g., microneedle patch) for local administration of factors, e.g., into a wrinkle, a particular skin layer, or tumor mass. In some variations, instead of being delivered through the needle lumen, the factors are coated on a needle(s), and are released when the needle(s) is placed into tissue.

[0274] In some variations, the factors are provided in conjunction with an implant. If the composition is an implant, the composition may be implanted/placed within a particular body

site or tissue. Sustained release of the factors may be achieved with implantable compositions, as well as other compositions described herein.

[0275] Alternatively, the factors may be formulated into compositions that are topically applied onto the skin or a mucosal surface, and include without limitation, water based gels or pastes, ointments, creams for dermatological use (anhydrous or hydrous), serums, lotions (anhydrous or hydrous), emulsions, sprays, solutions, aerosols, sticks (solid cream), films, bandages, towelletes, powders, skin sprays, nasal or throat sprays, oral drops, eye drops, ear drops, spreadable film-forming compositions, and transdermal patches.

[0276] When topically applied, delivery of the factors into the skin may be enhanced or assisted by various skin surface treatments preformed beforehand. The skin surface treatment may be performed prior to factor application. For example, the skin surface treatment may be performed up to two (2) hours before, up to one (1) hour before, up to 30 minutes before, up to 15 minutes before, up to 10 minutes before, or up to 5 minutes before factor application. The skin surface treatment can include without limitation, dermabrasion, laser resurfacing, and chemical peels. In some variations, the skin surface treatment includes micro-needling. Microneedling may be accomplished with any suitable derma roller. Derma rollers are commercially available devices that generally comprise a drum-shaped roller studded with microneedles arranged in rows around the roller, where the microneedles are about 0.5-1.5 mm in length and 0.1 mm in diameter. When rolled over the skin, the derma roller creates openings in the skin that allow for better penetration of the topically applied compositions. Here, microneedling with a derma roller can be performed prior to topical application of a factor composition to enhance penetration of the factors into the skin, and to also create micro-injuries, which trigger the inflammatory/healing process to produce collagen and other substances beneficial in rejuvenating the skin and improving skin appearance. In turn, the delivered factors can induce keratinocytes to produce growth factors including, but not limited to, PDGF, IL-1, TGF-α, and TGF-β, which have been shown to exert a paracrine effect on proliferation and activation of dermal fibroblasts, leading to skin regeneration and remodeling of dermal extracellular matrix.

[0277] The factor composition may be a topical composition, as previously stated. Exemplary topical compositions include, but are not limited to, water based gels or pastes, ointments, creams (anhydrous or hydrous), serums, lotions (anhydrous or hydrous), emulsions, sprays,

solutions, aerosols, sticks (solid cream), films, bandages, towelletes, powders, skin sprays, nasal or throat sprays, oral drops, eye drops, ear drops, spreadable film-forming compositions, and transdermal patches.

[0278] Creams are oil/water emulsions. They consist of an oil phase (internal phase), comprising typically fixed oils, hydrocarbons, and the like, such as waxes, petrolatum, mineral oil, and the like, and an aqueous phase (continuous phase), comprising water and any water-soluble substances, such as added salts. The two phases are stabilized by use of an emulsifying agent, for example, a surface active agent, such as sodium lauryl sulfate; hydrophilic colloids, such as acacia colloidal clays, veegum, and the like. Upon formation of the emulsion, the active ingredient (e.g., factor(s) or conditioned media) customarily is added in an amount to achieve the desired concentration.

[0279] Gels comprise a base selected from an oleaginous base, water, or an emulsion-suspension base. To the base is added a gelling agent which forms a matrix in the base, increasing its viscosity. Examples of gelling agents are hydroxypropyl cellulose, acrylic acid polymers, and the like. Customarily, the active ingredient (e.g., factor(s) or conditioned media) is added to the formulation at the desired concentration at a point preceding addition of the gelling agent.

[0280] Ointments generally are prepared using either (1) an oleaginous base, i.e., one consisting of fixed oils or hydrocarbons, such as white petrolatum or mineral oil, or (2) an absorbant base, i.e., one consisting of an anhydrous substance or substances which can absorb water, for example, anhydrous lanolin. Customarily, following formation of the base, whether oleaginous or absorbent, the active ingredient (e.g., factor(s) or conditioned media) is added in an amount affording the desired concentration.

[0281] Serums may be watery or thicker liquids, often clear in color. Serums are water based making them light in consistency. Serums may be layered under other serums as well as creams or lotions making them a very flexible product to incorporate into skin care regimens. Serums are tolerated well by all skin types as long as the individual is not sensitive to any of the ingredients. Serums may include glycerol or glycerine.

[0282] Some compositions of the invention can be applied as a thin homogeneous film, which does not require occlusion, bioadhesives, or other additives or devices to effect pharmacological action. The formulation may be applied through physical mechanical means including swab, applicator pad, syringe spreader, or like devices intended to apply liquids in a thin film.

[0283] The compositions may be formulated as desired with additives used commonly in the pharmaceutical sciences, such as penetration enhancers, surfactants, oils and fats, polyhydric alcohols, lower alcohols, thickening agents, UV absorbents, light scattering agents, preservatives, antioxidants, antibiotics, chelating agents, pH regulators, flavoring agents, pigments, and water.

[0284] Penetration enhancers suitable for use in the factor compositions include, but are not limited to, enhancers from any of the following classes: fatty alcohols, fatty acids (linear or branched); terpenes (e.g., mono, di and sequiterpenes; hydrocarbons, alcohols, ketones); fatty acid esters, organic acids, ethers, amides, amines, hydrocarbons, alcohols, phenols, polyols, surfactants (anionic, cationic, nonionic, bile salts).

[0285] Non limiting examples of surfactants include polyoxyethylene (hereinafter abbreviated as POE-branched alkyl ethers such as POE-octyldodecyl alcohol and POE-2-decyltetradecyl alcohol, POE-alkyl ethers such as POE-oleyl alcohol ether and POE-cetyl alcohol ether, sorbitan esters such as sorbitan monooleate, sorbitan monoisostearate and sorbitan monolaurate, POE-sorbitan esters such as POE-sorbitan monooleate, POE-sorbitan monoisostearate and POE-sorbitan monolaurate, fatty acid esters of glycerol such as glyceryl monooleate, glyceryl monostearate and glyceryl monomyristate, POE-fatty acid esters of glycerol such as POE-glyceryl monooleate, POE-glyceryl monostearate and POE-glyceryl monomyristate, POE-dihydrocholesterol ester, POE-hardened castor oil, POE-hardened castor oil fatty acid esters such as POE-hardened castor oil isostearate, POE-alkylaryl ethers such as POE-octylphenol ether, glycerol esters such as glycerol monoisostearate and glycerol monomyristate, POE-glycerol ethers such as POE-glycerol monoisostearate and POE-glycerol monomyristate, polyglycerol fatty acid esters such as diglyceryl monostearate, decaglyceryl decastearate, decaglyceryl decaisostearate and diglyceryl diisostearate and other nonionic surfactants; potassium salts, sodium salts, diethanolamine salts, triethanolamine salts, amino acid salts and other salts of higher fatty acids such as myristic acid, stearic acid, palmitic acid, behenic acid, isostearic acid and oleic acid, the above alkali salts of ether carboxylic acids, salts of N-

acylamino acids, N-acylsalconates, higher alkylsulfonates and other anionic surfactants; alkylamine salts, polyamine, aminoalcohol fatty acids, organic silicone resin, alkyl quaternary ammonium salts and other cationic surfactants; and lecithin, betaine derivatives, and other amphoteric surfactants.

[0286] Examples of oils and fats include vegetable oils and fats such as castor-oil, olive oil, cacao oil, camellia oil, coconut oil, wood wax, jojoba oil, grape seed oil and avocado oil; animal oils and fats such as mink oil and egg yolk oil; waxes such as beeswax, whale wax, lanolin, carnauba wax and candelilla wax; hydrocarbons such as liquid paraffin, squalene, microcrystalline wax, ceresine wax, paraffin wax and vaseline; natural or synthetic fatty acids such as lauric acid, myristic acid, stearic acid, oleic acid, isostearic acid and behenic acid; natural or higher alcohols such as cetanol, stearyl alcohol, hexyldecanol, octyldecanol and lauryl alcohol; and esters such as isopropyl myristate, isopropyl palmitate, octyldodecyl myristate, octyldodecyl oleate, and cholesterol oleate.

[0287] Examples of polyhydric alcohols include ethylene glycol, polyethylene glycol, propylene glycol, 1,3-butyrene glycol, 1,4-butyrene glycol, dipropylene glycol, glycerol, diglycerol, triglycerol, tetraglycerol and other polyglycerols, glucose, maltose, maltitose, sucrose, fructose, xylitose, sorbitol, maltotriose, threitol, and erythritol.

[0288] Examples of thickening agents include naturally-occurring high molecular substances such as sodium alginate, xanthene gum, aluminum silicate, quince seed extract, gum tragacanth, starch, collagen and sodium hyaluronate; semi-synthetic high molecular substances such as methyl cellulose, hydroxyethyl cellulose, carboxymethyl cellulose, soluble starch and cationized cellulose; and synthetic high molecular substances such as carboxyvinyl polymer, and polyvinyl alcohol.

[0289] Examples of UV absorbents include p-aminobenzoic acid, 2-ethoxyethyl p-methoxycinnamate, isopropyl p-methoxycinnamate, butylmethoxybenzoylmethane, glyceryl-mono-2-ethylhexanoyl-di-p-methoxybenzophenone, digalloyl trioleate, 2,2′-dihydroxy-4-methoxybenzophenone, ethyl-4-bishydroxypropylaminobenzoate, 2-ethylhexyl-2-cyano-3,3′-diphenyl acrylate, ethylhexyl p-methoxycinnamate, 2-ethylhexyl salicylate, glyceryl p-aminobenzoate, homomethyl salicylate, methyl o-aminobenzoate, 2-hydroxy-4-

methoxybenzophenone, amyl p-dimethylaminobenzoate, 2-phenylbenzoimidazole-5-sulfonic acid, and 2-hydroxy-4-methoxybenzophenone-5-sulfonic acid.

[0290] Examples of preservatives include benzoates, salicylates, sorbates, dehydroacetates, p-oxybenzoates, 2,4,4′-trichloro-2′-hydroxydiphenyl ether, 3,4,4′-trichlorocarbanilide, benzalkonium chloride, hinokitiol, resorcinol, and ethanol.

[0291] Examples of antioxidants include tocopherol, ascorbic acid, butylhydroxyanisole, dibutylhydroxytoluene, nordihydroguaiaretic acid and propyl gallate.

[0292] Examples of chelating agents include sodium edetate and sodium citrate.

[0293] In addition to those stated above, suitable vehicles, carriers, and adjuvants include water, vaseline, petrolatum, mineral oil, vegetable oil, animal oil, organic and inorganic waxes, polymers such as xanthanes, gelatin, cellulose, collagen, starch, kaolin, carrageenan, gum arabic, synthetic polymers, alcohols, polyols, and the like. The carrier can also include sustained release carrier such as lypizomes, microsponges, microspheres, or microcapsules, aqueous base ointments, water in oil or oil in water emulsions, gels or the like.

[0294] Additional agents that may be included in the factor compositions are vitamins, antioxidants, minerals, extracts, coenzyme Q10, caviar extract, shiitake extract, tripeptide (SYN-AKE), Matrixyl 3000 (palmitoyl oligopeptide and palmitoyl-tetrapeptide-7) (Sederma, Inc., Edison, NJ), and other compounds such as alpha-tocopherol (vitamin E), melanin, vitamin C, vitamin A, retinyl proprionate, retinoic acid, vitamin D3, nicotinamide (vitamin B), niacinaminde (Vit B3), d-panthenol, hyaluronic acid, ceramides, or seaweed (algae) extracts.

[0295] In some instances, the factors are unstable when combined with substances such as surfactants, oils, and/or other excipients. In these instances, the factors can be formulated into a composition that can be lyophilized and dissolved in 10% hyaluronic acid before use.

IV. Articles of Manufacture

[0296] The present application also provides articles of manufacture comprising any one of the devices or compositions described herein.

[0297] An exemplary kit can contain one or more of the following in a package or container: (1) an factor production unit cartridge; (2) one or more pharmaceutically acceptable buffers; and (3) instructions for installing the factor production unit cartridge, including instructions for modifying and/or adding the stem cells such as hADSCs.

[0298] Also provided herein are dermarollers, microneedles, creams, and transdermal patches for use with delivery of the any of the factor compositions provided herein.

[0299] It is to be understood that the terminology employed herein is used for the purpose of describing particular embodiments only and is not intended to be limiting since the scope of the present invention will be limited only by the appended claims and equivalents thereof. The following examples are for illustrative purposes. These are intended to show certain aspects and embodiments of the present invention but are not intended to limit the invention in any manner.

EXAMPLES

Example 1: Materials and Methods

[0300] This example provides the materials and methods subsequently used in Examples 2-9.

Isolation, culture and characterization of MSCs

[0301] MSCs used in this research were isolated from human adipose tissues obtained from healthy adult female donors age 32 and 49 undergoing routine liposuction procedures at the UCSD medical center, San Diego, CA. The MSC isolation protocol was approved by the local ethics committee and performed as previously described. Isolated adipose-derived stem cell lines were grown in DMEM/F12 medium (Life Technologies). In accordance with the MSC minimal definition criteria set by the International Society for Cellular Therapy, flow cytometric analysis showed that hADSCs express CD29, CD73, CD90 and CD105 but do not express CD11b, CD14, CD19, CD34, CD45, CD80, CD86 (antibodies from eBiosciense, USA). Morphological analysis showed that the cells present a fibroblast-like morphology, were plastic adherent and capable of adipogenic, chondrogenic and osteogenic differentiation under *in vitro* conditions using commercially available differentiation mediums (Invitrogen, USA). Cumulative population doublings (PD) were calculated as PD = log(N/NO) x 3.33 across the multiple passages as a function of the number of days of growth in culture, where NO is the number of

cells plated in the flask and N is the number of cells harvested at this passage. hADSCs PD 4 or PD 6 SR populations and PD 41 and 45 for SEN populations were used in all experiments. Treatment with recombinant IL-2 (Peprotech, USA) was performed as described in Deenick EK, Gett AV, Hodgkin PD (2003) Stochastic model of T cell proliferation: a calculus revealing IL-2 regulation of precursor frequencies, cell cycle time, and survival. J Immunol 170: 4963-4972. 20U/ml of IL-2 was added to the culturing media for 24 hours at 37°C.

Senescence—associated SA-β galactosidase assay

[0302] The assay for monitoring the expression of pH-dependent senescence-associated (3-galactosidase activity (SA-(βGal) was performed as described in manufacturer's kit (BioVision) and previously published in Wang J, Geesman GJ, Hostikka SL, Atallah M, Blackwell B, et al. (2011) Inhibition of activated pericentromeric SINE/ALU repeat transcription in SEN human adult stem cells reinstates self-renewal. Cell cycle 10: 3016-3030. The cultured hADSCs were washed with PBS for 15 minutes at room temperature, washed twice with PBS and stained with X-Gal containing supplement overnight at 37°C. The cells were washed twice with PBS, and the images were captured using a microscope (Nikons, TE300, DXM1200 Digital Camera, Japan).

Migration and invasion assay

[0303] Transwell filters were from Corning Incorporated (Acton, MA, USA) and all the cytokines in use were obtained from Peprotech Inc. (Rocky Hill, NJ, USA). The migration assay was performed as described in Perez LM, Bernal A, San Martin N, Galvez BG (2013), Arch Physiol Biochem 119: 195-201 using 8mm thick Transwell chambers. For the Transwell migration assay, 1.0 x 10^4 cells were suspended in 80ul of serum-free alpha-MEM and seeded in the upper chamber of 24-well Transwell plates containing 8 mm pore size filters (Corning, Costar, USA). In the lower chamber, 600 ul of DMEM or medium containing cytokines: IL-2, IL-6, IL-8, TNF-α, HMGβ1 was added. The concentrations in used were: 50ng/m1 IL-2, IL-6, IL-8 and HMGβ1; 30ng/m1 TNF-α as described in (Perez et al., 2013, Arch Physiol Biochem 119: 195- 201). hADSCs were incubated at 37°C for 16h. The cells retained in the upper chamber were removed by swab and those that had migrated through the filter were fixed with 4% paraformaldehyde for 20 minutes at room temperature and stained overnight with 5% toluidine blue. The cells were counted at the lower side; in five different randomly selected 10x fields using a bright-field microscope (Nikons, TE300, DXM1200 Digital Camera, Japan).

These experiments were done with hADSCs of two donors age 32 and 41, ether SR or SEN populations, with each donor sampled more than three times.

Enzyme-linked immunosorbent assays (ELISA)

[0304] hADSCs (SR or SEN) were plated at a density of 10^5 cells per 10 cm^2 dish and treated with 20 U/mL of IL-2 for 24 hour, with untreated controls as previously described in Deenick EK, Gett AV, Hodgkin PD (2003) Stochastic model of T cell proliferation: a calculus revealing IL-2 regulation of precursor frequencies, cell cycle time, and survival. J Immunol 170: 4963-4972. Then, cell membrane-associated protein fractions were prepared using MemPER Plus #89842 (ThermoFisher Scientific) following the manufacturer's protocol. Measurements of the concentrations of IL-2 receptors *alpha* and *beta* were obtained using human IL-2R *alpha* and human IL-2R *beta* ELISA kits #ELH-IL-2Ra and #ELH-IL-2Rb (RayBiotech, Inc) respectively. The optical densities for the standards (recombinant IL-2 receptors *alpha* and *beta)* as well as the experimental samples were measured at 450 nm by SPECTRA Max Plus (Molecular Devices) and concentrations were calculated as described in the manufacturer's protocol.

Real-time quantitative polymerase chain reaction

[0305] Total RNA was isolated from hADSCs using the RNeasy Mini Kit (Qiagen, Germany). cDNA was then synthesized using the RevertAid First Strand cDNA Synthesis Kit (Fermentas, USA). Real-time quantitative polymerase chain reaction (qPCR) was performed using TaqMan instrument. The expression levels were calculated as $2^{-\Delta\Delta Ct}$, where relative expression was determined by normalization to beta-actin gene expression. All assays were conducted in triplicates and negative control samples without cDNA were used. Primers for the qPCR were as follows:

[0306] IL-2 Receptor Alpha chain (IL-2Rα) For: 5'- CTGCCACTCGGAACACAAC-3' and Rev: 5'- TGGTCCACTGGCTGCATT-3'.

[0307] IL-2 Receptor Beta chain (IL-2Rβ) For: 5'- ACTCGAGAGCCAACATCTCC-3' and Rev: 5'- TCCGAGGATCAGGTTGCAG-3'.

[0308] IL-2 Receptor Gamma 1 chain (IL-2Rγ1) For: 5'- TGGATGGGCAGAAACGCTA-3' and Rev: 5'- GGCTTCCAATGCAAACAGGA-3'.

[0309] STAT 5A For: 5'- ACGCAGGACACAGAGAATGA -3' and Rev: 5'-CTGGGCAAACTGAGCTTGG-3'.

[0310] STAT 5B For: 5'- ACACAGCTCCAGAACACGT -3' and Rev: 5'-TGTTGGCTTCTCGGACCAA-3'.

[0311] VEGF A For: 5'- GGAGGAGGGCAGAATCATCA -3' and Rev: 5'-ATCAGGGGCACACAGGATG-3'.

Transcriptomic analysis

[0312] Transcriptomic analysis was performed with IL-2 treated and untreated (control group) SR and SEN-hADSCs as previously described in Deenick EK, Gett AV, Hodgkin PD (2003) Stochastic model of T cell proliferation: a calculus revealing IL-2 regulation of precursor frequencies, cell cycle time, and survival. J Immunol 170: 4963-4972. The two genotypes shown in FIG. 3A were used for the analysis of four different conditions: SR or SEN cells, with or without IL-2 stimulation, respectively. The same amount (10^6) cells was seeded in DMEM F12 media for each experimental condition, and IL-2 treatment was performed by adding 20U/m1 of recombinant IL-2 (Peprotech, USA) directly into the media for 24 hours as previously described in Deernick et al. 2003. Total RNA was isolated from samples using TRIzol reagent (Invitrogen, USA) according to the manufacturer's instructions. Samples from two different patients were combined together for the relevant conditions and RNA concentrations were measured with the Qubit 2.0 fluorimeter using the RNA HS Assay kit (Invitrogen, Life technologies, USA).

[0313] 100ng of total RNA of each sample was used to construct the libraries for sequencing on the Ion Proton™ System (Life technologies, USA) following the manufacturer's instructions. Prior to rRNA depletion and RNA-seq library construction, the ERCC RNA Spike-In Control mix (Ambion, Life Technologies) was added to total RNA for quality control analysis. The ERCC RNA Spike-In control mix contains 92 transcripts 250-2000 nt in length that mimic natural eukaryotic mRNAs. According to the protocol provided by manufacturer for 100 ng of total RNA was added to 2u1 of Mixl in dilution 1:1000 of spike-in. Afterwards, rRNA depletion was performed with the Low Input Ribominus Eukaryote System v2 (Ambion, Life technologies, USA). cDNA libraries were constructed with Ion total RNA-seq kit v2 (Ambion, Life technologies, USA), and barcoded with Ion Xpress RNA-seq barcode (Ambion, Life technologies). The size distribution and quantification of the libraries were performed on a

Bioanalyzer 2100 (Agilent technologies, USA). Library sequencing was performed on the Ion Proton™ System with P1 chip, and each library was sequenced 3 times.

RNA-seq data analysis

[0314] RNA-seq reads from individual Ion Proton™ System sequencing runs were combined for each of the four conditions. Sequence reads were mapped to the reference human genome assembly hgl9 (GRCh37) using the Torrent Mapping Alignment Program (TMAP, Life technologies). The quality of the four condition-specific combined RNA-seq runs was evaluated by comparing the expected counts of ERCC spike-in RNA sequences, obtained from the manufacturer's website, against the observed counts of RNA-seq tags that map to the same sequences. Initial gene expression levels were taken as the sum of exon-mapped reads for individual NCBI RefSeq gene models *(c),* and lowly expressed genes (read counts per million<1) were removed from subsequent analyses. For each library, individual gene expression levels were normalized using the beta-actin *(ACTB)* expression levels *(cACTB)* and the total exon length l of each gene. For library *j,* the beta-acting normalization factor s_j was calculated as

$$\frac{\frac{1}{n}\sum_{k=1}^{n} c_{ACTB,k}}{c_{ACTB,j}}$$

and the final normalized expression value for gene i in library j was calculated as

$$\text{as } e_{i,j} = \frac{c_{i,j} \times s_j}{l_i}$$

[0315] Differential gene expression analysis between pairs of libraries was performed using the program GFOLD v1.1.3, Feng J, Meyer CA, Wang Q, Liu JS, Shirley Liu X, et al. (2012) GFOLD: a generalized fold change for ranking differentially expressed genes from RNA-seq data. Bioinformatics 28: 2782-2788. GFOLD was chosen based on its demonstrated superior performance in characterizing differentially expressed genes in the absence of replicate data sets. GFOLD analysis yields a score that measures the extent of differential gene expression between conditions; the recommended GFOLD score cut-off of ±0.01 was used to define differentially expressed genes here. Functional enrichment analysis for differentially expressed genes between pairs of libraries was performed using the program GSEA v2.1.0. Specifically, individual pathways containing multiple genes that are up-regulated or down-regulated upon IL-2 treatment

in SR, SEN or both were identified in this way. Individual pathways for specific sets of differentially regulated genes (IL-2+ up-regulated in SR and/or SEN and IL-2+ down-regulated in SR and/or SEN) were related using networks where the nodes correspond to pathways and the edges correspond to the presence of shared genes between pathways.

[0316] FIG. 9 shows External RNA Controls Consortium (ERCC , a common set of external RNA controls) dose response used for quality control of RNA-seq experiments. For each of the four condition-specific RNA-seq pools, the expected counts of ERCC spike-in RNA sequences were regressed against the observed counts of RNA-seq tags that map to the same sequences. Observed versus expected counts were highly correlated, as indicated by the shape of the regression and the Pearson correlation r-values, consistent with high quality RNA-seq results.

Example 2: Characterization of the MSC senescent phenotype

[0317] Described in this example is a study that was conducted to evaluate the impact of replicative senescence on the transcriptional activity of human adipose-derived MSCs (hADSCs) in response to IL-2 signaling.

[0318] IL-2 signals via specific receptors, with three classes of cell surface receptors formed by various combinations of three IL-2R subunits: IL-2Ra (CD25), IL-2Rβ (CD 122) and IL-2Rg (CD 132). The experimental results indicate that hADSCs transcriptionally express all three receptors, however protein expression of the IL-2Ra in hADSCs is lower than seen for IL-2Rβ. These observations indicate that an IL-2 receptor composition consisting of IL-2Rβ and IL-2Rγ isoforms may mediate the predominant form of IL-2 cytokine recognition by hADSCs. The receptor composition changes only slightly upon replicative aging of the hADSCs, indicating that responsiveness of hADSCs to IL-2 does not change upon their senescence.

[0319] hADSCs were isolated and cultured as described above. *Ex vivo* replicative senescence led to decreased proliferation, accumulation of DNA damage and morphological changes: hADSCs became much larger with an irregular and flat shape, and nuclei became more circumscribed in phase contrast microscopy with the granular cytoplasm appearance of many inclusions and aggradations. The growth curve of hADSCs obtained from two different patients are shown in FIG. 3A. Typical staining for senescence-associated SA-β galactosidase activity for either hADSCs in linear growth rate, SR, or when cell lines cease their proliferation, SEN, is shown in FIG. 3B.

Example 3: SEN-MSCs demonstrate a higher propensity for migration

[0320] Migration assays were performed, using a set of cytokines and growth factors using the Transwell system as described in the Materials and Methods section, below. It was observed that adipose-derived MSCs undergoing replicative senescence demonstrated a higher propensity for migration. It was observed that SEN-hADSCs showed significantly higher basal migration capacity then their SR counterparts (FIG. 3C). FIG. 3C shows *ex vivo* migration assays for SR (left) and SEN (right) hADSCs. The black lines indicate the median values, and the whiskers indicate the range of values. Statistical differences were evaluated by a T-test with the p-value (p) as depicted.

[0321] In addition, the response of SEN-hADSCs to different cytokine chemo-attractants was measured. It was observed that hADSCs have an increased ability to migrate for late passages in comparison to early passages (FIG. 3D), indicating that replicative senescence increases the migratory properties of hADSCs in response to the tested chemo-attractants. IL-2 was the most potent chemo-taxis stimulant on SEN-MSCs, whereas the TNF-α was less potent among the tested chemo-attractants in these experiments (FIG. 3D). FIG. 3D shows the migration of self-renewing SR (on left) and senescence SEN (right) hADSCs. hADSCs were induced to migrate in the presence of different cytokines (50 ng/ml IL-2, IL-6, IL-8, HMGBl; 30 ng/ml TNF). The graphic represents the mean of ten independent experiments (n=10). P-values (p) related to experimental measurements are listed under the graphs.

[0322] Collectively, these data indicated that replicative senescence modifies the migratory properties of hADSCs and may influence the response of MSCs to the inflammatory environment and influence their immunomodulation output.

Example 4: Differential response to Il-2 stimulation in human adipose-derived MSCs upon replicative senescence

[0323] Assessment of the IL-2 receptor isoforms expression, by qPCR, demonstrated significant changes in expression of the IL-2Rα isoform in comparison to IL-2Rg and IL-2Rβ upon replicative senescence *ex vivo* (FIG. 4B). FIG. 4B shows IL-2 receptors α, β, and γ assessed by quantitative PCR (qPCR) in un-stimulated (IL-2-)SR cells (first bar) and SEN cells (third bar) and upon stimulation with 20ug/ml of recombinant IL-2 (IL-2+) (SR cells, second bar; SEN cells, fourth bar). Data shown as fold change ($\Delta\Delta CT$). Mean± SD from three

independent experiments is shown. Notably, the increased accumulation of the IL-2Rβ and IL-2Ra transcripts was recorded after IL-2 treatment in both SR and SEN-hADSCs, whereas IL-2Ra expression was abrogated when SEN cells were subjected to similar treatments (FIG. 4B).

[0324] However, the data indicated that protein level expression of the cellular membrane associated IL-2Rα receptor showed the opposite pattern (FIG. 4C). FIG. 4C shows the cellular membrane-associated levels of IL-2Rα and IL-2Rβ. The levels were quantified by ELISA in un-stimulated (IL-2-) SEN (third bar) and SR (first bar) hADSCs and upon stimulation with 20ug/ml of recombinant IL-2(IL-2+) SEN (fourth bar) and SR (second bar). Data are expressed as pictogram per milliliter. Results are the mean of three independent experiments (mean± SD). Statistical significance was estimated by a t-test, where ***p < 0.001, **p <0.01, *p<0.05.

[0325] Although the transcriptional status of IL-2 receptor isoforms does vary between the two different cell states (SR and SEN), it does not seem to be dependent upon IL-2 exposure (induction) as measured by the ELISA assay (described in the Materials and Methods, above). The data also demonstrated that protein encoding IL-2α receptor chain is less abundant than the IL-2Rβ isoform (compare 120 pg/ml of IL-2Rα to 350 pg/ml IL-2Rβ to 150 pg/ml of IL-2Rα and 440 pg/ml IL-2Rβ upon replicative senescence *ex vivo*) as shown in FIG. 4C. These data indicate that hADSCs response to IL-2 stimulation occurs through the intermediate-affinity receptor dimer composed of IL-2Rβ (CD 122) and the common IL-2Rg (CD 132).

[0326] IL-2 signals via JAKl and JAK3 to activate STAT5A and STAT5B, and additionally uses Ras-MAP kinase and phosphoinositol 3-kinase dependent signaling pathways. The expression of downstream target of IL-2, STAT5, is shown in FIGS. 5, 7A and 7B and the table of FIGS. 10A and 10B. In hADSCs, both STAT5A and STAT5B gene transcription follows the IL-2/STAT5 signaling axis.

[0327] FIG. 5 illustrates the effect of stimulation of the SR and SEN-hADSCs with IL-2. IL-2 upregulates mRNA of a mediator of IL-2 signaling STAT5 gene. STAT5A and STAT5B mRNA expression was assessed by quantitative RT-PCR in un-stimulated (IL-2-) SR (first bar) and SEN cells (third bar) and upon stimulation with 20ug/ml of recombinant IL-2 (IL-2+) (SR +IL-2, second bar; SEN + IL-2, third bar). Data are shown as fold change (ΔΔCT). Mean± SD from three independent experiments is shown. The position of the qPCR primers is depicted graphically. Statistical significance was estimated by the t-test, where ***p < 0.001, **p<0.01.

[0328] It was next investigated how IL-2 and its downstream target STAT5 affects transcriptional outcomes in hADSCs upon their replicative senescence *ex vivo*.

[0329] Exposure to IL-2 resulted in altered gene expression in human MCSs upon replicative senescence. To address how the transcriptional response to the IL-2/STAT5 axis changes upon replicative aging of hADSCs *ex vivo*, a RNA-seq transcriptome analysis was performed, using the Ion Proton™ System as described in Example 1 and shown in FIG. 8A. The gene expression levels in hADSCs across four conditions (libraries) was compared: self-renewal upon normal *ex vivo* culture (SR IL-2-), self-renewal upon 24 hrs recombinant IL-2 stimulation (SR IL-2+), replicative senescence upon normal *ex vivo* culture (SEN IL-2-), and replicative senescence upon 24 hrs recombinant IL-2 stimulation (SEN IL-2+). Distributions of the total read counts for the four conditions representing each condition are shown in FIG. 8B.

[0330] Beta-actin expression levels were used to normalize gene expression levels between conditions (as described in Example 1). This approach was taken to allow for the fact that overall gene expression levels may change upon IL-2 treatment. Beta-actin normalized gene expression distributions reveal overall up-regulation of gene expression upon IL-2 treatment in both SR and SEN states (FIG. 8D). However, comparison of individual gene expression levels among the four conditions indicates that IL-2 treatment more significantly affects SEN-compared to SR-hADSCs (FIG. 6A). FIG. 6A shows a hierarchical clustering showing the pairwise distance between conditions based on comparison of condition-specific gene expression profiles. The SR IL-2- and SR IL-2+ conditions group closely together when individual gene expression levels are compared followed by the SEN IL-2- condition. The SEN IL-2+ condition is an outlier amongst the four conditions showing a substantially divergent pattern of individual gene expression levels. This indicates that that the biological response to IL-2 treatment in hADSCs upon senescence may significantly impede MSC function via global transcriptional de-regulation in response to IL-2.

[0331] Expression levels were further compared between conditions in order to identify individual genes that are differentially expressed, up- and down-regulated, in response to IL-2 treatment in both SR and SEN states (FIG. 6B). FIG 6B is a Venn diagram showing the numbers of genes, which are up-regulated and downregulated upon IL-2 treatment. There are several more genes that are up-regulated (8,866) compared to down-regulated (2,296) upon IL-2 treatment in both SR and SEN-hADSCs. There is also a substantially higher proportion of genes

that are up-regulated in both SR and SEN-hADSCs (35%) compared to genes that are down-regulated in both states (4%). The greatest asymmetry is seen for genes that are down regulated in SEN-hADSCs upon IL-2 treatment (1,739); there are many more such genes than seen for the SR IL-2+ condition (649). This difference indicates that the overall divergence of the SEN IL-2+ condition is largely attributed to genes that are down-regulated upon IL-2 treatment, which is an unexpected result given the overall up-regulation across both SR and SEN upon IL-2 treatment (FIG. 6B and FIG. 8D).

[0332] FIGS. 6C-6D shows heat maps showing the expression levels of genes that are up-regulated (FIG. 6C) and down-regulated (FIG. 6D) upon IL-2 treatment. Normalized gene expression levels are shown as heat maps in grayscale. Groups correspond to genes that are up- or down-regulated in SR-only, SEN-only or both conditions.

[0333] Taken together, these data show that SEN-hADSCs have lost the ability to generate coordinated regulatory changes in response to IL-2 treatment to the same extent that exists for actively proliferating SR cells. The greater number of up-regulated genes seen for SR IL-2+, compared to SEN IL-2-, is consistent with this interpretation.

[0334] FIG. 10A shows a table (FIG. 10A) indicating biological pathways enriched for genes up-regulated upon IL-2 treatment in SR and SEN-hADSCs. In FIG. 10A, enriched pathways are shown along with the individual IL-2+ up-regulated genes belonging to the pathway and the pathway enrichment significance levels. Pathways with gene members up-regulated in SR are shown in the left column, and pathways with gene members up-regulated in SEN are shown in the right column. Pathways with gene members up-regulated in both SR and SEN are shown in the top row followed by pathways with gene members up-regulated only in SEN, and finally pathways with gene members up-regulated only in SR. Networks are shown relating pathways that are up-regulated in SR (left column) and pathways that are up-regulated in SEN (right column). The network nodes represent pathways, and the sizes of the nodes correspond to the number of up-regulated genes in that pathway. Pathway nodes are connected by edges if the pathways share up-regulated genes, and edge-weights correspond to the number of up-regulated genes shared between the pathways.

[0335] FIG. 10B illustrates biological pathways enriched for genes down- regulated upon IL-2 treatment in SR and SEN-hADSCs. Enriched pathways are shown along with the individual IL-

2+ down-regulated genes belonging to the pathway and the pathway enrichment significance levels. Pathways with gene members down-regulated in SR are shown in the left column, and pathways with gene members down-regulated in SEN are shown in the right column. Pathways with gene members down-regulated in both SR and SEN are shown in the top row followed by pathways with gene members down-regulated only in SEN, and finally pathways with gene members down-regulated only in SR. A network is shown relating pathways that are down-regulated in SEN (left column). The network nodes represent pathways, and the sizes of the nodes correspond to the number of SEN down-regulated genes in that pathway. Pathway nodes are connected by edges if the pathways share SEN down-regulated genes, and edge-weights correspond to the number of down-regulated genes shared between the pathways.

Example 5: Trophic properties of the hADSCs after Il-2 stimulation are susceptible to replicative aging *ex vivo*

[0336] FIGS. 7A-7D illustrate gene expression levels for SR and SEN cells upon IL-2 treatment among functionally coherent sets of genes. Expression levels are shown for sets of genes characterized as (in FIG. 7 A) trophic factors, (in FIG. 7B) anti-inflammatory and immunomodulatory, (as shown in FIG. 7C) anti-apoptotic and metastasis promoting, and (as shown in FIG. 7D) migration and angiogenesis promoting. Normalized gene expression levels are shown as heat maps in grayscale.

[0337] Table 1 shows the differential expression of trophic factors upon IL-2 treatment in SEN and SR cells. The SR GFold values represent the fold difference in SR cells treated with IL-2, relative to SR cells not treated with IL-2; the SEN GFold values represent the fold difference in SEN cells treated with IL-2, relative to SEN cells not treated with IL-2.

Table 1: Differential Expression of Trophic Factors Upon IL-2 Treatment

Gene Symbol	Gene ID	SR IL-2-	SR IL-2+	SEN IL-2-	SEN IL-2+	SR GFOLD	SEN GFOLD
TGFBRAP1	NM_001142621	941	1475	2242	2601	0.51	0.12
SDF2	NM_006923	685	992	1466	1516	0.37	0.00
IL17D	NM_138284	9	49	69	124	0.97	0.34
TGFA	NM_001099691	147	295	316	484	0.67	0.37
CSF1	NM_000757	1466	1691	3953	4906	0.09	0.24
TGFBR2	NM_001024847	3416	4028	20586	25244	0.16	0.26
LIF	NM_002309	163	227	942	1652	0.13	0.67
FGF1	NM_001144892	287	237	524	741	0.00	0.31

Gene Symbol	Gene ID	SR IL-2-	SR IL-2+	SEN IL-2-	SEN IL-2+	SR GFOLD	SEN GFOLD
EGFR	NM_005228	4980	5431	5971	5368	0.06	-0.09
SRF	NM_003131	1689	1742	2132	1957	0.00	-0.02
FGF7	NM_002009	756	766	1131	946	0.00	-0.11
FGF2	NM_002006	5573	5301	8776	8185	-0.01	-0.05
SFRP1	NM_003012	1351	1346	4190	3575	0.00	-0.15
PTGES2	NM_025072	521	746	1778	1699	0.33	0.00
PDGFRA	NM_006206	3877	4533	5085	3109	0.15	-0.63
PDGFA	NM_002607	612	866	790	682	0.32	-0.04
FGF5	NM_004464	4322	5738	3329	2895	0.34	-0.12
TGFB2	NM_001135599	352	422	166	314	0.02	0.60
TGFB1	NM_000660	4834	6297	3413	5582	0.32	0.64
IL11	NM_000641	583	758	152	950	0.19	2.35
IL1B	NM_000576	73	108	75	229	0.06	1.17
FGF14	NM_004115	61	69	89	255	0.00	1.11
TNFSF13B	NM_001145645	0	12	10	104	0.65	2.12
FGF11	NM_004112	67	48	10	198	0.00	3.09

[0338] The data indicated that the expression of growth factors in hADSCs upon stimulation with IL-2 is subjected to significant changes upon replicative senescence *ex vivo*. While the exposure of actively proliferating (SR) hADSCs to IL-2 resulted in increased expression of mitogenic proteins such as stromal cell-derived factor 2 (SDF2) and SDFL2, and prostaglandin E synthetase 2 (PTGES2), both SR and SEN-hADSCs are marked by significant increases of transforming growth factors alpha and beta (TGFa, TGFβl and TGFβ2), transforming growth factor beta receptor TGFBR2 and transforming growth factor beta receptor-associated protein TGFBRAPl, as well as transforming growth factor beta-induced (TGFBI) (FIG. 7A and Tables 6A-6D).

[0339] In addition, both SR and SEN IL-2 stimulated hADSCs were marked by up-regulation of colony stimulating factor 1 (CSF-1), LIF, IL-11, IL-17D, IL-1β and tumor necrosis factor (ligand) superfamily TNFSF13B, a cytokine encoding gene that stimulates B- and T-cell function (FIGS. 7A, 7B and FIGS. l0A-l0B).

[0340] Taking into account that paracrine IL-17D induces expression of IL-6, IL-8, and GM-CSF genes in endothelial cells, and IL-1β stimulates fibroblast growth factor activity (TGFa, TGFβ1 and TGFβ2 genes are notably up-regulated in IL-2-exposed hADSCs) in autocrine and paracrine fashion, along with thymocyte and B-cell proliferation and maturation by inducing release of IL-2 from these cells, the data indicate that the transcriptional status of

both SR and SEN-hADSCs may point to enhanced immunomodulatory properties of these cells after IL-2 exposure via a complex regulatory feed-back loop.

[0341] Both SR and SEN-hADSCs exposed to IL-2 are marked by significant increases in expression of transforming growth factors alpha and beta (TGFa, TGFβl and TGFβ2), transforming growth factor beta receptor TGFBR2 and transforming growth factor beta receptor-associated protein TGFBRAPl, as well as transforming growth factor beta-induced (TGFBI) genes (FIG. 7A).

[0342] In addition, essential differences in the IL-2 dependent expression of growth factors upon senescence of hADSCs that have not been observed in SR cells were also noted. This includes up-regulation of a subset of fibroblast growth factor family members (FGF l, FGF l 1, FGF 14) accompanied by down-regulation of other members, such as FGF2, FGF 5, FGF7, (FIG. 7 A, Table 1, and Tables 6A-6D).

[0343] IL-2 exposed SEN-hADSCs are marked by EGF mRNA up-regulation, but down-regulation of mRNA to its receptor EGFR, together a decrease in expression of the serum response factor SRF and the secreted modulator of WNT signaling SFRP1.The expression of both a potent mitogen for cells of mesenchymal origin that promotes wound healing, PDGFA, and its receptor, PDGFRA, is significantly suppressed in SEN-hADSCs in comparison to SR cells subjected to IL-2 exposure (FIG. 7A, FIG. 10A, Table 1, and Tables 6A-6D).

[0344] These data revealed senescence-related differences in the nature of IL-2 mediated transcriptional response in hADSCs that might impede these cells immunomodulatory properties *ex vivo* and, ultimately, *in vivo*.

[0345] A panel of anti-inflammatory and immunomodulatory markers for IL-2 treatment, IL-2 in combination with other drugs and IL-2 exposed human MSCs is shown (Table 2).

[0346] Differential gene expression analysis, comparing IL-2 treated versus untreated SR and SEN cells, allowed identification of individual genes that are up- or down-regulated upon IL-2 stimulation. Genes designated as up- or down-regulated in IL-2 treated SR and SEN-hADSCs were analyzed, using an integrated gene-set enrichment and pathway network approach in an attempt to capture the biological reality of coordinated cellular responses to IL-2 stimulation. To do this, pathways that were statistically enriched for up- or down-regulated genes were

identified, and then chosen based on the differentially expressed genes that they have in common (FIGS. l0A- l0B). The pathway network representation was weighted based on the numbers of differentially expressed genes in each pathway and the extent to which different pathways share sets of differentially expressed genes. This approach allowed identification of a highly connected network structure with numerous functionally related pathways as well as functionally relevant network substructures.

[0347] Upon senescence of hADSCs, IL-2 is less stimulatory for the gene pathways promoting proliferation (cell cycle pathway, q-value=l.54 e-5), imposing G2 checkpoint (G2 pathway, q-value=5.94e-4), p53 pathway (q-value=l.18e-2), major signal transduction MAPK pathway (MAPK, q-value=2.42e-4) and its major subgroup ERK pathway (ERK, q-value =2.62e-2), which regulate important cellular function such as survival, migration and proliferation. The analysis further corroborates the previous finding that PDGF-induced AKT and ERK pathways regulate opposing fate decisions of proliferation and differentiation in order to promote MSC self-renewal. Activation of the genes representing these pathways was observed only after *ex vivo* IL-2 exposure of actively SR-hADSCs but not their SEN counterparts (FIG. 10A, left side).

[0348] The data also provide information regarding the functionality of MSCs in carcinogenic settings. Both SR and SEN-hADSCs exposed to IL-2 are marked by significant increases in expression of transforming growth factors alpha and beta (TGF□, TGFβ1 and TGFβ2), transforming growth factor beta receptor TGFBR2 and transforming growth factor beta receptor-associated protein TGFBRAPl, as well as transforming growth factor beta-induced (TGFBI) genes (FIG. 7A). Secreted TGFP is believed to be important in regulation of the immune system by promoting differentiation of CD+4 T-cells and inhibiting immune-surveillance, thereby imposing immunosuppression. However, the higher level of TGFP expression in adipose-derived human MSCs after exposure to IL-2 might promote carcinogenesis. Since parts of the TGFP signaling pathway are shown to be mutated in cancer cells, this allows cancer cells to escape TGFP-induced cell cycle block, differentiation or apoptosis, while the surrounding stromal, immune, endothelial and smooth muscle cells still read the TGFP signaling as a potent suppressor of proliferation and trigger of differentiation causing immunosuppression and angiogenesis in the cancer cell microenvironment.

[0349] In IL-2 treated SEN-hADSCs prominent up-regulated genes are enriched for pathways associated with inflammation (IL-6 pathway, q-value=5.55e-3) and EGF signaling (q-

value=2.33e-4) that have been proven to provide a survival advantages to MSCs. The SEN-hADSCs exposed to IL-2 are also marked by increased expression of IL-1 R· IL-6 and IL-12 (FIG. 7B), cytokines known to stimulate IL-17 from lymphocytes. The data also indicate that lymphocytes are the only source of IL-17 production, and those MSCs, particularly upon their senescence, display high transcriptional activity of IL-17 when subjected to a pro-inflammatory environment (FIG. 7 A).

[0350] The observed connection to the angiogenic VEGF pathway (q-value=5.24e-3) (FIG. 10A, right side and FIG. 7D) and the enhanced capacity of SEN-hADSC to migration (FIGS. 3A, 3B) may indicate that IL-2 exposed SEN-MSCs could acquire properties necessary to support a tumorigenic environment and metastasis. In addition, up-regulation of the genes included in nitric oxide synthase pathway (iNOS) NOSl pathway (q-value=8.32e-2) in hADSC upon replicative senescence once again support that MSCs undergoing senescence can acquire metastasis-promoting properties via immunosuppression.

[0351] Pathways important for support of proliferation and DNA repair are down-regulated in hADCSs upon senescence: Cell Cycle pathway (q-value=2.52e-5), MCM pathway (q-value=l.62e-8), RB pathway (q-value=6.97e-5) ATM pathway (q-value=3.28e-2), p53 pathway (q-value=l.86 e-2) shown in FIG. l0 B. Overall, the data indicated that there are more biological pathways subjected to IL-2 triggered down-regulation in senescence then in self-renewal and these biological pathways are interconnected (FIG. l0B), further linking together a physiological impairment of IL-2 response upon replicative aging of hADSCs.

[0352] Table 2 shows the differential expression of anti-inflammatory and immunomodulatory factors upon IL-2 treatment in SEN and SR cells. The SR GFold values represent the fold difference in SR cells treated with IL-2, relative to SR cells not treated with IL-2; the SEN GFold values represent the fold difference in SEN cells treated with IL-2, relative to SEN cells not treated with IL-2.

Table 2: Differential Expression of Anti-Inflammatory and Immunomodulatory Factors Upon IL-2 Treatment

Gene Symbol	Gene ID	SR IL-2-	SR IL-2+	SEN IL-2-	SEN IL-2+	SR GFOLD	SEN GFOLD
CSF1R	NM_005211	80	43	189	455	-0.27	0.98
TNFSF13	NM_003808	69	55	104	172	0.00	0.31
HIVEP2	NM_006734	2739	2790	3876	5495	0.00	0.43
ITGAV	NM_002210	6797	7110	10656	17227	0.01	0.65
ITFG1	NM_030790	1067	1164	2398	3793	0.00	0.57
IL32	NM_001012631	404	422	526	1397	0.00	1.24
PTGER1	NM_000955	9	19	37	104	0.00	0.86
HIVEP1	NM_002114	1142	1217	1447	2046	0.00	0.38
CERCAM	NM_016174	6943	7119	12879	16369	0.00	0.31
CD99	NM_001277710	6948	7069	13830	16928	0.00	0.25
CD68	NM_001251	3830	3590	9144	11331	-0.02	0.26
IL6	NM_000600	434	502	782	996	0.00	0.19
CD83	NM_001040280	19	27	69	107	0.00	0.12
CD320	NM_016579	1068	782	990	1360	-0.29	0.32
CD72	NM_001782	61	36	73	122	-0.06	0.25
CHST3	NM_004273	2867	2935	2766	3706	0.00	0.34
TNFRSF25	NM_003790	61	68	56	98	0.00	0.25
CMIP	NM_198390	1503	1435	1289	2460	0.00	0.82
ESM1	NM_007036	2562	1887	1863	7612	-0.34	1.94
CCL28	NM_148672	68	37	44	170	-0.20	1.39
CLEC11A	NM_002975	1071	1403	1601	1449	0.25	-0.02
LRRC8A	NM_001127244	3710	4256	6709	6370	0.12	-0.02
IL33	NM_033439	55	84	220	198	0.03	0.00
IRAK1	NM_001569	5587	6539	9009	9094	0.17	0.00
TNFRSF21	NM_014452	244	331	636	616	0.16	0.00
IL12A	NM_000882	14	36	94	91	0.29	0.00
NOS3	NM_000603	48	83	137	142	0.19	0.00
MYL9	NM_006097	10584	19391	38407	32665	0.83	-0.21
IRAK3	NM_007199	181	304	613	488	0.43	-0.13
ILF3	NM_012218	5977	5913	6830	6368	0.00	-0.04
IL16	NM_001172128	129	72	150	120	-0.35	0.00
PEAR1	NM_001080471	1926	2387	510	187	0.21	-1.16
IL7R	NM_002185	831	954	634	545	0.04	-0.02
ILF2	NM_001267809	1344	1961	1878	1580	0.43	-0.13
CCL2	NM_002982	98	147	160	102	0.15	-0.23
KIF14	NM_014875	329	331	381	251	0.00	-0.33

Example 6: Anti-Inflammatory and immunomodulatory properties of IL-2 stimulated human MSCs

[0353] Next, it was investigated how exposure to the IL-2 pro-inflammatory environment, when imposed on replicative aging, affects the expression of the genes assigned to provide immunomodulatory properties of hADSCs (e.g., the anti-inflammatory and immunomodulatory properties of IL-2 exposed human MSC). The data demonstrated that the capacity for immunomodulation is affected by replicative aging of the human adipose-derived MCS during *ex vivo* passaging (FIG. 7B and Table 2).

[0354] IL-2 exposure in SR-hADSCs activates distinct set of genes attributed to T cell regulation. IL-2 exposure of SR-hADSCs results in up-regulation of genes, such as TNFRSF21 (involved in T cels differentiation), IL12A (T-cell activator), ILF2 (potent regulator of transcription of the IL-2 gene during T-cell activation), IL33 (paracrine inducer of T-helper type 2 associated cytokines) and down-regulation of CCL28 (chemotactic factor for CD+4, CD+8 T-cells), CD320 (receptor molecule with autocrine and paracrine function to augment the proliferation of plasma cells) shown in FIG. 7B, Table 2, and Tables 6A-6D.

[0355] Contrary to that, IL-2 exposed SEN-hADSCs were characterized by significant transcriptional up-regulation of CD320, a number of integrins which could be involved in modulation of T-cell function (ITG 11, ITGA V, ITFG 1), and genes encoding important regulatory molecules such as: the T-cell adhesion receptor (CD99), a factor attributed to the maintenance of naïve T-cells (CHST3), T-cell activators (HIVEP l and HIVEP2), a gene involved in T-cell signaling pathway (CMIP) and an autocrine/paracrine factor, PTGERl, involved in inhibition of CD+ cell proliferation (FIG. 7B, Table 2, and Tables 6A-6D).

[0356] The data also demonstrated that SR-hADSCs exposed to IL-2 trigger down-regulation of transcriptional activities of the genes encoding surface receptors that play a role in B-cell proliferation and differentiation (CD72) and horning macrophages (CD68). Both of these genes are significantly transcriptionally up-regulated in SEN cells upon similar treatment (FIG. 7B, Table 2, Tables 6A-6D). In addition, IL-2 treated SEN-hADSCs are set apart from similarly treated SR cells by transcriptional down-regulation of the genes required for pro-B to pre-B transitioning, the LRRC8A and PEARl genes, that regulate a number of non-adherent myeloid progenitors. In contrast, the genes involved in lymphocyte activation and homeostasis (CD83

and TNFRSF25) as well as leukocyte transmigration (CERCAM), and the genes responsible for endothelial cell-leukocyte interaction (ESM1), and a gene important for control monocytes/macrophage mediated immunological process (TNFSF 13), are up-regulated in SEN-hADSCs (FIG. 7B, Table 2, and Tables 6A-6D).

[0357] IL-2 exposure results in the differential expression of a number of cytokines and factors critical for chemotaxis (shown in FIG. 7B and Table 2).

[0358] SR-hADSCs are marked by up-regulation of IL-33, IL-12A, IL10RB, IL1RAP, IL7R, ILF2 and NOS3 genes, while IL-16 and CSF1R genes are down-regulated in these cells.

[0359] In SEN-hADSCs treated under similar conditions with IL-2, the genes encoding cytokines IL-32, IL-6, IL1RN, IL-20RB, IL-21R and inducers of inflammation TNFSF13 and TNFSF12, as well as the gene encoding extracellular matrix remodeler PLAU are up-regulated.

[0360] At the same time, several factors essential for cytokinesis such as MYL9, KIF14, IRAC3, as well as the genes encoding chemotactic factor that attracts monocytes and basophils (CCL2) and the CLEC11A gene regulating proliferation and differentiation of hematopoietic precursor cells, are down-regulated (FIG. 7B).

[0361] Similar down-regulation is also found for several interleukin receptor encoding genes IL7R, IL1R1, IL15RA, and interleukin enhancer binding factors ILF2 and ILF3.

[0362] These observations, together with IL-2 dependent differential transcriptional expression of cytokines in SEN-hADSCs (up-regulation of IL-32, IL-6, PLAU genes; down-regulation of CCL2, CLEC11A, ILF3, IRAK3, KIF14, MYL9 genes) and in SR-hADSCs (up-regulation of IL12A, IL7R, IRAK1, NOS3 genes; down-regulation of IL16, CSF1R genes), indicate that the immunomodulatory properties of hADSCs are susceptible to senescence imposed changes.

[0363] The observed connection to the angiogenic VEGF pathway (q-value=5.24e-3) (FIG. 10A, right side and FIG. 7D) and the enhanced capacity of SEN-hADSC to migration (FIGS. 4A,B) indicates that IL-2 exposed SEN-MSCs could acquire properties necessary to support a tumorigenic environment and metastasis. In addition, up-regulation of the genes included in nitric oxide synthase pathway (iNOS) NOS1 pathway (q-value=8.32e-2) in hADSC upon

replicative senescence also indicate that MSCs undergoing senescence can acquire metastasis-promoting properties via immunosuppression.

Example 7: Anti-apoptotic and metastasis promoting properties of IL-2-stimulated hADSCs upon replicative senescence

[0364] These experiments were also used to examine the anti-apoptotic and metastasis promoting properties of IL-2 exposed MSC upon replicative senescence.

[0365] The panel of anti-apoptotic and metastasis promoting markers for IL-2 treatment, IL-2 in combination with other drugs,or IL-2 in combination with MSC is shown in Table 3. The data provide a list of molecular marker targets important for assessment of anti- apoptotic and metastasis promoting events (e.g. for QC of SEN and SR stem cells for use in the invention).

[0366] Table 3 shows the differential expression of anti-apoptotic and metastasis factors upon IL-2 treatment in SEN and SR cells. The SR GFold values represent the fold difference in SR cells treated with IL-2, relative to SR cells not treated with IL-2; the SEN GFold values represent the fold difference in SEN cells treated with IL-2, relative to SEN cells not treated with IL-2.

Table 3: Differential Expression of Anti-Apoptotic and Metastasis Factors Upon IL-2 Treatment

Gene Symbol	Gene ID	SR IL-2-	SR IL-2+	SEN IL-2-	SEN IL-2+	SR GFOLD	SEN GFOLD
VEGFA	NM_001025366	5690	5914	5781	20606	0.00	1.78
PLEKHA1	NM_001195608	716	676	713	1096	0.00	0.46
VEGFB	NM_003377	989	1070	1832	2253	0.00	0.19
CRMP1	NM_001288661	168	209	401	547	0.00	0.23
FERMT1	NM_017671	76	70	264	325	0.00	0.02
CTSB	NM_147780	28365	28109	115877	138711	0.00	0.25
PLEKHA6	NM_014935	78	57	150	251	0.00	0.40
GNB2L1	NM_006098	16273	18409	33137	32212	0.14	-0.01
SIVA1	NM_006427	410	591	674	512	0.31	-0.20
TGFB1	NM_000660	4834	6297	3413	5582	0.32	0.64

[0367] For example, MSCs have been proven to assist reversal of apoptosis in cardiomyoblasts after ischemia, as well as damaged neurons and lung fibroblasts. Stanniocalcin1

(STC 1) has been identified as an essential factor capable of potent apoptotic reversal in fibroblasts damaged by UV and acidity.

[0368] The data indicate that IL-2 exposure transcriptionally upregulates both STC1 and STC2 genes, and such activation is not dependent on the replicative aging of hADSCs, at least *ex vivo* (Tables 6A-6D). In addition, paracrine effectors such as VEGF and TGFB1 have been implicated in the reversal of apoptosis in endothelial cells. The expression of genes encoding both of these factors is up-regulated in SR and SEN-hADSCs upon IL-2 treatment (FIG. 7C, FIG. 5, Table 3, and Tables 6A-6D).

[0369] The third graph of FIG. 5 shows that IL-2 upregulates transcription of the VEGFA gene upon replicative senescence of hADSCs. *VEFGA* gene expression was assessed by quantitative qPCR in unstimulated (IL-2-) SEN (dark) and SR (light) hADSCs and upon stimulation with 20ug/ml of recombinant IL-2 (IL-2+). Data shown as fold change $\Delta\Delta CT$ Mean ± SD from three independent experiments is shown. The position of the q-PCR primers are depicted graphically. Statistical significance was estimated by *t* - test, where $***p < 0.001$, $**p < 0.01$.

[0370] However, transcriptional activity of VEGFA is notably higher in senescence than in actively proliferating cells as further verified by qPCR analysis shown in FIG. 7C. Notably, the SIVA1 gene encoding a pro-apoptotic factor and a potent inducer of T lymphocytes apoptosis is significantly down-regulated in SEN cells upon IL-2 treatment in comparison to proliferating hADSCs (FIG. 7C, Table 3, and Tables 6A-6D). SIVA1 is not a strictly pro-apoptotic factor, but also a potent suppressor of tumor metastasis. Importantly, a number of the factors responsible for invasive growth and metastasis are significantly up-regulated in SEN-hADSCs exposed to IL-2 in comparison with similarly treated SR cells (FIG. 7C and Table 3). This includes RACKI, PLEKHAl, PLEKHA6, CTSB, CRMPl, FERMTl genes. These data indicated that pretreatment/exposure of hADSCs with IL-2 may enhance the antiapoptotic properties of these cells in general, and that such enhancement is affected by replicative senescence.

[0371] It was demonstrated that in IL-2 treated SEN-hADSCs, prominent up-regulated genes are enriched for pathways associated with inflammation (IL-6 pathway, q-value=5.55e-3) and EGF signaling (q-value=2.3 3 e-4) that have been proven to provide a survival advantages to

MSCs. The SEN-hADSCs exposed to IL-2 are also marked by increased expression of IL-1β, IL-6 and IL-12 (FIG. 7B), cytokines known to stimulate IL-17 from lymphocytes.

[0372] The data also indicated that lymphocytes are the only source of IL-17 production, and those MSCs, particularly upon their senescence, display high transcriptional activity of IL-17 when subjected to a pro-inflammatory environment (FIG. 7A).

Example 8: Transcriptional profiling indicates gene targets regulating enhanced migration and angiogenesis in IL-2 stimulated hADSCs upon replicative senescence

[0373] The panel of the markers indicating enhanced migration and angiogenesis in IL-2 treatments upon aging is shown (Table 4)

[0374] Transcriptional profiling indicates gene targets regulating enhanced migration and angiogenesis in IL-2 stimulated ADSCs upon replicative senescence. Further analysis of the transcriptional response indicates that IL-2 stimulation of SEN-hADSCs s enhances the expression of genes involved in vascular development and remodeling related to angiogenesis. It was observed significant up-regulation of the VEGFA, VEGFB, FBLNS, FBLN7, PGF, ANGPTl, ANGPT2, ANGPTL2, ANGPTL6, TNFSF12, PRKCA, PIK3CA, HRAS genes as well as a gene encoding a potent modulator of endothelial cell-leukocyte adhesion, ESM1 (FIG. 7D, FIGS. 10A- 10B, Table 4, and Tables 6A-6D).

[0375] Table 4 shows the differential expression of migration and angiogenesis factors upon IL-2 treatment in SEN and SR cells. The SR GFold values represent the fold difference in SR cells treated with IL-2, relative to SR cells not treated with IL-2; the SEN GFold values represent the fold difference in SEN cells treated with IL-2, relative to SEN cells not treated with IL-2.

Table 4: Differential Expression of Migration and Angiogenesis Promoting Factors Upon IL-2 Treatment

Gene Symbol	Gene ID	SR IL-2-	SR IL-2+	SEN IL-2-	SEN IL-2+	SR GFOLD	SEN GFOLD
PTGS1	NM_000962	1202	1233	2595	8456	0.00	1.63
CGREF1	NM_001166239	60	77	137	384	0.00	1.15
ROCK2	NM_004850	2014	2149	2171	2737	0.00	0.24
VEGFA	NM_001025366	5690	5914	5781	20606	0.00	1.78

Gene Symbol	Gene ID	SR IL-2-	SR IL-2+	SEN IL-2-	SEN IL-2+	SR GFOLD	SEN GFOLD
PLEKHA1	NM_001195608	716	676	713	1096	0.00	0.46
ESM1	NM_007036	2562	1887	1863	7612	-0.34	1.94
ANGPTL6	NM_031917	339	195	279	342	-0.50	0.02
PIK3CA	NM_006218	519	597	720	939	0.00	0.22
PGF	NM_002632	471	471	842	1503	0.00	0.69
TNK2	NM_005781	582	624	813	1176	0.00	0.38
FBLN7	NM_153214	201	195	268	353	0.00	0.13
PLEKHA6	NM_014935	78	57	150	251	0.00	0.40
PRKCA	NM_002737	3139	3258	4215	5298	0.00	0.26
ROCK1	NM_005406	2280	2326	2662	3068	0.00	0.12
CGNL1	NM_001252335	11	22	67	115	0.00	0.27
FGD6	NM_018351	419	411	749	1055	0.00	0.33
CRMP1	NM_001288661	168	209	401	547	0.00	0.23
CTSO	NM_001334	222	275	499	617	0.01	0.10
TNFSF12-TNFSF13	NM_172089	268	259	464	577	0.00	0.11
FAP	NM_004460	1810	1767	4594	6279	0.00	0.39
VEGFB	NM_003377	989	1070	1832	2253	0.00	0.19
FBLN5	NM_006329	5879	6117	8801	10137	0.00	0.15
ANGPT1	NM_001146	386	406	1069	1346	0.00	0.20
ANGPTL2	NM_012098	1241	1362	4927	5560	0.00	0.11
CTSB	NM_147780	28365	28109	115877	138711	0.00	0.25
FERMT1	NM_017671	76	70	264	325	0.00	0.02
HRAS	NM_176795	604	604	996	1124	0.00	0.03
MYL9	NM_006097	10584	19391	38407	32665	0.83	-0.21
TLN2	NM_015059	2058	2352	4839	4309	0.09	-0.10
ILK	NM_001014795	5437	6108	8647	8164	0.11	-0.03
PPAP2B	NM_003713	1703	2546	2327	1579	0.48	-0.45
CYR61	NM_001554	31391	30861	12856	12074	0.00	-0.05
RELN	NM_005045	2490	2989	925	671	0.17	-0.29
NEDD9	NM_006403	2617	3093	2123	1956	0.15	-0.01
TNFAIP8	NM_001077654	109	101	67	100	0.00	0.05
ANGPT2	NM_001118887	430	259	89	179	-0.47	0.58

[0376] The vascular endothelial growth factor, VEGF, released by MCSs, enables recruitment of endothelial lineage cells and initiation of vascularization as was previously reported. It is further demonstrated that up-regulation of VEGFA gene expression in SEN-hADSCs can be

detected by quantitative RT-PCR analysis and IL-2 exposure results in a statistically significant increase of VEGFA gene transcription in SR and SEN-hADSCs (FIG. 7D and Table 4).

[0377] It was further observed that in response to IL-2 exposure, a group of genes responsible for cell motility, migration and invasive growth are significantly up-regulated only in the hADSCs undergoing replicative senescence: CGNL l, CGREF l, CRMP l, FGD6, TNK2, PTGSl, TNFAIP8, CTSB, CTSO, FAP, FERMTl, PLEKHAl, PLEKHA6, ROCKl, ROCK2. A set of genes promoting cell adhesion, such as CHD24, CYR61, ILK, NEDD9, MYL9, PPAP2B, RELN and TLN2 were down-regulated (FIG. 7D, Table 4, and Tables 6A-6D). These data further the support experimental evidence for the enhanced migration capacity of SEN-hADSCs shown in FIG. 3B.

Example 9: Proteomic antibody array data

[0378] Table 7 provides the raw values for all proteomic antibody array data.

[0379] FIG. 2B shows the five factor production units used for collection of these data. All 5 factor production units contained stem cells from a 38year old patient in 10% PRP containing StemPro MSC SFM Xeno-free medium except A (no cell control). Factor production units were populated with SR or SEN-hADSC 2500 cells /cm^3 in 700ul/cm^3 of 10% PRP containing StemPro MSC SFM Xeno-free medium. Referring to FIG. 2B, factor production units C and E, the cells of the factor production units were stimulated with IL-2 for 24 hrs, after which media was exchanged to the 10% PRP containing StemPro MSC SFM Xeno-free medium. Factor production units were kept at 37°C and 5% CO2 for 24, 48, and 72 hrs after which media was collected and analyzed.

[0380] Equal volumes of medium from the factor production units were analyzed on a RayBio C-Series Human Cytokine Antibody Array AAH-CYT-2000 (RayBiotech, Inc). The C-Series Human Cytokine Antibody Array AAH-CYT-2000 is based on chemiluminescence assay principle and contains antibodies to 174 protein of interest. Data were extracted from the membranes using LI-COR Biosciences densitometry software (Li-COR). The raw data were normalized by taking the ratio between Average Intensity of the given protein signal/ to Average Intensity Negative Control, to account for differences in exposure and array to array variation.

[0381] The factor production unit represented as A contained no cells, as a control. This factor production unit was set-up with 700ul/cm^2 of 10% PRP containing StemPro MSC SFM Xeno-free medium. The medium was collected at 24, 48 and 72 hrs and total protein was quantified by Qubit fluorimetric quantification using Qubit 2.0 (Thermofisher), applied on RayBio C-Series Human Cytokine Antibody Array AAH-CYT-2000 and data were extracted as described above and analyzed.

[0382] The factor production unit labeled as B contained SR-hADSCs not treated with IL-2. This factor production unit was populated with patient specific hADSC 2500 cells /cm^3 in 700ul/cm^3 of 10% PRP containing StemPro MSC SFM Xeno-free medium. The samples were collected at 24hr, 48hr or 72hrs.

[0383] The factor production unit labeled as C was a factor production unit containing SR-hADSCs treated with IL-2. This factor production unit contained 2500 cells /cm^3 of patient specific SR-hADSCs in 700ul/cm^3 of 10% PRP containing StemPro MSC SFM Xeno-free medium. The cells in the factor production unit were treated with IL-2. For the IL-2 treatment, the factor production unit was treated with 20U/ml IL-2 (Peprotech) in 10% PRP in StemPro MSC SFM Xeno-free medium at 37°C for 24h. IL-2 was removed post-treatment with 2 washes of PBS-cmf. Fresh medium was added at 700ul/cm^3. The samples were collected 24hr, 48hr or 72hr later.

[0384] The factor production unit labeled as D contained senescent hADSCs (SEN-hADSCs). This factor production unit contained SEN-hADSC at 2500 cells /cm^3 in 700ul/cm^3 of 10% PRP containing StemPro MSC SFM Xeno-free medium. Samples were collected at 24h, 48h or 72h.

[0385] The factor production unit labeled as E contained SEN-hADSCs treated with IL-2 as described above for the factor production unit labeled as C. Samples were collected at 24h, 48h or 72h.

[0386] The factors collected from factor production units A-E represented in FIG. 2B are characterized in detail below.

[0387] FIGS. 11-17 show the increase in secretion of the below named proteins (factors) from SR-hADSCs maintained in a factor production unit of the invention, 24 hours post incubation with media containing 10% PRP (platelet-rich plasma) alone (no IL-2 stimulation). Secretion

levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support. FIG. 11 shows the increase in secretion of Interleukin 5 (IL5) and Interleukin 6 (IL6). FIG. 12 shows the increase in secretion of Interleukin 1 receptor 4 (IL1R4). FIG. 13 shows the increase in secretion of Neurotrophin 3 (NT3), platelet derived growth factor A alpha (PDGF AA), platelet derived growth factor A beta (PDGF AB), and pro-platelet basic protein (PPBP). FIG. 14 shows the increase in secretion of Chemokine (C-C motif) ligand 18 (CCL18), Chemokine (C-Cmotif) ligand 25 (CCL25), Chemokine (C-C motif) ligand 27 (CCL27), and CXC chemokine ligand 11 (CXCL11). FIG. 15 shows the increase in secretion of Intercellular Adhesion Molecule 1 (ICAM-1) and Metalloproteinase inhibitor 2 (TIMP-2). FIG. 16 shows the increase in secretion of Metalloproteinase inhibitor 1 (TIMP-1). FIG. 17 shows the increase in secretion of vascular epithelium (VE) Cadherin (calcium dependent cell adhesion protein).

[0388] FIGS. 18-19 show the increase in secretion of the below named proteins (factors) from SR-hADSCs, 24 hours post incubation with 10% PRP alone (no IL-2 stimulation). These proteins were found to not be present in PRP. FIG. 18 shows the increase in secretion of Interleukin 4 (IL4). FIG. 19 shows the increase in secretion of insulin-like growth factor-binding protein-1 (IGFBP1).

[0389] FIGS. 20-31 show an increase in the below named proteins (factors) from SR-hADSCs maintained in a factor production unit of the invention, 48 hours post incubation with 10% PRP alone (no IL-2 stimulation). Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support. FIG. 20 shows the increase in secretion of Interleukin 9 (IL9) and Interleukin 18 binding protein alpha (IL18BPa). FIG. 21 shows the increase in secretion of Interleukin 1 receptor type II (IL1R2), Interleukin 2 receptor beta (IL-2Rb), Interleukin 2 receptor gamma (IL-2Rg), Interleukin 5 receptor alpha (IL5Ra), Interleukin 10 receptor beta (IL10Rb), Interleukin 18 receptor accessory protein (IL18Rb), and Interleukin 21 receptor (IL-21R). FIG. 22 shows the increase in secretion of Insulin-like growth factor 2 (IGF2), Transforming growth factor alpha (TGFa), Transforming growth factor beta 1/latency-associated peptide (LAP) (TGFb1), and Transforming growth factor beta 2 (TGFb2). FIG. 23 shows the increase in secretion of Receptor tyrosine-protein kinase ErbB-3 (ErbB3), Fas ligand (Fas LG), Leukemia inhibitory factor (LIF), Prolactin (PRL) factor, platelet-derived growth factor receptor alpha (PDGFRa), platelet-derived

growth factor receptor beta (PDGFRb), Stem cell factor kit receptor (SCFR), and Sialic acid-binding Ig-like Lectin 5 (Siglec 5). FIG. 24 shows the increase in secretion of CXC chemokine ligand 16 (CXCL16). FIG. 25 shows the increase in secretion of activated leukocyte cell adhesion molecule (ALCAM), E selectin (cell surface glycoprotein in immune-adhesion), Intercellular adhesion molecule 2 (ICAM2), L selectin (Lymphocyte adhesion molecule), and Platelet endothelial cell adhesion molecule (PECAM 1). FIG. 26 shows the increase in secretion of Activin A (INHBA), Insulin-like growth factor 2 (IGF-2), and Leptin Receptor (LEPR). FIG. 27 shows the increase in secretion of Bone morphogenetic protein 5 (BMP5), Bone morphogenetic protein 7 (BMP7), Macrophage colony-stimulating factor 1 receptor (MCSFR), matrix metalloproteinase 1 (MMP1), matrix metalloproteinase 3 (MMP3), matrix metalloproteinase 9 (MMP9), and matrix metalloproteinase 13 (MMP13). FIG. 28 shows the increase in secretion of monocyte differentiation antigen (CD14), cell differentiation antigen (CD80), Cardiotrophin-1 (CT-1), and Leukemia inhibitory factor (LIF). FIG. 29 shows the increase in secretion of Endoglin (ENG). FIG. 30 shows the increase in secretion of Tyrosine kinase with immunoglobulin-like and EGF-like domains 1 (TIE1) and Tyrosine kinase with immunoglobulin-like and EGF-like domains 2 (TIE2). FIG. 31 shows the increase in secretion of Activin A (Inhibin beta A, INHBA), Leptin Receptor (Leptin R), and Transforming growth factor beta 1 (TGFb1).

[0390] FIG. 32 shows the increase in secretion of Nerve growth factor receptor (NGFR) from SR-MSCs maintained in a factor production unit of the invention, 48 hours post incubation with 10% PRP alone (no IL-2 stimulation). NGFR was found to not be present in in PRP.

[0391] FIGS. 33-39 show the increase in secretion of the below named proteins (factors) from SR-hADSCs maintained in a factor production unit of the invention, 72 hours post incubation with 10% PRP alone (no IL-2 stimulation). Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support. FIG. 33 shows the increase in secretion of Interleukin 1 beta (IL1b), Interleukin 3 (IL3), Interleukin-13 Receptor subunit alpha-2 (IL13Rα2), and Interleukin 1 receptor alpha (IL1Rα). FIG. 34 shows the increase in secretion of Probetacellulin (BTC), Colony stimulating factor (CSF1), Fibroblast growth factor 6 (FGF6), Glial cell line-derived neurotrophic factor (GDNF), insulin-like growth factor 1 (IGF-1), Leptin, and platelet-derived growth factor B beta (PDGF BB). FIG. 35 shows the increase in secretion of stem cell factor/c-kit ligand (SCF),

Stromal Cell-Derived Factor-1 alpha (SDF1a), Stromal Cell-Derived Factor-1 beta (SDF1b), Transforming growth factor beta 1 (TGFb1), Transforming growth factor beta 3 (TGFb3), and tumor necrosis factor superfamily member 14 (TNFSF14). FIG. 36 shows the increase in secretion of Insulin-like growth factor 1 (IGF1). FIG. 37 shows the increase in secretion of Transforming growth factor beta 1 (TGFb1) and platelet-derived growth factor B beta (PDGF BB). FIG. 38 shows the increase in secretion of Chemokine (C-C motif) ligand 2 (CCL2), Chemokine (C-C motif) ligand 5 (CCL5), Chemokine (C-C motif) ligand 7 (CCL7), Chemokine (C-C motif) ligand 8 (CCL8), and Chemokine (C-C motif) ligand 11 (CCL11). FIG. 39 shows the increase in secretion of Chemokine (C-C motif) ligand 13 (CCL13), Chemokine (C-C motif) ligand 22 (CCL22), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C motif) ligand 24 (CCL24), and CXC Chemokine ligand 10 (CXCL10).

[0392] FIGS. 40-42show the increase in secretion of the below named proteins (factors) from SR-hADSCs maintained in a factor production unit of the invention, 72 hours post incubation with 10% PRP alone (no IL-2 stimulation). These factors were found to not be present in PRP. FIG. 40 shows the increase in secretion of Brain-derived neurotrophic factor (BDNF), Bone morphogenetic protein 4 (BMP4), Bone morphogenetic protein 6 (BMP6), Ciliary neurotrophic factor (CNTF), Epidermal growth factor (EGF), Fibroblast growth factor 7 (FGF7), and insulin-like growth factor-binding protein-4 (IGFBP4). FIG. 41 shows the increase in secretion of chemokine (C-X-C motif) ligand 13 (BLC), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C motif) ligand 28 (CCL28), chemokine (C-C motif) ligand 11 (Eotaxin 1), Chemokine (C-X-C motif) ligand 6 (GCP-2), FLT3LG (Fms-Related Tyrosine Kinase 3 Ligand), and Fractalkine (CX3CL1). FIG. 42 shows the increase in secretion of Angiotensin (ANG) and colony stimulating factor 2 (CSF2).

[0393] FIG. 43 shows the increase in secretion of Chemokine (C-C motif) ligand 27 (CCL27) and TNFRSF1B (Tumor Necrosis Factor Receptor Superfamily, Member 1B) from SR-hADSCs maintained in a factor production unit of the invention, 24 hours post stimulation with IL-2. Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support.

[0394] FIGS. 44-53 show the increase of the below named proteins (factors) from SR-hADSCs maintained in a factor production unit of the invention, 48 hours post stimulation with IL-2. Secretion levels are shown relative to the amount of the corresponding protein present at

basal levels in the 10% PRP containing media, used for hADSC support. FIGS. 44 shows the increase in secretion of Interleukin 9 (IL9), Interleukin 11 (IL11), Interleukin 12 alpha (IL12a), Interleukin 12 beta (IL12b), and Interleukin 18 binding protein alpha (IL18BPa). FIG. 45 shows the increase in secretion of Interleukin 1 receptor type I (IL1R1), Interleukin 1 receptor type II (IL1R2), Interleukin 1 receptor type IV (IL1R4), Interleukin 2 receptor beta (IL-2Rb), Interleukin 2 receptor gamma (IL-2Rg), Interleukin 5 receptor alpha (IL5Ra) Interleukin 10 receptor beta (IL10Rb), Interleukin 18 receptor beta (IL18Rb), and Interleukin 21 receptor (IL-21R). FIG. 46 shows the increase in secretion of Fibroblast growth factor 4 (FGF4), FGF9, MSP alpha/HGF like factor (HGF like), Insulin-like growth factor 1 (IGF1), IGF2, insulin-like growth factor-binding protein-6 (IGFBP6), LAP (TGF beta family), and platelet derived growth factor A alpha (PDGFAA). FIG. 47 shows the increase in secretion of platelet derived growth factor A beta (PDGFAB), platelet derived growth factor B beta (PDGFBB), Stromal Cell-Derived Factor-1 alpha (SDF1a), Sialic acid-binding Ig-like Lectin 5 (Siglec 5), Transforming growth factor alpha (TGFa), Transforming growth factor beta 2 (TGFb2), Vascular endothelial growth factor (VEGF), and Vascular endothelial growth factor D (VEGFD). FIG. 47 also shows the increase in secretion of DR6, Dtk, EGFR, Endoglin, ErbB3, Fas, Fas LG, and IGF1 sr. FIG. 48 shows the increase in secretion of Leptin (LEP), Leptin Receptor (LEPR), Macrophage colony-stimulating factor 1 receptor (MCSFR), Neurotrophin 4 (NT4), Osteoprotegerin (OPG), platelet-derived growth factor receptor alpha (PDGFRa), platelet-derived growth factor receptor beta (PDGFRb), and Prolactin (PRL). FIG. 49 shows the increase in secretion of Stem cell factor receptor (SCFR), Angiopoietin 1 receptor (TIE1), Angiopoietin 1 receptor (TIE2), TNF superfamily member 10C (TNFSF10C), TNF superfamily member 10D (TNFSF10D), TNF superfamily member 14 (TNFSF14), urokinase plasminogen activator receptor (uPAR), and Vascular endothelial growth factor receptor-2 (VEGFR2). FIG. 50 shows the increase in secretion of Chemokine (C-C motif) ligand 2 (CCL2), CCL3, CCL5, CCL8, CCL17, CCL20, CCL25, CXC chemokine ligand 5 (CXCL5), CXCL11, and CXCL16. FIG. 51 shows the increase in secretion of activated leukocyte cell adhesion molecule (ALCAM), Bone morphogenetic protein 5 (BMP5), BMP7, E selectin (endothelial cell adhesion molecule), Intercellular adhesion molecule 2 (ICAM2), ICAM3, L selectin (Lymphocyte adhesion molecule), and matrix metalloproteinase 1 (MMP1). FIG. 52 shows the increase in secretion of matrix metalloproteinase 13 (MMP13), MMP3, MMP9, Platelet endothelial cell adhesion molecule (PECAM 1), Metalloproteinase inhibitors TIMP 1, TIMP 2, TIMP 4, and vascular

epithelium (VE) Cadherin (calcium dependent cell adhesion protein). FIG. 53 shows the increase in secretion of monocyte differentiation antigen (CD14), cell differentiation antigen (CD80), Cardiotrophin-1 (CT-1), Leukemia inhibitory factor (LIF), Macrophage migration inhibitory factor (MIF), Thrombopoietin (THPO), and Lymphotactin (XCL1).

[0395] FIG. 54 shows the increase in secretion of Nerve growth factor receptor (NGFR) from SR-hADSCs maintained in a factor production unit of the invention, 48 hours post stimulation with IL-2. FIG. 54 also shows increase in the secretion of IL8 and TNFRSF1A with IL-2 at 24h post-IL-2 stimulation. NGFR, IL8 and TNFRSF1A were found to not be present in PRP.

[0396] FIGS. 55-57 show the increase in the secretion of the below named proteins (factors) from SR-hADSCs maintained in a factor production unit of the invention, 72 hours post stimulation with IL-2. Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support. FIG. 55 shows the increase in secretion of Interleukin 1 receptor alpha (IL1Ra), Interleukin 6 (IL6), and Interleukin-13 receptor subunit alpha-2 (IL13Ra2). FIG. 56 shows the increase in secretion of Fibroblast growth factor 6 (FGF6), pro-platelet basic protein (PPBP), stem cell factor (SCF), and Vascular endothelial growth factor receptor-3 (VEGFR3). FIG. 57 shows the increase in secretion of Chemokine (C-C motif) ligand 22 (CCL22), CCL23, CCL24, CCL26, and CXC chemokine ligand 10 (CXCL10).

[0397] FIG. 58 shows the increase in secretion of Angiotensin (ANG), Brain-derived neurotrophic factor (BDNF), Bone morphogenetic protein 4 (BMP4), colony stimulating factor 2 (CSF2), Epidermal growth factor (EGF), Fibroblast growth factor 7 (FGF-7), Interferon gamma (IFNγ), insulin-like growth factor-binding protein-1 (IGFBP 1), and IGFBP 2 from SR-hADSCs maintained in a factor production unit of the invention, 72 hours post stimulation with IL-2. These factors were found to not be present in PRP.

[0398] FIG. 59 shows the increase in secretion of Fibroblast growth factor 6 (FGF6), CXC chemokine ligand 16 (CXCL16), and Stromal Cell-Derived Factor-1 alpha (SDF1a) from SEN-hADSCs maintained in a factor production unit of the invention, 24 hours post incubation with 10% PRP alone (no IL-2 stimulation). Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support.

[0399] FIG. 60 shows the increase in secretion of Brain-derived neurotrophic factor (BDNF), B lymphocyte chemokine (CXCL13; BLC), Chemokine (C-C motif) ligand 1 (CCL1), Flt-3 LG (Fms-Related Tyrosine Kinase 3 Ligand), Fractalkine (T-cell chemokine CX3CL1), granulocyte chemotactic protein 2 (GCP-2)/CXCL6, Interleukin 1 alpha (IL1a), Interleukin 4 (IL4), IL15, and Interferon gamma (IFNγ) from SEN-hADSCs maintained in a factor production unit of the invention, 24 hours post incubation with 10% PRP alone (no IL-2 stimulation). These factors were found to not be present in PRP.

[0400] FIGS. 61-70 show the increase in the secretion of the below named proteins (factors) from SEN-hADSCs maintained in a factor production unit of the invention, 48 hours post incubation with 10% PRP alone (no IL-2 stimulation). Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support. FIG. 61 shows the increase in secretion of Interleukin 2 beta (IL-2b), IL3, IL5, and IL6. FIG. 62 shows the increase in secretion of Interleukin 1 receptor type II (IL1R2), Interleukin 2 receptor gamma (IL-2Rg), Interleukin 5 receptor alpha (IL5Ra), Interleukin 10 receptor beta (IL10Rb), Interleukin 18 receptor binding protein alpha (IL18BPa), Interleukin 18 receptor beta (IL18Rb), and Interleukin 21 receptor (IL-21R).FIG. 63 shows the increase in secretion of Insulin-like growth factor 1 (IGF1), IGF2, LAP (TGF beta family), Leptin (LEP), Leptin Receptor (LEPR), platelet derived growth factor A alpha (PDGFAA), platelet derived growth factor A beta (PDGFAB), and platelet derived growth factor B beta (PDGFBB).FIG. 64 shows the increase in secretion of platelet-derived growth factor receptor alpha (PDGFRa), Stem cell factor (SCF), Stem cell factor receptor (SCFR), Transforming growth factor beta 1 (TGF b1), Transforming growth factor beta 2 (TGF b2), Transforming growth factor alpha (TGFa), Vascular endothelial growth factor receptor-2 (VEGFR2), and VEGFR3.FIG. 65 shows the increase in secretion of Death receptor 6 (DR6; TNF receptor superfamily member 21), Glial cell line-derived neurotrophic factor (GDNF), Neurotrophin 3 (NT3), Tyrosine kinase with immunoglobulin-like and EGF-like domains 1 (TIE1), TIE2, and TNF superfamily member 14 (TNFSF14).FIG. 66 shows the increase in secretion of Chemokine (C-C motif) ligand 2 (CCL2), CCL5, CCL8, CCL17, CCL18, and CCL23.FIG. 67 shows the increase in secretion of Chemokine (C-C motif) ligand 24 (CCL24), CCL25, CCL26, CCL27, CXC Chemokine ligand 10 (CXCL10), and CXCL11.FIG. 68 shows the increase in secretion of activated leukocyte cell adhesion molecule (ALCAM), Bone morphogenetic protein 5 (BMP5), BMP7, E selectin (endothelial cell adhesion molecule), Intercellular adhesion

molecule 1 (ICAM1), ICAM2, L selectin (Lymphocyte adhesion molecule), and matrix metalloproteinase 1 (MMP1).FIG. 69 shows the increase in secretion of matrix metalloproteinase 3 (MMP3), MMP9, MMP13, Platelet endothelial cell adhesion molecule (PECAM 1), Metalloproteinase inhibitors TIMP 1, TIMP 2, and TIMP 4.FIG. 70 shows the increase in secretion of monocyte differentiation antigen (CD14), monocyte differentiation antigen (CD80), Cardiotrophin-1 (CT-1), and Leukemia inhibitory factor (LIF).

[0401] FIGS. 71-72 show the increase in the secretion the below named proteins (factors) from SEN-hADSCs maintained in a factor production unit of the invention, 48 hours post incubation with 10% PRP alone (no IL-2 stimulation). These factors were found to not be present in PRP. FIG. 71 shows the increase in secretion of Bone morphogenetic protein 4 (BMP4), Chemokine (C-C motif) ligand 11 (CCL11), CCL23, Ciliary neurotrophic factor (CNTF), Epidermal growth factor (EGF), Fibroblast growth factor 7 (FGF7), insulin-like growth factor-binding protein-1 (IGFBP1), IGFBP2, IGFBP4, and Nerve growth factor receptor (NGFR). FIG. 72 shows the increase in secretion of Interleukin 7 (IL7), IL10, IL13, and IL16.

[0402] FIG. 73 shows the increase in secretion of Probetacellulin (BTC), Interleukin-13 receptor subunit alpha-2 (IL13Ra2), and Stromal Cell-Derived Factor-1 beta (SDF1b) from SEN-hADSCs maintained in a factor production unit of the invention, 72 hours post incubation with 10% PRP alone (no IL-2 stimulation). Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support.

[0403] FIG. 74 shows the increase in secretion of Hepatocyte growth factor (HGF), Interleukin 8 (IL8), and TNFRSF1A (Tumor Necrosis Factor Receptor Superfamily, member 1A) from SEN-hADSCs maintained in a factor production unit of the invention, 72 hours post incubation with 10% PRP alone (no IL-2 stimulation). These factors were found to not be present in PRP.

[0404] FIG. 75 shows the increase in secretion of Chemokine (C-C motif) ligand 23 (CCL23), Ciliary neurotrophic factor (CNTF), Epidermal growth factor (EGF), CCL11 (Eotaxin 1), IL4, and Nerve growth factor receptor (NGFR) from SEN-hADSCs maintained in a factor production unit of the invention, 24 hours post stimulation with IL-2. These factors were found to not be present in PRP. These factors were found to not be present in PRP.

[0405] FIG. 75 also shows the increase in secretion of CXCL16, HCC4, sgp130, and TNFRSF1B at 24h post IL-2 stimulation. Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media.

[0406] FIGS. 76-86 show the increase in the secretion of the below named proteins (factors) from SEN-hADSCs, 48 hours post stimulation with IL-2. Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support. FIG. 76 shows the increase in secretion of Interleukin 1 beta (IL1b), IL3, IL5, IL6, IL9, IL10, IL12b, and Interleukin 18 binding protein alpha (IL18BPa). FIG. 77 shows the increase in secretion of Interleukin 1 receptor alpha (IL1Ra), IL1R4, IL10Rb, IL18Rb, IL1R2, IL-21R, IL-2Rb, IL-2Rg, and IL5Ra. FIG. 78 shows the increase in secretion of Fibroblast growth factor 6 (FGF6), insulin-like growth factors IGF1 and IGF2, LAP (TGF beta family), Neurotrophin 3 (NT3), platelet derived growth factor A alpha (PDGFAA), platelet derived growth factor A beta (PDGFAB), and platelet-derived growth factor receptor alpha (PDGFRa). FIG. 79 shows the increase in secretion of Stem cell factor (SCF), Transforming growth factor 2 (TGF2), TGFa, TGFb1, TGFb3, Tumor necrosis factor beta (TNFb), Vascular endothelial growth factor receptor-2 (VEGF R2), and VEGF R3. FIG. 80 shows the increase in secretion of DR6 (TNF receptor superfamily member 21), Endoglin (ENG), Receptor tyrosine-protein kinase erbB-3 (ErbB3), Fas ligand (Fas LG), Glial cell line-derived neurotrophic factor (GDNF), GITR ligand (GITR LG), and Leptin receptor (LEPR). FIG. 81 shows the increase in secretion of Prolactin (PRL), Stem cell factor receptor (SCFR), Sialic acid-binding Ig-like Lectin 5 (Siglec 5), Angiopoietin 1 receptor (TIE1), and Angiopoietin 1 receptor (TIE2). FIG. 82 shows the increase in secretion of Chemokine (C-C motif) ligand 8 (CCL8), CCL13, CCL15, CCL17, CCL18, and CCL20. FIG. 83 shows the increase in secretion of Chemokine (C-C motif) ligand 22 (CCL22), CCL24, CCL26, CXC chemokine ligand 9 (CXCL9), and CXCL11. FIG. 84 shows the increase in secretion of Activin A (INHBA), Bone morphogenetic protein 5 (BMP5), E selectin (endothelial cell adhesion molecule), Intercellular adhesion molecule 1 (ICAM 1), ICAM 2, L selectin (Lymphocyte adhesion molecule), and Macrophage colony-stimulating factor (MCSF). FIG. 85 shows the increase in secretion of matrix metalloproteinase 1 (MMP1), MMP13, MMP3, MMP9, Platelet endothelial cell adhesion molecule (PECAM 1), and Metalloproteinase inhibitor 4 (TIMP-4). FIG. 86 shows the increase in secretion of monocyte differentiation antigen (CD14), Lymphotactin (XCL1), Cardiotrophin-1

(CT-1), Leukemia inhibitory factor (LIF), Macrophage Migration Inhibitory Factor (MIF), and pro-platelet basic protein (PPBP).

[0407] FIG. 87 shows the increase in secretion of Brain-derived neurotrophic factor (BDNF), Bone morphogenetic protein 4 (BMP4), Fibroblast growth factor 7 (FGF7), insulin-like growth factor-binding protein-2 (IGFBP2), IL-2, IL16, and Interferon gamma (INF gamma) from SEN-hADSCs maintained in a factor production unit of the invention, 48 hours post stimulation with IL-2. These factors were found to not be present in PRP.

[0408] FIGS. 88-89 show the increase in secretion of the below named proteins (factors) from SEN-hADSCs maintained in a factor production unit of the invention, 72 hours post stimulation with IL-2. Secretion levels are shown relative to the amount of the corresponding protein present at basal levels in the 10% PRP containing media, used for hADSC support. FIG. 88 shows the increase in secretion of Adiponectin (Acrp30), Agouti-related protein (AgRP), ANGPT2 (Angiopoietin 2), basic-Fibroblast Growth Factor (bFGF), Probetacellulin (BTC), Interleukin-13 receptor subunit alpha-2 (IL13Ra2), Leptin (LEP), Neurotrophin 4 (NT4), and Stromal Cell-Derived Factor-1 alpha (SDF1a). FIG. 89 shows the increase in secretion of Chemokine (C-C motif) ligand 2 (CCL2), CCL4, CCL5, CCL23, CCL25, CCL27, CXC Chemokine ligand 10 (CXCL10), Stromal Cell-Derived Factor-1 beta (SDF1b), Metalloproteinase inhibitors 1 (TIMP1), TIMP2, and tumor necrosis factor superfamily member 14 (TNFSF14).

[0409] FIG. 90 shows the increase in secretion of Granulocyte-macrophage colony-stimulating factor (GM-CSF) and IL13 from SEN-hADSCs maintained in a factor production unit of the invention, 72 hours post stimulation with IL-2. These factors were found to not be present in PRP.

Example 10: Induction of senescence using microRNAs

[0410] The SEN phenotype can be achieved by transfection of a range of concentrations (1pm to 1000uM) of senescence-associated micro RNAs (SA-miRNAs) or SA-miRNA mimics.

[0411] This example shows that SA-miRNAs originating from MIRG17HG and MIR100HG clusters can coordinately regulate gene targets to induce senescence. Transient delivery of SA-miRNAs to SR-ADSCs is sufficient to induce SEN phenotypes. Delivery of the miRNA mimics of SA-miRNAs from either *MIR100HG* or *MIR17HG* clusters separately does not result in a

SEN phenotype as detected by SA-βgal (FIG. 108, Panel A). When SA-miRNAs from both clusters were transfected into SR-hADSCs, about 40% of the cells became marked by expression of senescence-associated β-galactosidase (SA-βgal). FITC-labeled random RNAs were used as a control for the transfection efficiency in all of these experiments, which ranges from 50 to 60% (FIG. 108, Panel B). The SEN phenotype was achieved by a range of concentrations (5pM or 10pM combined with SA-miRNA mimics).

Cell Culture

[0412] SR-hADSCs are seeded on 4-well slides at a density of about 1×10^4cells/well one day before transfection. Transfection is carried out with 5pmol or 10pmol of one or more senescence associated microRNA mimics using a transfection reagent such as Fugene 6 (Promega).

RT-PCR

[0413] Total cellular RNA was extracted from cells using the TRIzol reagent™ (Life Technologies) according to manufacturer's instructions. The microRNA was isolated using a mirPremier microRNA isolation kit (Sigma-Aldrich), RNA and microRNA were quantified with a NanoDrop ND-2000 Spectrophotometer (Thermo Scientific). The cDNA was synthesized by adding the purified RNA and oligo (dT) primers by using superscript III reverse transcriptase (Life Technologies). Primers were designed by primer3 software and shown in Table S1. For miRNA cDNA synthesis, the *Mystic microRNA cDNA synthesis* Mix kit (Sigma-Aldrich) was used. All microRNA assay primers were bought from Sigma-Aldrich.

Real-time Quantitative PCR

[0414] Quantification of mRNA and microRNA expression for candidate genes was performed by real-time quantitative PCR (qRT-PCR) using the LightCycler® 480 Real-Time PCR System (Roche). Total RNA and microRNA was reverse transcribed by using the high capacity superscript III reverse transcriptase (Life Technologies) and the *Mystic microRNA cDNA synthesis* Mix kit (Sigma-Aldrich), respectively. Primers were designed by primer3 software , and sequences are provided below in Table 5. All microRNA assay primers were bought from Sigma-Aldrich. qRT-PCR reactions were performed with the power SYBR® green PCR master mix and the mystic microRNA SYBR green qPCR ReadyMix in a MicroAmp optical 96-well reaction plate. The PCR amplification of total RNA was performed in a

LightCycler® 480 Real-Time PCR System (Roche) using the following program: Cycle 1, 95°C for 10 min. Cycle 2, 40 cycles of 95°C for 15 sec, 60°C for 60 sec. CT values were automatically obtained. Relative expression values of RNA were obtained by normalizing CT values of the mRNA genes in comparison with CT values of the endogenous control (beta-actin) using the CT method. The PCR amplification of microRNA was performed in a LightCycler® 480 Real-Time PCR System (Roche) using the following program: Cycle 1, 95°C for 2 min. Cycle 2, 40 cycles of 95°C for 5 sec, 60°C for 30 sec. Relative expression values of microRNA were obtained by normalizing CT values of the microRNA genes in comparison with CT values of the endogenous control (U6) using the CT method.

Table 5: qPCR primers

Gene	Forward Primer	Reverse Primer
NAP1L1	5' CTGGCTCCCCATACTAGTCG 3'	5'CTTGAAGGGCTGCAAGAATC 3'
USP6	5' ACCATCACAGGCTCTTCA CC 3'	5' AACGATCAATGCTGCTGTTG 3'
SMARCD2	5' ACCCCATTGTCATCAACCAT 3'	5' TCTCTGGGTCTTCAGCTGGT 3'
CHD2	5'GATGACGAAGCTCCCAAAG 3'	5'TAGATGCTCCAGTGGCTCCT 3'
CHD4	5'CATCGATGGTGGAATCACTG 3'	5'ATCCGGTGAGCTCTGCTAAA 3'
CHD8	5'ATGCGGATTGTGAAGAAGGA3'	5'GGCTCTTCATCCTCATGGAA3'
HDAC3	5'TGGCTTCTGCTATGTCAACG 3'	5'TCTCTGCCCCGACTTCATAC3'
HDAC5	5'TCTGAACCACTGCATTTCCA 3'	5'GCCTGGACCGTAATTTCAGA 3'
HDAC9	5'CAGGCGGAAGGATGGAAATG3'	5'ATGCGTTGCTGTGAAACCAT3'
WDR44	5'TCTCTCCTAACCGCAAGCAT3'	5'AGCTCTCTCCCAGAGTTGGA 3'
SAP18	5'CCACTGTTGCTACGGGTCTT 3'	5'CCACTGTTGCTACGGGTCTT 3'
SUZ12	5'GCCTTTGAGAAGCCAACACA3'	5'CTGCAAATGAGCTGACAAGC3'
SMARCA1	5'AGGGCGAGAAGAAGAAGGAG3'	5'TCTGTGCTGAAGGCTGAATG3'
IGF2BP3	5'TCCAAGCAGAAACCATGTGA3'	5'ACTTACAAGCCGCAGAGGTG3'

Results

[0415] SA-miRNA mimics that can be used to induce senescence include mir-17-5p, mir-18a-5p, mir-19a-3p, mir-20a-5p and mir-92a1-5p, mir-125b1-5p, mir-1let7a-2-3p, and mir-100-5p (referred to in this Example as the set of SA-miRNA mimics).

[0416] FIG. 108 illustrates that senescence associated-miRNAs from oncogenic MIR17HG and tumori-suppressive MIR100HG clusters function to establish the hADSC SEN phenotype. Panel A shows the percentage of SA-β-Gal positive cells among the total amount of cells counted after transient transfection of mimics of SA-miRNA from either the MIR17HG (mir-17-5p, mir-18a-5p, mir-19a-3p, mir-20a-5p and mir-92a1-5p) or the MIR100HG (mir-125b1-5p, mir-1let7a-2-3p, mir-100-5p) clusters separately or after simultaneous transfection by the set of SA-miRNA mimics from both clusters in SR hADSCs. SA-miRNA mimics were transfected with FITC-labeled control to account for transfection efficiency as described in Experimental Procedures. Transfection efficiency for each combination is shown in (B) and expressed as a percentage of green cells among the total amount of cells (n) counted under the fluorescent microscope.

[0417] FIG. 109 illustrates a field depicting SA-β-Gal positivity and conversion of SR-hADSCs into SEN-hADSCs after transfection by 5pM or 10 pM of mimics of SA-miRNAs into SR-hADSCs.

[0418] The SEN phenotype induced under these conditions is similar to replicative senescence as demonstrated by downregulation of a handful of selected genes (FIGS. 110-112). In SR-hADSCs transfected with a full set of SA-miRNA mimics, downregulation of endogenous mRNA from the enriched functional network that represents SA-miRNA target genes such as SUZ12, NAP1L1, SMARCD2, SAP18, IGF2BP3, CHD2, and CHD4 (FIG. 110 and FIG. 113), as well as a number of the genes not targeted by SA-miRNAs but, nevertheless, shown to be downregulated upon replicative senescence, such as SMARCA1, CHD8, HDAC3, HDAC5, and HDAC9 (FIG. 111 and FIG. 113) was observed.

[0419] FIG. 110 demonstrates the direct influence of SA-miRNAs on gene transcription. Expression of SA-miRNA target genes was measured by qPCR analysis in SR-hADSCs (SR,

light bars) and in SR-hADSCs transiently transfected with the set of SA-miRNA mimics (SR+miRNA, dark bars).).

[0420] FIG. 111 demonstrates the indirect influence of SA-RNAs on gene transcription. Expression of genes previously shown to be downregulated in SEN-hADSCs but not identified as SA-miRNA targets was measured by qPCR analysis in SR-hADSCs (SR, light bars) and in SR-hADSCs transiently transfected with the set of SA-miRNA mimics (SR+miRNA, dark bars). RNA was isolated from the cells 48h post transfection. Samples were normalized against *β-actin*. Mean expression levels ± SEM (n=3) are shown as fold change ($\Delta\Delta C\tau$). Statistical differences were evaluated, where ***$p < 0.001$, **$p < 0.01$, *$p < 0.05$.

[0421] FIG. 112 shows the mean normalized protein expression levels ± SEM (n=3) in SR-hADSCs (light bars) and SEN- hADSCs (dark bars) transfected with SA-miRNAs. Results are shown for SA-miRNA direct and indirect target genes. Statistical differences were evaluated by Student's *t*-test, where ***$p < 0.001$, **$p < 0.01$, *$p < 0.05$.

[0422] FIG. 113 illustrates the novel genes that are the targets of SA-miRNA in replicative senescence, and their functional relationships and enrichment. Four functional categories of genes were evaluated for their relationships and functional enrichment using a network-based approach as described above. The network nodes represent genes and are categorized based on their functional category. Gene nodes are labeled in regards to targeted miRNA. Edges represent annotated protein relationships from the STRING database. Black solid edges represent connections of the sub-network minimal spanning trees (*i.e.* Steiner trees), dark gray dashed edges show additional sub-network connections, and light gray dashed edges represent connections between function-specific sub-networks. *P*-values indicate the extent to which each function-specific sub-network is enriched for genes from that particular functional category. Steiner nodes are shown in grey. Downregulated genes, which are not targeted by SA-miRNAs are shown based on their functional category.

Example 11: Factor-dependent immunostimulation of human PBMCs to increase production of Treg cells

[0423] The inventors show here (in FIG. 98) that factors produced by SR MSCs + IL-2 in an exemplary factor production unit of the invention has the ability to modulate the production of

Tregs cells. Treg cells are defined here by CD4+ CD25+FoxP3+ (Forkhead box P3 (FoxP3)+ expression) and CD4+ CD25-FoxP3+. CD4+ regulatory T cells (Treg cells) expressing the transcription factor FoxP3 are highly immune suppressive and play central roles in the maintenance of self-tolerance and immune homeostasis.

[0424] Described below are materials and methods for the production of factors that can influence Treg differentiation and production.

Isolation, culture and characterization of hADSCs

[0425] MSCs used in this example were isolated from human adipose tissues obtained from healthy adult female donors age 38, 45 and 49 undergoing routine liposuction procedures at the UCSD medical center, San Diego, CA. The MSC isolation protocol was approved by the local ethics committee and performed as previously described (Wang et al., Cell Cycle, 2011). Isolated adipose-derived stem cell lines were grown in DMEM/F12 medium (Life Technologies). In accordance with the MSC minimal definition criteria set by the International Society for Cellular Therapy (Dominici et.al. 2006, Cytotherapy 8: 315-317), flow cytometric analysis showed that hADSCs expressed CD29, CD73, CD90 and CD105 but do not express CD11b, CD14, CD19, CD34, CD45, CD80, CD86 (antibodies from eBiosciense, USA). Morphological analysis showed that the cells present a fibroblast-like morphology, were plastic adherent and capable of adipogenic, chondrogenic and osteogenic differentiation under *in vitro* conditions using commercially available differentiation mediums (Invitrogen, USA). Cumulative population doublings (PD) were calculated as PD = log(N/N0) x 3.33 across the multiple passages as a function of the number of days of growth in culture as described (Wang et al., Cell Cycle, 2011; Niu et al., 2015 , Oncotarget), where N0 is the number of cells plated in the flask and N is the number of cells harvested at this passage. hADSCs PD 4 or PD 6 for SR populations.

Induction of senescence using a genotoxic agent

[0426] To induce genotoxic senescence, the cells were treated with a genotoxic agent, Bleomycin (Cayman chemical) an anticancer chemotherapy drug. The factor production unit (containing 3-D scaffolds made from polycaprolactone (PCL) matrix/fibers that mimic 3-D ECM), populated with patient hADSCs was treated with 50ug/ml of bleomycin in 10% PRP

containing StemPro MSC SFM xeno-free medium for 2h at 37C (Niu et al., Oncotarget, 2015). Following the genotoxic exposure, the factor production unit was washed twice with PBS-cmf and fresh medium was replaced. The factor production unit was maintained for 5 days to achieve complete genotoxic-induced senescence, then the factor production unit with SEN cells were either left untreated (SEN) or treated with 20U/ml IL-2 for 24h (SEN+IL-2) as described below. The assay for monitoring the expression of pH-dependent senescence-associated β-galactosidase activity (SA-βGal) was performed as described in manufacturer's kit (BioVision) and previously published in (Wang et al., 2011, Cell Cycle 10: 3016-3030). The cultured hADSCs were washed with PBS for 15 minutes at room temperature, and stained with X-Gal containing supplement overnight at 37°C. The cells were washed twice with PBS, and the images were captured using a microscope (Nikons, TE300, DXM1200 Digital Camera, Japan).

IL-2 Stimulation/Treatment

[0427] Stimulation with recombinant IL-2 (Peprotech, USA) was performed as described (Deenick et al., 2003, J Immunol 170: 4963-4972; Niu et al., 2015, Oncotarget). 20U/ml of IL-2 was added to the culturing media for 24 hours at 37°C. For the IL-2 treatment, the factor production unit containing hADSCs was treated with 20U/ml IL-2 (Peprotech) in 10% PRP in StemPro MSC SFM xeno-free medium at 37°C for 24h. IL-2 was removed post-treatment with 2 washes of PBS-cmf and cells were co-cultured with PBMCs in 10% PRP in StemPro MSC SFM xeno-free medium.

Co-Culture with PBMCs for Immunomodulation

[0428] Four factor production units were populated with cells for the four conditions and shown in FIG. 2C: untreated SR-hADSCs, untreated genotoxic-induced SEN-hADSCs, SR-hADSCs treated with Il-2, and SEN-hADSCs treated with IL-2. Factors produced by the cells were used to guide Treg production in PBMC population. For each condition, 50,000 hADSCs were co-cultured for 72h with 500,000 viable Normal Peripheral Blood Mononuclear Cells (PBMCs). PBMCs from a single healthy 32 years old male donor were purchased from AllCells, Alameda, CA. A fresh Vial was thawed for each experiment and viability and cell count was performed using a Biorad TC20 cell counter after staining with trypan blue. Controls were run with PBMCs alone (FIG. 2C). Cells were collected by trypsinization at 24h or 72h time points and Tregs were stained using anti-human-FoxP3 Staining kit (BD Biosciences) containing

FoxP3 Alexa Fluor 647, PE Mouse Anti-Human CD25, FITC Mouse Anti-Human CD4, Isotype FITC-Mouse IgG1, Isotype PE-Mouse IgG1, Isotype Alexa 647-Mouse IgG1 k following maunfacturer's recommendations as demonstrated in FIG. 97 and FIG. 99.

FACS data analysis strategy – analysis for Treg production

[0429] Cells were collected by trypsinization at 24h and 72h time points and Tregs were stained with anti-human-FoxP3 Staining kit (BD Biosciences) containing FoxP3 Alexa Fluor 647, PE Mouse Anti-Human CD25, FITC Mouse Anti-Human CD4, Isotype FITC- Mouse IgG1, Isotype PE- Mouse IgG1, Isotype Alexa 647- Mouse IgG1 k following manufacturer's recommendations. Briefly, the cells were incubated with human Fc-receptor block (BD Biosciences) diluted 1:50 in staining Buffer (BD Biosciences, CA) for 10 min on ice to block the non-specific receptor binding. The cells were incubated on ice, in dark for 30 min with 20ul each surface antibody against CD4(FITC) or CD25(PE) or both and isotype-matched control antibodies. The cells were then washed with 1ml staining buffer and fixed with fixation buffer that was supplied in the FoxP3 Staining kit (BD Biosciences) for 10 min at 4°C in the dark. The cells were permeabilized using permeabilization buffer (BD Biosciences) for 30min at room temperature and then washed with 1ml staining buffer. After washing, the cells were incubated with 20ul of FoxP3- Alexa Fluor 647 antibody for 30min at room temperature in dark. At the end of the incubation period, the PBMCS were washed and resuspended into 500ul of fixative buffer and flow cytometry was performed on a FACS Canto II flow cytometer (BD Biosciences.

[0430] Data were collected on a FACS Canto II flow cytometer (BD Biosciences) at UCSF core facility. Onecomp ebeads (eBioscience) were used for compensation following manufactures protocol. Briefly, 1 drop of beads was added to in a separate tube and a single antibody was added to each tube at a concentration that was used for PBMCs. The samples were incubated at 4C for 15min, then washed with 2ml of staining buffer, resuspended in staining buffer and used to set-up the optimal fluorescence detector (PMT) voltages for PE, FITC and Alexa -647 fluorochromes used for PBMCs staining.

[0431] Analysis for Tregs was performed as outlined in the FACS analysis gating strategy in FIG. 97B using FlowJo software (Tree Star Inc). Lymphocytes were gated on forward and side scatter from the total PBMC population. Then, lymphocytes population expressing CD4-FITC population was gated to identify CD25-PE Tcells: CD4+ CD25+ Tcells or CD4+ CD25- T cells.

The populations expressing FoxP3 protein were identified as Tregs (shown in FIG. 97). The Treg population can be defined as CD4+ CD25-FoxP3+ and triple positive CD4+ CD25+FoxP3+ lymphocytes.

[0432] FIG. 98 illustrates that factors produced in an exemplary factor production unit of the invention influences production of Tregs. This figure shows that factors collected from SR hADSCs 72 hours after stimulation with IL-2 (for 24 hours) were optimal for increased production of Tregs, out of the conditions tested.

FIG. 99 shows representative data from the FACS analysis. The numbers inside the plots represent the number of cells in the population expressing the marker. The table provides a summary of the number of cells expressing the marker on Panels A-D. In this gating, lymphocytes were gated based on the light scatter plot distribution (SSC-A vs. FSC-A) (A). The lymphocyte population from panel A was further analyzed for CD4+ lymphocytes based on bound CD4 FITC and is shown as a histogram plot (B). CD4+ Lymphocytes were then sequentially analyzed for CD25 expression (D) followed by analysis of Foxp3 expressing Tregs based on positive Alexa-Fluor 647 anti-FoxP3 antibody binding. Panels E-H show the dot plot for lymphocytes for the expression of 2 markers. CD4+ lymphocytes are shown on the x-axis and CD25 expression is on the y-axis (E). The CD4+ CD25+ lymphocytes are in Q2. Foxp3+ positive T-Regs expressing CD25+ or CD25 negative are represented (panels F and G). Total CD4+ CD25+ FoxP3+ Tregs are plotted in panel H.

Table 6A: Differentially Upregulated Genes in SR + IL-2

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_015665	AAAS	0.24	0.00	622	830	1129	1229
NM_023928	AACS	0.09	0.00	863	1023	1254	1336
NM_001286682	AADAT	0.15	0.00	59	96	283	275
NM_001087	AAMP	0.20	0.00	2016	2486	3001	2832
NM_015511	AAR2	0.40	0.00	938	1367	1922	1835
NM_020745	AARS2	0.06	-0.07	476	575	736	616
NM_001261434	AARSD1	0.16	-0.03	274	369	518	436
NM_001271696	ABCB7	0.12	-0.02	153	212	406	338
NM_001198934	ABCC10	0.07	0.00	734	865	1813	1673
NM_005845	ABCC4	0.19	0.00	731	935	1337	1362
NM_020297	ABCC9	0.23	-0.22	721	949	2161	1723
NM_001040876	ABCE1	0.32	-0.05	852	1178	1312	1152
NM_007189	ABCF2	0.06	0.00	1964	2207	3296	3251
NM_032750	ABHD14B	0.17	0.00	611	779	1630	1558
NM_005158	ABL2	0.06	0.00	6606	7144	9240	9584
NM_000019	ACAT1	0.20	0.00	706	912	1884	1878
NM_005891	ACAT2	0.08	0.00	533	646	1362	1255
NM_032360	ACBD6	0.30	0.00	350	508	772	867
NM_001082486	ACD	0.23	0.00	347	479	453	425
NM_001098	ACO2	0.34	0.00	1994	2706	4798	4689
NM_001037171	ACOT9	0.08	-0.09	949	1114	1897	1645
NM_003501	ACOX3	0.25	0.00	344	483	973	878
NM_016361	ACP6	1.16	0.00	18	73	164	179
NM_033068	ACPT	0.30	0.00	40	77	54	48
NM_001288968	ACSF2	0.43	0.00	37	79	200	214
NM_001076552	ACSS2	0.53	0.01	338	571	1373	1503
NM_001100	ACTA1	0.31	-0.15	91	153	108	68
NM_001141945	ACTA2	0.28	-0.30	3308	4240	4529	3486
NM_005159	ACTC1	0.52	-0.29	1327	2069	807	582
NM_001199954	ACTG1	0.15	-0.20	124973	139507	229718	199115
NM_001024675	ACTL10	0.47	0.00	40	86	37	41
NM_004924	ACTN4	0.34	0.00	18951	24599	25070	25242
NM_005736	ACTR1A	0.38	-0.10	2851	3921	8462	7590
NM_005735	ACTR1B	0.09	0.00	2057	2353	2887	2987
NM_005721	ACTR3	0.40	0.00	2780	3875	7678	7468
NM_024855	ACTR5	0.10	0.00	159	217	241	211
NM_022899	ACTR8	0.20	0.00	752	968	1190	1218
NM_000666	ACY1	0.25	-0.06	258	371	1171	1017

Table 6A: Differentially Upregulated Genes in SR + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_203488	ACYP1	0.16	-0.15	55	91	133	87
NM_000022	ADA	0.19	0.00	482	634	817	736
NM_030955	ADAMTS12	0.17	0.00	1480	1804	2313	2201
NM_014244	ADAMTS2	0.09	-0.06	10108	11082	9512	8822
NM_014243	ADAMTS3	0.23	-0.10	40	74	31	13
NM_182920	ADAMTS9	0.27	0.00	49	89	46	50
NM_001025107	ADAR	0.17	0.00	5109	6000	8672	8943
NM_182503	ADAT2	0.03	0.00	99	137	166	163
NM_052853	ADCK2	0.79	0.00	269	552	514	462
NM_000671	ADH5	0.52	-0.23	1369	2133	3629	2924
NM_032804	ADO	0.65	0.00	367	671	894	884
NM_001619	ADRBK1	0.11	0.00	1607	1875	1924	2044
NM_000026	ADSL	0.07	-0.14	873	1019	1545	1288
NM_001126	ADSS	0.40	0.00	373	576	1094	1081
NM_022767	AEN	0.13	-0.17	1828	2156	2358	1946
NM_152406	AFAP1L1	0.28	0.00	643	883	761	819
NM_006796	AFG3L2	0.60	-0.12	965	1606	2423	2081
NM_006076	AGFG2	0.18	0.00	377	502	453	440
NM_018238	AGK	0.28	-0.03	238	351	551	466
NM_024758	AGMAT	0.21	0.00	45	80	125	96
NM_006411	AGPAT1	0.29	0.00	1767	2318	3968	3865
NM_006412	AGPAT2	0.26	0.00	542	742	2096	2194
NM_020133	AGPAT4	0.74	0.00	103	227	626	599
NM_178819	AGPAT6	0.05	0.00	2204	2446	4257	4264
NM_032717	AGPAT9	0.54	0.01	28	68	129	170
NM_000029	AGT	0.50	0.00	10	37	351	316
NM_015446	AHCTF1	0.02	0.00	782	887	1027	1000
NM_000687	AHCY	0.03	-0.15	1941	2136	3261	2765
NM_020731	AHRR	0.12	-0.27	687	842	1572	1192
NM_012111	AHSA1	0.31	0.00	1465	1974	2516	2567
NM_001130847	AIFM1	0.36	0.00	577	840	1350	1244
NM_003977	AIP	0.10	0.00	1033	1221	1709	1671
NM_032876	AJUBA	0.10	0.00	937	1113	799	823
NM_174858	AK5	0.35	-0.61	837	1181	4461	2767
NM_003488	AKAP1	0.43	0.00	503	775	977	945
NM_005100	AKAP12	0.08	-0.03	2308	2601	5209	4882
NM_001198656	AKAP2	0.24	-0.16	8623	10504	23286	20445
NM_001202414	AKR1A1	0.05	0.00	1332	1504	2165	2283
NM_001628	AKR1B1	0.30	0.00	3801	4907	10810	10662

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001353	AKR1C1	0.43	-0.40	11991	16663	17729	13053
NM_001354	AKR1C2	0.27	-0.18	6380	7987	7310	6198
NM_003739	AKR1C3	0.61	0.00	1265	2095	2071	2009
NM_001818	AKR1C4	0.62	0.00	302	549	472	418
NM_032375	AKT1S1	0.08	0.01	1078	1251	1953	2115
NM_000031	ALAD	0.17	-0.02	404	530	1622	1473
NM_000688	ALAS1	0.07	0.00	2108	2372	3720	3920
NM_000689	ALDH1A1	0.54	0.00	19	51	0	0
NM_000693	ALDH1A3	0.16	-0.69	502	645	4477	2617
NM_000692	ALDH1B1	0.44	-0.42	1656	2418	2957	2067
NM_001031806	ALDH3A2	0.14	0.00	440	564	1175	1248
NM_000694	ALDH3B1	0.21	-0.18	365	494	1870	1523
NM_001182	ALDH7A1	0.30	0.00	182	280	356	336
NM_019109	ALG1	0.21	0.00	446	598	1142	1039
NM_032834	ALG10	0.19	0.00	61	101	69	72
NM_144988	ALG14	0.89	0.00	46	127	252	238
NM_013338	ALG5	0.02	0.00	544	632	761	848
NM_001007027	ALG8	0.26	-0.02	313	444	886	780
NM_032306	ALKBH7	0.26	0.00	295	421	630	601
NM_052947	ALPK2	0.16	-0.16	3052	3605	4188	3558
NM_020919	ALS2	0.21	0.00	1107	1402	1678	1708
NM_005782	ALYREF	0.15	-0.12	1078	1312	1524	1285
NM_001267782	AMBRA1	0.32	-0.08	686	959	1574	1370
NM_001634	AMD1	0.27	-0.15	1591	2068	2543	2144
NM_016201	AMOTL2	0.26	-0.51	7839	9743	6636	4447
NM_001635	AMPH	0.27	0.00	103	166	241	266
NM_000481	AMT	0.25	0.00	27	55	94	68
NM_022662	ANAPC1	0.15	-0.04	985	1211	1460	1298
NM_001242374	ANAPC13	0.55	-0.08	611	1010	1291	1107
NM_001278485	ANAPC15	0.03	0.00	282	346	661	675
NM_013366	ANAPC2	0.11	-0.06	740	899	1674	1481
NM_001286756	ANAPC4	0.57	0.00	200	363	584	608
NM_016238	ANAPC7	0.31	-0.23	812	1118	1999	1577
NM_015305	ANGEL1	0.64	0.00	205	391	705	774
NM_020987	ANK3	0.44	0.00	18	46	89	81
NM_001257999	ANKFY1	0.25	0.00	1886	2414	4739	4961
NM_020319	ANKMY2	0.34	0.00	323	483	753	799
NM_033121	ANKRD13A	0.20	0.00	3303	3994	4987	4900
NM_030816	ANKRD13C	0.28	-0.11	565	779	1029	854

Table 6A: Differentially Upregulated Genes in SR + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_019046	ANKRD16	0.27	0.00	97	158	164	177
NM_032139	ANKRD27	0.01	0.00	1123	1247	2080	1937
NM_032290	ANKRD32	0.31	0.00	109	179	154	120
NM_144698	ANKRD35	0.02	0.00	49	76	202	244
NM_052855	ANKRD40	0.53	0.00	1139	1801	2086	2185
NM_017704	ANKRD49	0.19	0.00	81	128	127	102
NM_020337	ANKRD50	0.13	-0.05	1241	1488	2344	2116
NM_173595	ANKRD52	0.05	-0.03	5569	6021	6208	5828
NM_015245	ANKS1A	0.21	0.00	463	617	780	858
NM_018685	ANLN	0.15	-1.06	3260	3819	3309	1477
NM_001286615	ANO4	0.09	-0.55	112	159	179	91
NM_006305	ANP32A	0.09	0.00	500	613	1119	1198
NM_006401	ANP32B	0.18	-0.05	759	961	1002	869
NM_012403	ANP32C	0.07	0.00	96	137	168	176
NM_007193	ANXA10	0.33	-0.10	3	17	158	111
NM_145869	ANXA11	0.02	-0.02	4548	4854	8306	7896
NM_001283	AP1S1	0.21	0.00	1496	1878	4669	4654
NM_004069	AP2S1	0.46	-0.17	1784	2636	5133	4338
NM_001271769	AP3B1	0.36	0.00	1007	1422	2514	2688
NM_001134296	AP3M2	0.01	0.00	380	451	1198	1266
NM_004722	AP4M1	0.32	-0.02	195	302	732	638
NM_001204446	AP5S1	0.09	0.00	264	340	464	518
NM_013229	APAF1	0.10	0.00	483	595	447	518
NM_019043	APBB1IP	0.10	0.01	915	1089	942	1050
NM_006051	APBB3	0.03	0.00	159	207	279	275
NM_014481	APEX2	0.26	-0.07	498	682	705	591
NM_015957	APIP	0.14	0.00	61	98	160	161
NM_001270517	APITD1-CORT	0.16	0.01	58	95	116	155
NM_014508	APOBEC3C	0.44	-0.29	317	509	1408	1050
NM_001136540	APOL1	0.33	-0.35	246	374	713	488
NM_030882	APOL2	0.01	-0.03	998	1114	1728	1560
NM_001251904	APPL2	0.16	0.00	2299	2747	3712	3926
NM_000485	APRT	0.21	0.00	1326	1671	3213	3368
NM_000044	AR	0.60	0.00	217	400	867	874
NM_001039479	AREL1	0.03	0.00	1435	1599	2941	2882
NM_001024226	ARF1	0.50	-0.01	8861	12952	18255	17737
NM_001662	ARF5	0.28	0.00	1473	1936	3311	3335
NM_032389	ARFGAP2	0.23	0.00	1101	1419	2283	2144
NM_001287432	ARFIP1	0.07	0.00	469	570	1038	1107

Table 6A: Differentially Upregulated Genes in SR + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_018011	ARGLU1	0.36	-0.06	648	938	1169	1017
NM_004308	ARHGAP1	0.18	-0.06	4080	4872	9533	8859
NM_033515	ARHGAP18	0.11	0.00	1154	1365	3357	3166
NM_020809	ARHGAP20	0.51	0.00	101	191	568	591
NM_001025616	ARHGAP24	0.13	0.00	1172	1402	2780	2719
NM_004815	ARHGAP29	0.31	0.00	1234	1674	3481	3619
NM_020754	ARHGAP31	0.33	-0.29	2208	2953	4527	3510
NM_001172630	ARHGAP33	0.63	0.00	42	99	131	131
NM_025251	ARHGAP39	0.30	0.00	31	63	156	146
NM_152432	ARHGAP42	0.54	0.00	22	57	69	68
NM_004309	ARHGDIA	0.21	-0.09	7926	9529	12881	11758
NM_199002	ARHGEF1	0.17	0.00	1639	1993	1803	1834
NM_018125	ARHGEF10L	0.67	0.00	363	674	1400	1495
NM_153213	ARHGEF19	0.23	0.00	133	202	79	79
NM_001080479	ARHGEF28	0.10	0.00	782	940	1291	1329
NM_005435	ARHGEF5	0.25	0.00	261	374	601	667
NM_002892	ARID4A	0.16	0.00	144	207	435	490
NM_001244638	ARID5B	0.19	0.00	2713	3296	4873	5026
NM_006321	ARIH2	0.16	0.00	919	1140	1813	1728
NM_001667	ARL2	0.31	0.00	892	1223	1622	1582
NM_015161	ARL6IP1	0.23	-0.14	1327	1696	2084	1760
NM_001199196	ARMC6	0.60	-0.33	506	873	1404	1018
NM_001271466	ARMC9	0.09	-0.45	627	757	3232	2220
NM_016608	ARMCX1	0.18	-0.02	570	735	1160	1037
NM_016607	ARMCX3	0.19	0.00	1186	1477	2986	3122
NM_001168479	ARMCX5	0.22	0.00	113	174	181	200
NM_001199818	ARMCX5-GPRASP2	0.06	0.00	213	274	709	686
NM_001190996	ARPC1A	0.17	0.00	1262	1546	3159	3055
NM_005718	ARPC4	0.17	-0.24	2515	3019	6199	5029
NM_001198793	ARPC4-TTLL3	0.30	0.00	1111	1497	3038	3057
NM_001270439	ARPC5	0.11	0.00	4798	5410	7245	7418
NM_030978	ARPC5L	0.17	-0.04	871	1087	1753	1569
NM_182616	ARPIN	0.29	-0.09	529	737	1248	1067
NM_001257328	ARRB2	0.25	0.00	186	275	216	229
NM_152285	ARRDC1	0.38	0.00	260	408	453	503
NM_001079516	ASAH2B	0.29	0.00	26	55	60	57
NM_001247996	ASAP1	0.21	-0.05	3120	3808	6549	6061
NM_001142733	ASB14	1.05	0.00	37	118	112	129

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_080863	ASB16	0.27	0.00	37	71	102	118
NM_017873	ASB6	0.12	-0.07	1758	2067	3271	2928
NM_001198798	ASCC1	0.47	0.00	171	296	522	486
NM_032204	ASCC2	0.22	0.00	1042	1333	2263	2299
NM_004674	ASH2L	0.05	0.00	758	883	1206	1153
NM_001095	ASIC1	0.65	-0.20	35	87	227	155
NM_004192	ASMTL	0.11	0.00	637	781	1398	1392
NM_004317	ASNA1	0.15	-0.17	1310	1586	3030	2521
NM_001251888	ASPSCR1	0.19	0.00	271	372	665	654
NM_014010	ASTN2	0.52	0.00	55	115	231	205
NM_018164	ASUN	0.17	-0.04	432	562	925	802
NM_018188	ATAD3A	0.21	0.00	782	1010	913	906
NM_031921	ATAD3B	0.42	0.00	448	692	574	590
NM_024857	ATAD5	0.02	-0.20	230	287	125	78
NM_001136153	ATF6B	0.05	0.00	1483	1671	3128	3257
NM_001190266	ATG16L1	0.29	0.00	658	909	1481	1394
NM_052936	ATG4A	0.06	0.00	225	289	449	457
NM_006395	ATG7	0.17	0.00	1126	1388	2136	2103
NM_004044	ATIC	0.59	0.00	705	1185	2059	2113
NM_032827	ATOH8	0.39	0.00	935	1348	1996	1978
NM_004045	ATOX1	0.13	0.00	486	611	1094	1148
NM_024524	ATP13A3	0.07	0.00	7540	8187	7289	7506
NM_001677	ATP1B1	0.06	0.00	1237	1408	1025	1098
NM_001257335	ATP5A1	0.33	-0.34	3012	4000	7262	5506
NM_001686	ATP5B	0.21	-0.06	10702	12780	23492	21985
NM_001687	ATP5D	0.25	0.00	587	790	1067	1055
NM_001190329	ATP5G3	0.56	-0.32	1599	2539	4750	3614
NM_006356	ATP5H	0.32	-0.14	422	611	1458	1205
NM_007100	ATP5I	0.30	-0.13	656	910	1635	1372
NM_001003703	ATP5J	0.20	0.00	513	676	1165	1205
NM_001003713	ATP5J2	0.38	0.00	364	555	1015	924
NM_001697	ATP5O	0.04	0.00	654	761	1543	1438
NM_018035	ATP5SL	0.41	-0.09	561	846	1364	1172
NM_001696	ATP6V1E1	0.26	0.00	1730	2232	4195	4142
NM_001198909	ATP6V1F	0.04	-0.28	1068	1207	2660	2041
NM_000053	ATP7B	0.24	0.00	219	317	422	492
NM_005603	ATP8B1	0.14	-0.11	3192	3725	4369	3841
NM_001184	ATR	0.29	0.00	571	795	1331	1231
NM_130384	ATRIP	0.08	0.00	361	451	489	473

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001137675	ATXN1L	0.05	0.00	976	1117	1368	1399
NM_153340	ATXN7L2	0.18	0.00	86	134	121	116
NM_001136262	ATXN7L3B	0.02	0.00	1192	1330	1516	1575
NM_001287490	AUNIP	0.09	0.00	168	227	389	366
NM_021913	AXL	0.26	-0.30	24844	30431	25272	20136
NM_152490	B3GALNT2	0.20	0.00	496	655	794	854
NM_194318	B3GALTL	0.03	0.00	216	272	368	399
NM_001288722	B3GAT3	0.34	0.00	390	576	1044	978
NM_198540	B3GNT8	0.62	0.00	14	44	83	67
NM_033309	B3GNT9	0.32	0.00	725	1015	1576	1562
NM_212543	B4GALT4	0.47	0.00	876	1344	1121	1201
NM_001243475	B9D1	0.32	0.00	73	128	212	213
NM_001033549	BABAM1	0.18	0.00	1026	1282	2525	2440
NM_004322	BAD	0.30	0.00	398	569	1383	1353
NM_001172415	BAG1	0.25	0.00	310	439	645	726
NM_004282	BAG2	0.03	-0.30	802	916	1375	1013
NM_001188	BAK1	0.30	-0.15	395	566	747	591
NM_003860	BANF1	0.17	-0.27	1226	1505	2250	1737
NM_006317	BASP1	0.46	-0.03	3439	4992	5336	4993
NM_031885	BBS2	0.02	0.00	710	814	1612	1577
NM_176824	BBS7	0.04	0.00	264	328	699	769
NM_001013257	BCAM	0.73	0.00	37	96	69	46
NM_001170714	BCAR1	0.09	0.00	2190	2500	3712	3656
NM_003567	BCAR3	0.15	-0.06	3909	4555	6958	6407
NM_078468	BCCIP	0.34	0.00	474	689	1096	1111
NM_015367	BCL2L13	0.34	0.00	986	1372	2922	3000
NM_001199864	BCL2L2-PABPN1	0.20	0.00	1113	1405	1926	2052
NM_004765	BCL7C	0.29	-0.04	232	345	668	567
NM_182557	BCL9L	0.09	0.00	3336	3740	4629	4758
NM_014739	BCLAF1	0.06	0.00	1521	1726	3011	3096
NM_020139	BDH2	1.24	-0.13	19	80	200	142
NM_018429	BDP1	0.29	0.00	718	981	1285	1331
NM_005868	BET1	0.07	0.00	351	434	514	530
NM_018476	BEX1	0.19	0.00	76	122	21	15
NM_016561	BFAR	0.21	0.00	1199	1522	2731	2800
NM_001003800	BICD2	0.33	-0.22	2183	2932	5180	4253
NM_018688	BIN3	0.28	0.00	362	514	1044	1140
NM_017693	BIVM	0.20	0.00	437	580	1169	1187
NM_001167820	BLCAP	0.28	0.00	958	1286	2375	2431

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_000057	BLM	0.31	0.00	143	227	62	87
NM_001487	BLOC1S1	0.15	0.00	479	614	1048	1059
NM_001282436	BLOC1S2	0.37	0.00	278	429	905	922
NM_001253823	BLVRA	0.16	-0.11	454	586	1341	1129
NM_005180	BMI1	0.13	0.00	568	708	1111	1227
NM_133468	BMPER	0.06	0.00	1468	1659	1208	1103
NM_013979	BNIP1	0.03	0.00	249	309	333	359
NM_138369	BOD1	0.05	0.00	758	881	1077	1126
NM_032515	BOK	0.81	0.00	597	1176	1770	1669
NM_001286746	BORA	0.06	-0.24	94	134	146	91
NM_006085	BPNT1	0.85	-0.05	291	617	728	621
NM_152743	BRAT1	0.47	-0.16	387	622	1329	1081
NM_004899	BRE	0.66	0.00	163	321	842	924
NM_001519	BRF1	0.53	0.00	317	540	638	649
NM_032043	BRIP1	0.04	-0.24	483	575	275	187
NM_015399	BRMS1	0.38	0.00	731	1064	1630	1573
NM_017797	BTBD2	0.32	0.00	1784	2394	3625	3725
NM_001002860	BTBD7	0.11	0.00	1091	1298	2032	2150
NM_001037637	BTF3	0.32	0.01	1453	1970	2656	2847
NM_004336	BUB1	0.07	-1.05	926	1081	911	383
NM_001211	BUB1B	0.03	-0.98	602	698	514	216
NM_004725	BUB3	0.25	-0.13	3362	4208	4245	3676
NM_001261835	BZRAP1	0.65	0.00	21	59	62	63
NM_001159767	BZW2	0.67	-0.11	583	1049	1348	1137
NM_014267	C11orf58	0.24	0.00	377	522	965	972
NM_001135635	C11orf68	0.05	-0.06	1741	1941	2379	2124
NM_207645	C11orf87	0.85	0.00	21	67	42	52
NM_021640	C12orf10	0.03	0.00	621	720	1061	1111
NM_001286198	C12orf43	0.85	0.00	151	341	370	349
NM_152318	C12orf45	0.31	-0.38	79	136	256	155
NM_024738	C12orf49	0.09	0.00	1045	1228	1553	1691
NM_138425	C12orf57	0.13	0.00	937	1135	1445	1499
NM_001135570	C12orf73	0.43	0.00	75	141	164	163
NM_001102366	C14orf159	0.22	-0.09	325	447	1275	1089
NM_024644	C14orf169	0.35	0.00	271	415	516	558
NM_001199058	C15orf38-AP3S2	0.14	0.00	895	1092	2206	2303
NM_022744	C16orf58	0.08	0.00	2197	2486	3294	3440
NM_020314	C16orf62	0.55	0.00	995	1602	3575	3429
NM_001001436	C16orf87	0.09	0.00	190	253	245	283

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001272051	C16orf91	0.34	0.00	136	222	270	226
NM_001193655	C17orf62	0.04	0.00	737	853	1481	1571
NM_017941	C17orf80	0.01	-0.06	241	297	418	338
NM_001114118	C17orf85	0.23	0.00	693	914	1366	1431
NM_001201475	C18orf21	0.08	0.00	171	229	285	255
NM_017914	C19orf24	0.51	0.00	266	454	736	828
NM_152482	C19orf25	0.56	0.00	118	227	387	340
NM_032207	C19orf44	0.33	0.00	100	168	193	181
NM_001290149	C19orf48	0.21	-0.16	687	895	510	390
NM_138358	C19orf52	0.04	0.00	219	278	410	440
NM_001100418	C19orf60	0.26	0.00	153	233	412	427
NM_199341	C19orf68	0.16	0.00	52	87	96	104
NM_205767	C19orf70	0.38	-0.34	248	390	923	647
NM_017891	C1orf159	0.62	0.00	49	112	177	153
NM_207356	C1orf174	0.34	0.00	379	561	624	695
NM_152374	C1orf216	0.12	0.00	317	411	1225	1237
NM_024319	C1orf35	0.31	0.00	218	331	270	220
NM_001098616	C1orf43	0.25	0.01	2556	3232	4914	5172
NM_017860	C1orf56	0.29	0.00	109	177	318	318
NM_001282671	C1orf86	0.03	0.00	249	310	545	593
NM_001212	C1QBP	0.02	-0.16	1402	1552	1888	1558
NM_030968	C1QTNF1	0.23	0.00	143	215	449	383
NM_021254	C21orf59	0.04	0.00	455	541	657	577
NM_024627	C22orf29	0.16	0.00	648	820	977	926
NM_001286577	C2CD3	0.40	0.00	345	535	851	867
NM_001286174	C2CD5	0.25	0.00	381	528	749	693
NM_013310	C2orf27A	0.27	0.00	24	51	94	120
NM_025203	C2orf44	0.53	0.00	185	331	308	272
NM_024520	C2orf47	0.13	0.00	129	184	281	301
NM_001286537	C2orf49	0.35	0.00	210	328	491	536
NM_001145054	C2orf81	0.77	0.00	50	125	266	253
NM_032321	C2orf88	0.37	0.00	329	502	838	876
NM_020685	C3orf14	0.25	0.00	29	58	168	179
NM_173657	C3orf33	0.32	0.00	36	72	110	105
NM_001099777	C3orf55	0.58	0.00	35	83	187	165
NM_001206997	C4orf22	0.32	0.00	40	78	92	113
NM_018356	C5orf22	0.40	0.00	300	469	493	564
NM_033211	C5orf30	0.06	0.00	2346	2608	5197	5346
NM_001277348	C5orf66	0.57	0.00	111	216	268	292

Table 6A: Differentially Upregulated Genes in SR + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_178508	C6orf1	0.20	-0.35	529	693	1647	1185
NM_001161376	C6orf136	0.87	0.00	120	283	277	327
NM_021184	C6orf47	0.24	0.00	320	448	559	536
NM_145267	C6orf57	0.94	0.00	19	66	69	91
NM_024067	C7orf26	0.06	0.00	501	602	632	662
NM_001243749	C7orf49	0.22	0.00	627	828	1160	1152
NM_001134395	C7orf50	0.06	0.00	511	613	1422	1299
NM_197964	C7orf55	0.55	0.00	99	193	287	253
NM_001130929	C7orf73	0.12	0.00	509	634	888	900
NM_177965	C8orf37	0.04	-0.45	26	47	92	44
NM_016390	C9orf114	0.07	-0.01	1047	1211	1720	1571
NM_001193329	C9orf3	0.47	0.00	362	587	859	852
NM_017998	C9orf40	0.17	-0.55	195	272	314	172
NM_032307	C9orf64	0.32	-0.06	335	494	603	501
NM_032310	C9orf89	0.25	0.00	478	653	1148	1065
NM_198584	CA13	0.71	0.00	20	59	54	59
NM_016289	CAB39	0.20	0.00	1085	1370	1797	1911
NM_001080543	CACTIN	0.19	-0.11	397	528	595	479
NM_004341	CAD	0.07	-0.07	2925	3251	3519	3159
NM_001009571	CADPS2	0.33	0.00	50	94	17	9
NM_033138	CALD1	0.29	-0.03	11161	14028	19721	18841
NM_015916	CALHM2	0.61	0.00	445	779	1662	1773
NM_005184	CALM3	0.11	-0.15	6502	7321	12973	11353
NM_001256139	CAPG	0.05	0.00	958	1097	3556	3530
NM_005186	CAPN1	0.33	0.00	4130	5456	9843	9636
NM_024537	CARS2	0.13	-0.25	1424	1696	3508	2782
NM_144508	CASC5	0.15	-0.86	529	674	670	314
NM_020764	CASKIN1	0.02	0.00	276	339	362	390
NM_032982	CASP2	0.42	0.00	625	945	925	924
NM_004346	CASP3	0.02	0.00	639	733	593	567
NM_001225	CASP4	0.46	0.00	578	900	1115	1017
NM_001267056	CASP7	0.14	0.00	316	413	445	425
NM_001080125	CASP8	0.47	-0.04	86	162	272	214
NM_001752	CAT	0.27	0.00	519	717	2510	2628
NM_170662	CBLB	0.22	0.00	980	1257	2620	2540
NM_001284291	CBLL1	0.11	0.00	518	640	753	828
NM_001286789	CBR1	0.36	0.00	1619	2244	4163	4216
NM_001127228	CBX1	0.50	0.00	494	797	1067	1030
NM_007276	CBX3	0.10	0.00	821	984	1181	1201

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_014292	CBX6	0.18	-0.06	1274	1571	2851	2566
NM_032449	CC2D1B	0.34	0.00	1019	1423	2246	2259
NM_021174	CCAR2	0.11	-0.13	2194	2538	3438	2972
NM_133459	CCBE1	0.25	-0.34	2421	3064	4280	3203
NM_001008661	CCBL2	0.45	0.00	162	278	391	421
NM_013301	CCDC106	0.64	0.00	11	41	187	227
NM_001163323	CCDC120	0.69	0.00	35	89	60	85
NM_176816	CCDC125	0.05	0.00	94	133	260	261
NM_024821	CCDC134	0.42	0.00	106	188	162	205
NM_025004	CCDC15	0.03	-0.42	114	155	146	79
NM_016474	CCDC174	0.15	0.00	148	211	279	323
NM_025057	CCDC176	0.02	0.01	31	53	123	163
NM_152492	CCDC27	1.25	0.00	22	90	58	55
NM_024296	CCDC28B	0.23	-0.33	79	129	160	94
NM_001256964	CCDC51	0.20	0.00	191	273	327	375
NM_001017928	CCDC58	0.90	0.00	23	74	44	31
NM_014167	CCDC59	0.41	0.00	125	215	210	233
NM_175884	CCDC71L	0.06	-0.15	508	607	1117	909
NM_138770	CCDC74A	0.88	0.00	14	52	381	431
NM_001130147	CCDC77	0.04	0.00	222	282	302	360
NM_001080433	CCDC85A	0.50	-0.58	335	558	603	346
NM_006848	CCDC85B	0.42	-0.18	669	1004	965	762
NM_024098	CCDC86	0.08	-0.21	1184	1371	1310	1031
NM_001135597	CCDC88A	0.03	-0.06	1271	1424	2379	2122
NM_152723	CCDC89	1.11	0.00	13	58	67	65
NM_018074	CCDC94	0.29	-0.02	239	354	435	364
NM_052848	CCDC97	0.14	0.00	438	561	628	579
NM_001105564	CCHCR1	0.38	-0.08	500	743	988	837
NM_002982	CCL2	0.15	-0.23	98	147	160	102
NM_001237	CCNA2	0.28	-0.80	898	1208	778	388
NM_031966	CCNB1	0.24	-0.93	1156	1499	1849	880
NM_004701	CCNB2	0.20	-0.57	355	481	489	277
NM_005190	CCNC	0.43	0.00	349	550	568	628
NM_057749	CCNE2	0.20	0.00	203	289	108	89
NM_001761	CCNF	0.02	0.00	701	800	428	412
NM_001199189	CCNH	0.12	0.00	476	595	774	728
NM_014711	CCP110	0.02	0.00	301	366	401	431
NM_006431	CCT2	0.15	-0.02	2352	2781	3571	3327
NM_006430	CCT4	0.21	-0.03	3016	3695	5648	5292

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_012073	CCT5	0.36	-0.26	4545	6112	6971	5599
NM_001762	CCT6A	0.32	-0.05	1760	2369	3232	2937
NM_001166285	CCT7	0.19	-0.08	3521	4249	7420	6747
NM_001282907	CCT8	0.13	0.00	1184	1417	1568	1630
NM_133493	CD109	0.03	-0.05	1845	2033	8131	7582
NM_020404	CD248	0.02	-0.68	5111	5422	9229	5532
NM_014143	CD274	0.08	0.00	329	414	168	166
NM_001024736	CD276	0.15	0.00	6196	7135	11178	11347
NM_006110	CD2BP2	0.10	-0.08	1254	1468	2123	1871
NM_030911	CDADC1	0.14	0.00	100	149	189	176
NM_138477	CDAN1	0.07	0.00	457	557	734	826
NM_006023	CDC123	0.67	0.00	690	1227	1838	1880
NM_003672	CDC14A	0.39	0.00	31	67	83	100
NM_001255	CDC20	0.11	-1.31	886	1061	786	270
NM_001789	CDC25A	0.15	0.00	547	692	160	126
NM_139286	CDC26	0.46	0.00	76	145	152	185
NM_001114091	CDC27	0.43	0.00	940	1396	1963	2022
NM_004359	CDC34	0.01	0.00	1345	1482	1645	1665
NM_007065	CDC37	0.16	0.00	2525	3002	4309	4490
NM_017913	CDC37L1	0.20	0.00	186	267	410	421
NM_001039802	CDC42	0.22	-0.02	2680	3308	5632	5301
NM_152243	CDC42EP1	0.36	-0.17	1763	2434	2699	2238
NM_006779	CDC42EP2	0.14	0.00	1151	1389	1212	1201
NM_006449	CDC42EP3	0.32	-0.14	1544	2083	3261	2780
NM_001038707	CDC42SE1	0.04	0.00	2000	2209	3290	3364
NM_001254	CDC6	0.31	0.00	845	1162	223	229
NM_152562	CDCA2	0.36	-0.21	336	508	626	471
NM_031299	CDCA3	0.19	-0.91	344	463	445	194
NM_017955	CDCA4	0.31	0.00	648	906	713	734
NM_080668	CDCA5	0.10	-0.72	803	965	753	397
NM_001127370	CDCA7L	0.23	-0.10	697	921	370	287
NM_001796	CDH8	0.24	0.00	234	336	258	266
NM_001786	CDK1	0.08	-0.42	349	437	314	189
NM_052988	CDK10	0.48	0.00	588	924	984	974
NM_001798	CDK2	0.30	-0.34	1220	1639	1040	734
NM_000075	CDK4	0.28	-0.29	1626	2130	3438	2643
NM_004935	CDK5	0.58	0.00	47	105	185	155
NM_001278167	CDK5RAP1	0.46	-0.03	264	434	751	651
NM_001278216	CDK5RAP3	0.34	0.00	375	554	1011	1083

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001261	CDK9	0.11	0.00	1139	1352	2211	2146
NM_001220778	CDKN1A	0.13	-0.03	13883	15626	32012	30770
NM_004064	CDKN1B	0.08	0.00	434	534	426	442
NM_017632	CDKN2AIP	0.25	0.00	248	358	389	407
NM_080656	CDKN2AIPNL	0.03	-0.03	189	242	343	279
NM_001262	CDKN2C	0.22	-0.33	430	579	339	220
NM_005192	CDKN3	0.03	-0.99	275	339	331	131
NM_001134422	CDV3	0.27	0.00	3561	4532	3851	3970
NM_152342	CDYL2	0.08	0.00	446	545	674	721
NM_005195	CEBPD	0.42	-0.23	62	119	125	76
NM_018689	CEMIP	0.17	-0.38	9699	11231	3955	2869
NM_001812	CENPC	0.58	0.00	76	157	135	152
NM_024053	CENPM	0.55	-0.91	230	407	329	139
NM_001100624	CENPN	0.17	-0.24	1035	1282	1179	900
NM_001012267	CENPP	0.22	0.00	123	187	337	299
NM_025082	CENPT	0.53	-0.03	741	1193	1984	1806
NM_024629	CENPU	0.44	0.00	140	243	191	152
NM_181716	CENPV	0.02	0.00	299	363	316	316
NM_001012507	CENPW	0.38	-0.96	141	235	237	92
NM_014956	CEP164	0.12	0.00	806	980	1583	1510
NM_032142	CEP192	0.17	0.00	648	824	1102	1190
NM_018718	CEP41	0.38	-0.04	141	235	618	525
NM_015147	CEP68	0.03	0.00	246	306	701	773
NM_001098802	CEP78	0.30	-0.02	203	308	514	436
NM_022778	CEP85	0.48	0.00	542	856	564	645
NM_032816	CEP89	0.19	-0.08	334	450	990	841
NM_005507	CFL1	0.17	-0.09	15387	17812	29260	26863
NM_001243645	CFL2	0.32	-0.13	1962	2633	4663	4042
NM_033043	CGB5	0.71	0.00	20	59	17	17
NM_033183	CGB8	0.48	0.00	21	53	27	33
NM_001008390	CGGBP1	0.13	0.00	1496	1774	2889	2937
NM_138481	CHADL	0.94	0.00	13	52	110	83
NM_005483	CHAF1A	0.09	-0.13	1046	1225	707	566
NM_005441	CHAF1B	0.19	-0.34	332	447	272	172
NM_001164144	CHAMP1	0.31	0.00	620	869	1000	915
NM_203298	CHCHD1	0.06	0.00	547	653	817	835
NM_017812	CHCHD3	0.07	-0.03	540	649	1171	1035
NM_001011667	CHCHD7	0.41	0.00	121	210	356	318
NM_001005735	CHEK2	0.48	0.00	118	214	154	133

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_014043	CHMP2B	0.19	0.00	580	752	759	797
NM_001144073	CHORDC1	0.09	0.00	231	301	258	244
NM_019886	CHST7	0.38	0.00	91	160	229	270
NM_175856	CHSY3	0.12	0.00	427	539	439	497
NM_022092	CHTF18	0.05	0.00	298	370	229	183
NM_001039690	CHTF8	0.26	0.00	2001	2575	3236	3281
NM_001206612	CHTOP	0.02	0.00	1419	1572	1788	1895
NM_001278	CHUK	0.09	0.00	591	718	938	876
NM_144697	CIART	0.03	0.00	174	225	460	479
NM_032630	CINP	0.17	-0.08	411	539	1017	865
NM_004882	CIR1	0.03	0.00	181	232	399	396
NM_018464	CISD1	0.10	0.00	158	216	343	388
NM_001136498	CISD3	0.12	-0.22	716	875	1647	1299
NM_013324	CISH	0.93	-0.42	31	95	56	24
NM_001206999	CIT	0.26	-0.99	1141	1497	1739	791
NM_001131016	CIZ1	0.17	0.00	2897	3451	7302	7246
NM_001098525	CKAP2	0.02	-0.03	967	1090	1115	985
NM_152515	CKAP2L	0.05	-0.42	621	729	493	311
NM_001008938	CKAP5	0.10	0.00	3832	4318	6114	5967
NM_007056	CLASRP	0.13	0.00	610	758	622	617
NM_001127899	CLCN5	0.11	0.00	413	521	555	623
NM_005602	CLDN11	0.07	-1.05	4182	4626	2909	1299
NM_002975	CLEC11A	0.25	-0.02	1071	1403	1601	1449
NM_175060	CLEC14A	0.02	-1.46	125	167	370	104
NM_015226	CLEC16A	0.21	0.00	648	844	944	996
NM_001004419	CLEC2D	0.08	0.00	193	255	349	305
NM_001287594	CLIC1	0.31	-0.40	6592	8471	17949	13255
NM_015526	CLIP3	0.09	-0.21	487	596	2493	2015
NM_000086	CLN3	0.15	-0.09	666	836	1454	1250
NM_001293	CLNS1A	0.75	0.00	323	636	740	787
NM_006831	CLP1	0.29	0.00	249	368	430	488
NM_001258394	CLPB	0.19	-0.13	743	953	1414	1181
NM_006012	CLPP	0.31	0.00	986	1343	1406	1311
NM_022111	CLSPN	0.14	-0.26	892	1088	507	362
NM_007096	CLTA	0.35	0.00	1734	2377	3829	3956
NM_015229	CLUH	0.20	0.00	1725	2138	2556	2536
NM_182523	CMC1	0.43	-0.27	40	84	141	85
NM_032359	CMSS1	0.58	0.00	228	414	628	689
NM_017801	CMTM6	0.04	0.00	1148	1295	2217	2359

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001099642	CMTR2	0.37	0.00	236	371	507	573
NM_018235	CNDP2	0.01	-0.17	1479	1621	2903	2418
NM_001168647	CNKSR2	0.27	0.00	33	65	56	68
NM_173515	CNKSR3	0.07	-0.07	435	530	320	250
NM_004368	CNN2	0.11	-0.61	2892	3309	5484	3425
NM_033133	CNP	0.07	0.00	2696	3004	5243	5261
NM_006586	CNPY3	0.43	0.00	803	1200	2028	2176
NM_015463	CNRIP1	0.34	0.00	731	1037	1333	1299
NM_152609	CNST	0.28	0.00	1781	2324	2105	2211
NM_007018	CNTRL	0.04	-0.33	273	340	443	296
NM_001040431	COA3	0.13	0.00	311	405	1181	1105
NM_016565	COA4	0.25	-0.07	630	845	1198	1033
NM_001206641	COA6	1.93	0.00	36	208	204	203
NM_023077	COA7	0.45	-0.13	292	474	611	484
NM_015386	COG4	0.31	-0.02	924	1270	2489	2292
NM_153603	COG7	0.10	0.00	696	843	1160	1209
NM_032382	COG8	0.19	0.00	624	806	1248	1244
NM_001854	COL11A1	0.31	0.00	2126	2815	3910	3924
NM_001849	COL6A2	0.03	0.00	17602	18385	31346	31434
NM_152516	COMMD1	0.19	-0.18	270	371	803	627
NM_001287392	COMMD6	0.18	0.00	218	304	699	651
NM_144589	COMTD1	0.50	0.00	17	46	87	65
NM_007263	COPE	0.11	0.00	3180	3636	5840	6035
NM_016128	COPG1	0.30	0.00	8316	10594	13545	13268
NM_012133	COPG2	0.06	0.00	246	312	709	802
NM_003653	COPS3	0.28	0.00	738	1002	1314	1340
NM_006833	COPS6	0.03	-0.16	1970	2160	4889	4159
NM_001282950	COPS7B	0.02	0.00	749	851	1266	1153
NM_001099337	COQ10A	0.07	0.00	97	138	148	144
NM_016035	COQ4	0.04	-0.29	203	260	1023	750
NM_001018070	CORO1B	0.18	0.00	1592	1956	3161	3129
NM_014325	CORO1C	0.33	0.00	17437	22410	26274	25663
NM_052820	CORO2A	0.04	-0.12	201	257	383	294
NM_024535	CORO7	0.90	0.00	166	383	722	691
NM_001201479	CORO7-PAM16	0.54	0.00	348	590	1015	1004
NM_001303	COX10	0.22	0.00	244	346	331	375
NM_004375	COX11	0.18	0.00	293	398	566	579
NM_078470	COX15	0.16	0.00	562	715	1208	1150
NM_001863	COX6B1	0.40	-0.12	1002	1459	3288	2848

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001865	COX7A2	0.28	0.00	732	996	1346	1229
NM_004718	COX7A2L	0.79	0.00	775	1488	2092	1998
NM_001866	COX7B	0.61	0.00	410	723	1011	985
NM_001867	COX7C	0.05	-0.03	662	776	1123	996
NM_004074	COX8A	0.58	-0.40	1081	1764	2993	2116
NM_024913	CPED1	0.04	0.00	1125	1268	1934	1911
NM_003915	CPNE1	0.20	0.00	3287	3981	5580	5490
NM_152727	CPNE2	0.11	-0.07	599	734	851	719
NM_001122633	CPS1	0.28	-0.13	102	166	320	240
NM_013291	CPSF1	0.05	0.00	2011	2238	3090	3209
NM_017437	CPSF2	0.14	0.00	1234	1487	2263	2340
NM_016207	CPSF3	0.37	0.00	452	675	1025	1103
NM_001256456	CPSF3L	0.57	-0.09	995	1625	2406	2107
NM_007007	CPSF6	0.24	0.00	1047	1356	1822	1830
NM_001136040	CPSF7	0.24	0.00	1257	1620	1537	1671
NM_001876	CPT1A	0.04	-0.06	2237	2467	4074	3697
NM_001136052	CPT1C	0.51	0.00	83	162	208	207
NM_000098	CPT2	0.04	0.00	288	356	657	590
NM_001029885	CPTP	0.18	0.00	351	470	757	745
NM_198148	CPXM2	0.07	-1.27	73	109	237	72
NM_001144958	CRACR2A	0.23	-0.01	174	256	514	438
NM_003805	CRADD	0.15	0.00	217	297	304	349
NM_194071	CREB3L2	0.25	0.00	9787	12023	11617	11621
NM_015986	CRLF3	0.06	0.00	388	475	428	486
NM_014675	CROCC	0.03	-0.02	136	181	387	320
NM_001098482	CRTC1	0.08	0.00	260	333	534	538
NM_001130042	CRYZ	0.22	0.00	311	432	1102	1018
NM_004077	CS	0.13	-0.15	1943	2282	3980	3408
NM_001316	CSE1L	0.14	-0.14	2065	2432	3818	3283
NM_022048	CSNK1G1	0.15	-0.03	755	936	1425	1277
NM_001897	CSPG4	0.12	0.00	2905	3339	7803	7933
NM_020536	CSRP2BP	0.29	0.00	465	655	998	980
NM_001324	CSTF1	0.08	0.00	517	628	759	795
NM_001325	CSTF2	0.21	-0.06	333	455	709	599
NM_015235	CSTF2T	0.18	0.00	534	690	882	854
NM_001326	CSTF3	0.17	0.00	314	421	568	616
NM_001012614	CTBP1	0.15	0.00	2861	3363	4706	4693
NM_015343	CTDNEP1	0.36	-0.22	854	1217	1593	1250
NM_001008392	CTDSPL	0.12	0.00	723	881	1235	1325

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001085458	CTNND1	0.23	0.00	2836	3534	5823	5965
NM_175859	CTPS2	0.33	-0.04	240	365	620	525
NM_001814	CTSC	0.19	-0.35	921	1163	607	412
NM_004079	CTSS	0.20	0.00	14	34	137	146
NM_005231	CTTN	0.23	-0.04	8090	9832	20056	19079
NM_033427	CTTNBP2	0.51	0.00	19	50	435	460
NM_145232	CTU1	0.24	0.00	46	83	46	59
NM_024040	CUEDC2	0.26	-0.37	596	811	2075	1486
NM_001079872	CUL4B	0.23	-0.06	1410	1799	3558	3222
NM_020943	CWC22	0.02	0.00	236	293	412	453
NM_199168	CXCL12	0.04	0.00	3249	3535	3022	3081
NM_001171907	CXorf40A	0.58	0.00	215	391	412	397
NM_001013845	CXorf40B	0.26	0.00	392	549	678	599
NM_001161454	CYB561A3	0.02	0.00	952	1073	1932	1813
NM_001914	CYB5A	0.63	-0.16	109	221	576	445
NM_030579	CYB5B	0.47	-0.06	890	1366	2360	2113
NM_016229	CYB5R2	0.28	0.00	136	213	287	259
NM_032412	CYSTM1	0.29	-0.15	473	665	3088	2612
NM_145056	DACT3	0.29	0.00	47	87	250	237
NM_033657	DAP3	0.33	0.00	1061	1460	2579	2579
NM_014326	DAPK2	1.38	0.00	6	49	89	91
NM_001348	DAPK3	0.29	-0.04	1889	2474	3371	3100
NM_001141969	DAXX	0.30	0.00	1039	1411	2036	2081
NM_018959	DAZAP1	0.10	-0.26	1886	2179	1612	1231
NM_001178042	DBI	0.32	0.00	475	683	1142	1068
NM_001048222	DBNDD2	0.05	0.00	804	928	595	566
NM_001014436	DBNL	0.45	0.00	1548	2279	6118	5946
NM_025230	DCAF11	0.14	0.00	851	1041	1932	1926
NM_015397	DCAF12	0.37	0.00	802	1151	1264	1368
NM_015420	DCAF13	0.44	0.00	418	657	969	900
NM_017741	DCAF16	0.26	-0.04	492	678	747	643
NM_005828	DCAF7	0.17	0.00	2298	2766	3843	3797
NM_000788	DCK	0.79	0.00	393	782	826	876
NM_152640	DCP1B	0.22	0.00	183	267	543	553
NM_001261412	DCTN2	0.43	-0.06	2286	3274	6249	5754
NM_001281426	DCTN3	0.30	0.00	510	716	1508	1536
NM_001199743	DCTN5	0.17	0.00	1795	2171	4047	4126
NM_024096	DCTPP1	0.57	-0.17	422	723	809	636
NM_032299	DCUN1D5	0.30	0.00	511	722	751	797

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001195218	DCXR	0.33	0.00	429	625	792	702
NM_024050	DDA1	0.01	0.00	739	837	1079	1168
NM_013974	DDAH2	0.16	0.00	794	994	1828	1911
NM_000107	DDB2	0.33	0.00	570	814	932	1000
NM_032341	DDI2	0.12	0.00	260	341	497	556
NM_145244	DDIT4L	0.33	0.00	113	187	146	139
NM_001014796	DDR2	0.10	0.00	3392	3842	10259	9911
NM_023935	DDRGK1	0.08	0.00	516	626	1383	1312
NM_007242	DDX19B	0.02	0.00	621	717	998	1004
NM_007204	DDX20	0.24	0.00	366	508	476	469
NM_004728	DDX21	0.39	-0.01	3021	4194	3937	3717
NM_004818	DDX23	0.18	-0.01	1253	1549	2019	1863
NM_022779	DDX31	0.35	0.00	250	386	695	678
NM_005804	DDX39A	0.23	-0.58	1537	1946	2019	1238
NM_004640	DDX39B	0.07	-0.06	1352	1552	2489	2229
NM_014829	DDX46	0.01	0.00	1239	1369	1285	1320
NM_001111322	DDX54	0.05	0.00	1723	1922	2446	2327
NM_020936	DDX55	0.25	0.00	347	487	524	479
NM_019082	DDX56	0.14	0.00	1199	1445	1818	1885
NM_014314	DDX58	0.09	0.00	119	167	420	362
NM_017631	DDX60	0.23	0.00	120	185	281	235
NM_032998	DEDD	0.20	0.00	661	854	1354	1270
NM_020946	DENND1A	0.34	0.00	506	732	1142	1194
NM_001195215	DENND1B	0.02	0.00	218	273	430	494
NM_014957	DENND3	0.13	0.00	485	612	720	704
NM_014856	DENND4B	0.08	0.00	1043	1219	1237	1253
NM_152678	DENND6A	0.09	-0.17	227	297	347	255
NM_018369	DEPDC1B	1.39	0.00	27	115	54	48
NM_001077242	DEPDC7	0.60	0.00	70	148	227	237
NM_022783	DEPTOR	0.09	-0.24	42	70	96	55
NM_015954	DERA	0.29	0.00	407	578	749	717
NM_001927	DES	0.43	-0.07	362	569	135	94
NM_213566	DFFA	0.09	-0.01	886	1047	1840	1691
NM_022719	DGCR14	0.58	0.00	258	462	688	671
NM_001199266	DGKZ	0.37	0.00	135	225	287	251
NM_000791	DHFR	0.13	0.00	320	415	331	346
NM_001930	DHPS	0.05	0.00	1104	1262	2159	2013
NM_001136050	DHRS1	0.57	0.00	153	286	1071	1046
NM_024308	DHRS11	0.74	-0.17	35	92	154	102

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001193636	DHRS4L2	0.17	-0.42	103	156	308	185
NM_001358	DHX15	0.11	-0.01	3010	3437	4321	4085
NM_003587	DHX16	0.40	-0.03	1402	2005	2196	2006
NM_019030	DHX29	0.29	0.00	550	768	1117	1233
NM_020162	DHX33	0.25	0.00	687	921	880	893
NM_014681	DHX34	0.18	0.00	472	616	638	682
NM_032656	DHX37	0.30	0.00	865	1178	1468	1381
NM_004941	DHX8	0.13	-0.16	1247	1494	2219	1852
NM_005219	DIAPH1	0.45	0.00	4232	6062	7185	7037
NM_001042517	DIAPH3	0.03	-0.63	1363	1521	1050	603
NM_014473	DIMT1	0.08	-0.02	680	809	1034	917
NM_001931	DLAT	0.22	0.00	785	1023	1506	1444
NM_006094	DLC1	0.25	0.00	7520	9279	8412	8517
NM_004405	DLX2	0.74	0.00	19	58	125	155
NM_019100	DMAP1	0.52	0.00	315	534	1138	1148
NM_001174116	DMXL2	0.34	0.00	367	544	1333	1340
NM_001080449	DNA2	0.20	0.00	145	214	114	146
NM_207437	DNAH10	0.16	0.00	63	102	183	196
NM_001002762	DNAJB12	0.06	0.00	1360	1542	2597	2547
NM_018198	DNAJC11	0.09	-0.06	1429	1652	2298	2055
NM_018163	DNAJC17	0.15	-0.01	146	208	266	213
NM_152686	DNAJC18	0.20	0.00	118	178	441	449
NM_145261	DNAJC19	0.38	0.00	29	63	116	92
NM_003315	DNAJC7	0.20	0.00	782	1003	1672	1608
NM_014280	DNAJC8	0.39	0.00	806	1174	1701	1634
NM_015190	DNAJC9	0.09	0.00	499	610	557	573
NM_005740	DNAL4	0.74	0.00	85	192	356	386
NM_194249	DND1	0.38	0.00	147	243	200	222
NM_001278464	DNM1L	0.13	-0.02	1825	2155	3107	2880
NM_001130823	DNMT1	0.04	-0.19	3614	3923	2566	2102
NM_006892	DNMT3B	0.97	0.00	52	148	96	96
NM_006443	DNPH1	0.36	0.00	177	284	720	778
NM_001282062	DOC2A	0.51	-0.08	100	189	225	168
NM_001290223	DOCK1	0.20	0.00	2592	3172	5650	5560
NM_144658	DOCK11	0.17	0.00	128	188	474	506
NM_001145165	DOHH	0.28	0.00	121	192	210	170
NM_005128	DOPEY2	0.03	-0.13	917	1037	2926	2512
NM_001384	DPH2	0.10	0.00	538	659	636	689
NM_080650	DPH6	0.22	0.00	31	60	87	59

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_003863	DPM2	0.42	-0.18	544	826	1377	1103
NM_153741	DPM3	0.54	-0.20	176	319	745	569
NM_005700	DPP3	0.02	0.00	818	926	1599	1595
NM_004147	DRG1	0.21	-0.12	963	1227	1689	1427
NM_001388	DRG2	0.10	-0.18	761	914	1564	1261
NM_032160	DSEL	0.02	-0.19	2349	2550	4151	3460
NM_080820	DTD1	0.08	0.00	785	926	1508	1623
NM_080664	DTD2	0.19	-0.06	155	225	387	311
NM_016448	DTL	0.28	-0.37	839	1135	518	342
NM_001271667	DTNBP1	0.36	0.00	171	275	258	268
NM_020892	DTX2	0.21	0.00	459	614	564	616
NM_138287	DTX3L	0.02	0.00	523	610	759	689
NM_012145	DTYMK	0.19	-0.05	705	901	1177	1028
NM_022156	DUS1L	0.07	0.00	854	1001	1104	1105
NM_020175	DUS3L	0.17	-0.08	342	455	408	325
NM_007240	DUSP12	0.14	0.00	215	291	343	396
NM_007026	DUSP14	0.12	-0.24	3052	3523	6002	4867
NM_001142314	DUSP19	1.19	0.00	10	57	52	65
NM_001947	DUSP7	0.10	0.00	937	1115	807	847
NM_001271786	DYNC1I2	0.55	0.00	334	575	1210	1122
NM_016141	DYNC1LI1	0.11	0.00	681	831	1121	1225
NM_001281729	DYNLRB1	0.09	0.00	1688	1939	3334	3384
NM_006519	DYNLT1	0.23	-0.13	1405	1787	2627	2240
NM_198968	DZIP1	0.16	0.00	944	1165	1986	1887
NM_001950	E2F4	0.36	-0.04	1548	2145	2394	2179
NM_022659	EBF2	0.07	0.00	502	605	356	373
NM_001398	ECH1	0.09	0.00	1234	1439	1537	1625
NM_001002030	ECHDC1	0.20	0.00	556	726	936	946
NM_024693	ECHDC3	0.44	0.00	42	88	31	48
NM_001258316	ECT2	0.35	-0.01	599	862	940	835
NM_001142443	EDC3	0.26	0.00	1042	1369	1553	1475
NM_018217	EDEM2	0.48	0.00	334	548	1146	1131
NM_001959	EEF1B2	0.46	-0.03	684	1058	2015	1835
NM_032378	EEF1D	0.19	-0.14	1974	2423	3321	2834
NM_004280	EEF1E1	0.90	0.00	80	202	173	214
NM_001404	EEF1G	0.44	-0.04	6878	9651	16581	15728
NM_032437	EFCAB7	0.34	0.00	16	40	79	111
NM_015137	EFR3A	0.34	0.00	1394	1918	4394	4397
NM_001258354	EFTUD2	0.26	-0.02	2650	3368	5207	4906

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_005228	EGFR	0.06	-0.09	4980	5431	5971	5368
NM_080732	EGLN2	0.04	-0.10	1313	1473	2365	2059
NM_006795	EHD1	0.24	0.00	2726	3424	3275	3390
NM_139265	EHD4	0.27	0.00	1874	2429	3729	3617
NM_014335	EID1	0.23	0.00	1313	1680	3411	3558
NM_001008394	EID3	0.19	0.00	47	82	108	120
NM_001242481	EIF1AD	0.11	0.00	618	757	655	636
NM_005875	EIF1B	0.14	0.00	526	662	576	599
NM_032025	EIF2A	0.11	0.00	863	1034	1564	1597
NM_002759	EIF2AK2	0.02	0.00	751	854	1510	1408
NM_001013703	EIF2AK4	0.30	0.00	2757	3603	6578	6493
NM_014239	EIF2B2	0.06	0.00	919	1063	1807	1885
NM_020365	EIF2B3	0.17	0.00	505	653	1123	1128
NM_006893	EIF2D	0.33	-0.17	682	966	1481	1201
NM_004094	EIF2S1	0.09	0.00	1730	1983	2477	2615
NM_001415	EIF2S3	0.49	0.00	692	1090	1576	1619
NM_003753	EIF3D	0.36	0.00	4345	5823	10710	10506
NM_003754	EIF3F	0.22	-0.28	748	977	1239	924
NM_003755	EIF3G	0.26	-0.05	2266	2896	4078	3747
NM_003756	EIF3H	0.49	0.00	1673	2530	3637	3623
NM_003757	EIF3I	0.18	-0.09	3964	4708	7709	6965
NM_003758	EIF3J	0.38	0.00	456	684	659	640
NM_013234	EIF3K	0.52	-0.10	661	1064	2071	1793
NM_016091	EIF3L	0.38	-0.03	1911	2668	4835	4508
NM_006360	EIF3M	0.03	0.01	1732	1908	2354	2529
NM_001416	EIF4A1	0.43	-0.29	5254	7364	12022	9547
NM_014740	EIF4A3	0.01	0.00	2140	2314	1868	1926
NM_001417	EIF4B	0.46	-0.01	2393	3490	6037	5747
NM_001130679	EIF4E	0.32	0.00	315	467	730	732
NM_001282958	EIF4E2	0.13	0.00	1109	1334	1242	1364
NM_003732	EIF4EBP3	0.18	0.00	44	77	212	213
NM_001970	EIF5A	0.28	-0.18	3606	4616	7495	6346
NM_001099692	EIF5AL1	0.08	-0.01	4612	5115	8013	7662
NM_002212	EIF6	0.13	-0.01	3082	3571	5636	5338
NM_018127	ELAC2	0.14	0.00	2123	2505	3606	3732
NM_001114123	ELK1	0.21	0.00	1292	1633	1452	1484
NM_006532	ELL	0.23	0.00	481	649	990	891
NM_025165	ELL3	1.07	0.00	15	61	106	137
NM_153702	ELMOD2	0.25	0.00	250	361	611	664

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001278939	ELN	0.50	-0.41	2316	3480	641	416
NM_203413	ELP5	0.18	0.00	631	810	1038	935
NM_006067	EMC8	0.02	0.00	734	837	869	874
NM_001257370	EME2	0.64	0.00	8	37	98	131
NM_001193268	EML2	0.05	0.00	515	614	1027	945
NM_001424	EMP2	0.12	-0.08	1343	1591	1533	1329
NM_001426	EN1	0.49	-0.09	285	475	930	778
NM_015036	ENDOD1	0.05	0.00	1321	1493	4041	4142
NM_004435	ENDOG	0.18	0.01	582	750	971	1081
NM_000118	ENG	0.13	-0.05	13055	14733	15252	14379
NM_001977	ENPEP	0.51	0.00	28	67	31	41
NM_006209	ENPP2	0.05	-0.31	491	587	1547	1137
NM_207043	ENSA	0.39	0.00	472	709	1044	1139
NM_001098175	ENTPD1	0.05	0.00	353	433	430	455
NM_001128930	ENTPD4	0.06	0.00	2349	2624	3051	3242
NM_001247	ENTPD6	0.17	0.00	1414	1735	2733	2850
NM_001278689	EOGT	0.09	0.00	493	603	1175	1203
NM_001430	EPAS1	0.35	0.00	2929	3958	8874	9052
NM_001431	EPB41L2	0.16	0.00	1206	1479	2134	2205
NM_018424	EPB41L4B	0.09	0.00	38	65	58	85
NM_004431	EPHA2	0.21	0.00	2827	3467	1283	1384
NM_004444	EPHB4	0.15	-0.15	402	521	468	359
NM_014805	EPM2AIP1	0.36	0.00	341	516	840	928
NM_001130072	EPN1	0.09	0.00	1684	1935	2516	2643
NM_001258374	EPS15L1	0.07	0.00	817	961	1246	1368
NM_004447	EPS8	0.22	-0.12	2317	2882	5800	5102
NM_005702	ERAL1	0.24	-0.03	824	1084	1524	1372
NM_004448	ERBB2	0.18	-0.01	1706	2090	3953	3726
NM_000400	ERCC2	0.21	-0.18	2075	2576	4122	3460
NM_000122	ERCC3	0.09	0.00	1226	1424	1961	2039
NM_005236	ERCC4	0.27	0.00	293	421	497	477
NM_001432	EREG	0.63	0.00	108	220	46	68
NM_006494	ERF	0.18	0.00	826	1042	1578	1623
NM_004450	ERH	0.07	0.00	306	383	634	597
NM_006459	ERLIN1	0.02	0.00	1609	1768	3257	3205
NM_005238	ETS1	0.19	-0.06	4177	5002	4465	4065
NM_005239	ETS2	0.28	0.00	839	1133	769	758
NM_001987	ETV6	0.14	0.00	771	952	984	1063
NM_001135032	EVA1A	0.32	-0.09	2051	2744	3371	2991

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_018166	EVA1B	0.04	-0.32	593	696	1160	839
NM_013986	EWSR1	0.40	-0.34	1983	2806	3094	2296
NM_017820	EXD3	0.11	-0.10	60	95	220	161
NM_130398	EXO1	0.29	-0.43	322	467	171	94
NM_016046	EXOSC1	0.42	0.00	261	418	903	835
NM_001001998	EXOSC10	0.08	0.00	1825	2073	2560	2429
NM_014285	EXOSC2	0.28	-0.23	524	726	1002	762
NM_058219	EXOSC6	0.47	-0.16	332	540	626	488
NM_015004	EXOSC7	0.22	-0.07	373	510	780	656
NM_001034194	EXOSC9	0.27	0.00	812	1089	905	826
NM_001440	EXTL3	0.40	-0.11	1829	2599	5143	4530
NM_000137	FAH	0.36	-0.30	302	460	2019	1519
NM_016044	FAHD2A	0.02	-0.25	249	307	620	451
NM_001098832	FAM104A	0.14	0.00	534	671	1065	1030
NM_001282696	FAM107B	0.04	0.00	249	312	46	55
NM_014719	FAM115A	0.07	0.00	736	870	2560	2527
NM_024556	FAM118B	0.09	0.00	357	447	682	669
NM_001286722	FAM120A	0.27	0.00	6257	7828	11552	11833
NM_198841	FAM120AOS	0.11	0.00	826	995	1728	1745
NM_032448	FAM120B	0.13	0.00	901	1093	2213	2248
NM_017848	FAM120C	0.41	0.00	143	242	299	309
NM_138333	FAM122A	0.49	0.00	213	366	543	508
NM_032581	FAM126A	0.13	0.00	1280	1533	2435	2368
NM_001078172	FAM127B	0.16	0.00	464	597	884	933
NM_001078173	FAM127C	0.42	0.00	591	897	1002	1011
NM_052966	FAM129A	0.23	-0.19	1922	2428	5659	4730
NM_001031690	FAM131B	1.36	0.00	16	77	316	281
NM_022749	FAM160B2	0.26	0.00	1027	1353	2518	2510
NM_001085480	FAM162B	0.04	0.00	49	77	2	9
NM_032648	FAM167B	0.31	0.00	60	108	83	74
NM_198475	FAM171A2	1.17	0.00	10	56	195	201
NM_023933	FAM173A	0.87	0.00	19	63	112	116
NM_207446	FAM174B	0.01	0.00	39	63	64	79
NM_139076	FAM175A	0.32	0.00	82	141	262	242
NM_032182	FAM175B	0.32	0.01	463	666	717	811
NM_032222	FAM188B	0.07	0.00	24	45	152	128
NM_006589	FAM189B	0.05	0.00	843	971	2088	2150
NM_024946	FAM192A	0.13	0.00	433	550	940	876
NM_207368	FAM195B	0.50	-0.10	991	1540	3354	2952

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001129891	FAM196B	0.16	0.00	794	994	2011	2018
NM_017832	FAM206A	0.47	0.00	116	210	399	383
NM_001243746	FAM20A	0.30	0.00	44	83	58	67
NM_020223	FAM20C	0.04	0.00	2522	2762	5790	6063
NM_001005751	FAM21A	0.28	0.00	594	816	1585	1455
NM_015262	FAM21C	0.20	0.00	612	795	1633	1571
NM_001291328	FAM228B	0.67	-0.20	100	211	618	466
NM_001033564	FAM229B	0.22	0.00	46	82	164	176
NM_152644	FAM24B	0.36	0.00	55	104	92	83
NM_153711	FAM26E	0.46	-0.16	270	443	942	752
NM_014077	FAM32A	0.47	0.00	988	1500	2094	2205
NM_019054	FAM35A	0.02	0.00	276	339	424	434
NM_153690	FAM43A	0.16	0.00	189	264	245	214
NM_052943	FAM46B	0.73	-0.36	175	360	127	70
NM_001256763	FAM49B	0.25	0.00	267	383	312	296
NM_001013622	FAM53A	0.97	-0.17	17	62	42	20
NM_016605	FAM53C	0.25	0.00	925	1217	2061	2007
NM_001130997	FAM58A	0.56	0.00	279	490	574	599
NM_019013	FAM64A	0.16	-1.32	173	244	245	72
NM_001193523	FAM65A	0.43	-0.02	2191	3147	4211	3944
NM_001100910	FAM72B	0.19	0.00	29	56	56	41
NM_032809	FAM73B	0.53	-0.10	321	544	836	693
NM_030919	FAM83D	0.12	-0.70	450	566	545	283
NM_201400	FAM86A	0.20	0.00	407	543	840	769
NM_001083537	FAM86B1	0.06	0.00	22	42	100	94
NM_001099653	FAM86C1	0.18	0.00	104	158	231	190
NM_144963	FAM91A1	0.45	0.00	403	637	882	937
NM_001289108	FAM96A	0.27	0.00	204	303	497	442
NM_015475	FAM98A	0.18	0.00	1861	2266	2373	2501
NM_000135	FANCA	0.17	0.00	845	1059	695	641
NM_001018115	FANCD2	0.16	-0.38	317	421	327	205
NM_001113378	FANCI	0.06	0.00	1065	1224	1165	1055
NM_005766	FARP1	0.16	0.00	3748	4406	5754	6026
NM_006567	FARS2	0.09	0.00	159	215	568	521
NM_004461	FARSA	0.25	0.00	1422	1840	1722	1821
NM_005687	FARSB	0.23	-0.21	627	832	1518	1201
NM_000043	FAS	0.18	0.00	502	653	1460	1462
NM_001136193	FASTKD2	0.26	-0.12	649	879	1266	1054
NM_024091	FASTKD3	0.16	0.00	87	134	162	165

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_021826	FASTKD5	0.31	0.00	323	473	532	553
NM_001291285	FAT4	0.10	-0.50	1098	1297	1512	974
NM_001997	FAU	0.95	0.00	360	805	1069	1055
NM_001080542	FBF1	0.68	0.00	69	154	210	198
NM_001436	FBL	0.34	-0.01	1064	1480	1221	1098
NM_017556	FBLIM1	0.40	-0.02	968	1412	3271	3044
NM_001004019	FBLN2	0.16	0.00	6669	7750	2768	2769
NM_017703	FBXL12	0.38	-0.01	232	367	686	597
NM_001278716	FBXL4	0.20	0.00	274	378	597	680
NM_001193534	FBXL5	0.16	0.00	1270	1552	2855	2874
NM_032807	FBXO18	0.19	0.00	1782	2185	3860	3871
NM_147188	FBXO22	0.11	0.00	412	519	930	919
NM_012175	FBXO3	0.16	0.00	302	404	690	780
NM_030793	FBXO38	0.28	0.00	721	983	1208	1316
NM_018998	FBXW5	0.30	-0.15	2712	3547	5736	4928
NM_153348	FBXW8	0.43	0.01	459	710	1073	1190
NM_001136019	FCGRT	0.11	0.00	764	923	2213	2346
NM_001002901	FCRLB	0.08	0.00	61	94	171	139
NM_001135821	FDPS	0.09	0.00	655	790	1437	1429
NM_004109	FDX1	0.06	0.00	61	93	179	166
NM_001031734	FDX1L	0.14	-0.13	258	345	838	677
NM_001258013	FDXR	0.10	-0.47	119	168	430	259
NM_018708	FEM1A	0.20	0.00	1111	1401	1628	1634
NM_004111	FEN1	0.19	-0.46	1865	2292	1339	880
NM_001042548	FEZ2	0.10	0.00	1599	1858	3404	3237
NM_004463	FGD1	0.18	0.00	700	890	1221	1318
NM_004464	FGF5	0.34	-0.12	4322	5738	3329	2895
NM_001113411	FGGY	0.34	0.00	38	76	258	262
NM_000143	FH	0.29	0.00	1346	1793	1185	1091
NM_004214	FIBP	0.49	0.00	801	1251	2421	2320
NM_001080472	FITM2	0.24	0.00	130	199	287	266
NM_015258	FKBP15	0.25	-0.05	1391	1797	3111	2835
NM_002014	FKBP4	0.16	0.00	740	928	1395	1355
NM_025207	FLAD1	0.10	-0.08	426	532	1034	878
NM_005803	FLOT1	0.39	-0.15	1488	2112	4993	4283
NM_015033	FNBP1	0.02	0.00	1181	1315	1526	1649
NM_001024948	FNBP1L	0.28	0.00	164	252	374	436
NM_002028	FNTB	0.16	0.00	833	1038	1456	1573
NM_000804	FOLR3	0.31	0.00	115	188	707	765

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_006732	FOSB	0.04	0.00	66	98	54	70
NM_005438	FOSL1	0.33	-0.16	4479	5899	3947	3338
NM_005253	FOSL2	0.13	0.00	3486	4019	5515	5296
NM_004472	FOXD1	0.14	0.00	1633	1950	2279	2442
NM_005250	FOXL1	0.06	0.00	662	779	1192	1311
NM_202002	FOXM1	0.26	-0.86	2104	2690	2175	1098
NM_001018078	FPGS	0.23	-0.23	1094	1406	2521	2006
NM_001193306	FPR1	0.52	0.00	34	78	158	155
NM_012083	FRAT2	0.76	0.00	32	87	79	102
NM_174938	FRMD3	0.15	-0.29	654	819	851	614
NM_018027	FRMD4A	0.05	0.00	3154	3449	3822	4015
NM_001267046	FRMD6	0.24	-0.05	10248	12522	23265	21989
NM_014728	FRMPD4	0.05	0.00	216	277	308	259
NM_001013660	FRRS1	0.29	0.00	51	93	237	222
NM_006653	FRS3	0.16	0.00	64	103	79	92
NM_023037	FRY	0.10	-0.22	263	342	674	503
NM_003088	FSCN1	0.12	-0.22	5767	6530	6033	4967
NM_013393	FTSJ2	0.05	0.00	495	592	711	769
NM_003902	FUBP1	0.06	-0.16	2579	2854	3157	2651
NM_003934	FUBP3	0.11	0.00	1631	1901	2955	2823
NM_001170634	FUS	0.08	-0.03	4400	4886	5644	5299
NM_032664	FUT10	0.06	0.00	219	282	433	499
NM_001013439	FXR1	0.06	0.00	1488	1685	2762	2885
NM_024513	FYCO1	0.24	0.00	694	921	2880	2808
NM_003468	FZD5	0.42	0.00	47	95	89	91
NM_003508	FZD9	0.91	0.00	13	51	10	15
NM_005754	G3BP1	0.55	-0.06	1586	2498	2968	2675
NM_007278	GABARAP	0.23	-0.03	1187	1521	3402	3155
NM_005254	GABPB1	0.37	0.00	310	474	607	671
NM_015675	GADD45B	0.26	0.00	2057	2633	1404	1416
NM_052850	GADD45GIP1	0.10	0.00	588	715	1447	1340
NM_005255	GAK	0.17	0.00	1908	2302	3772	3750
NM_024637	GAL3ST4	0.17	0.00	136	198	493	434
NM_000403	GALE	0.11	-0.23	637	779	938	713
NM_001001556	GALK2	0.02	0.00	350	419	522	475
NM_054110	GALNT15	0.36	-0.65	79	140	749	414
NM_004482	GALNT3	0.50	0.00	91	174	54	79
NM_000155	GALT	0.04	-0.12	248	311	830	677
NM_000156	GAMT	0.07	-0.22	105	148	630	468

Table 6A: Differentially Upregulated Genes in SR + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_198141	GANC	0.61	0.00	246	450	765	749
NM_014364	GAPDHS	0.24	-0.27	37	70	131	78
NM_018983	GAR1	0.08	0.00	130	179	148	126
NM_001136005	GART	0.25	0.00	1086	1421	1803	1856
NM_006478	GAS2L1	0.09	-0.01	612	738	1154	1035
NM_174942	GAS2L3	0.38	-0.70	136	228	191	87
NM_017660	GATAD2A	0.06	0.00	3058	3368	4147	4347
NM_004564	GATB	0.26	-0.29	303	433	853	619
NM_001282629	GBGT1	0.66	-0.03	60	136	141	102
NM_003203	GCFC2	0.04	0.00	152	201	287	294
NM_006836	GCN1L1	0.11	0.00	7506	8432	12330	12454
NM_004962	GDF10	0.62	0.00	25	66	35	44
NM_001288824	GDF9	0.34	0.00	122	202	327	338
NM_001494	GDI2	0.22	-0.02	4008	4895	6391	6041
NM_001252156	GEMIN5	0.11	-0.09	910	1090	1439	1233
NM_024775	GEMIN6	0.04	0.00	123	167	241	209
NM_017856	GEMIN8	0.33	0.00	147	236	464	536
NM_001130009	GEN1	0.04	0.00	193	248	229	226
NM_024996	GFM1	0.30	-0.01	961	1308	1832	1682
NM_005110	GFPT2	0.28	0.00	1557	2038	4055	4140
NM_001099781	GGT5	0.15	-0.90	21	43	81	26
NM_001080383	GJC1	0.11	-0.08	1437	1688	1720	1497
NM_000169	GLA	0.35	0.00	416	615	1183	1250
NM_001003722	GLE1	0.21	0.00	705	917	1279	1198
NM_005270	GLI2	0.10	0.00	1090	1289	1707	1706
NM_006708	GLO1	0.37	-0.09	892	1280	2770	2440
NM_016080	GLOD4	0.12	0.00	711	868	1389	1329
NM_197962	GLRX2	0.85	0.00	45	121	127	120
NM_016417	GLRX5	0.03	0.00	541	631	665	654
NM_001256310	GLS	0.07	0.00	6267	6870	7611	7628
NM_015710	GLTSCR2	0.79	-0.03	368	736	990	871
NM_002065	GLUL	0.31	-0.41	2045	2708	3789	2686
NM_032569	GLYR1	0.03	0.00	1637	1811	3136	2991
NM_000405	GM2A	0.17	0.00	900	1125	3396	3416
NM_013334	GMPPB	0.01	0.00	678	774	1106	1079
NM_003875	GMPS	0.39	0.00	779	1141	1142	1192
NM_002069	GNAI1	0.22	0.00	820	1062	1460	1519
NM_053004	GNB1L	0.27	0.00	130	204	198	176
NM_006098	GNB2L1	0.14	-0.01	16273	18409	33137	32212

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_021629	GNB4	0.20	0.00	2087	2568	2676	2530
NM_004126	GNG11	0.02	-0.03	1274	1410	4480	4166
NM_005274	GNG5	0.53	0.00	246	429	767	808
NM_013285	GNL2	0.09	0.00	2079	2377	2252	2111
NM_001184819	GNL3L	0.20	0.00	1299	1631	2048	1926
NM_014236	GNPAT	0.38	0.00	575	851	2080	2159
NM_005471	GNPDA1	0.33	-0.23	963	1332	2510	2000
NM_002077	GOLGA1	0.21	0.00	534	708	1325	1401
NM_001174124	GOLGA7	0.45	0.00	538	837	1302	1296
NM_031899	GORASP1	0.34	0.00	1191	1648	2331	2310
NM_018559	GPALPP1	0.03	0.00	128	171	360	336
NM_018040	GPATCH2	0.63	0.01	115	232	418	490
NM_005708	GPC6	0.13	-0.30	505	636	1206	885
NM_019593	GPCPD1	0.37	0.00	228	358	643	688
NM_001083112	GPD2	0.20	0.00	774	995	1004	1020
NM_015698	GPKOW	0.45	0.00	360	574	836	819
NM_001080452	GPR108	0.38	0.00	697	1014	2435	2512
NM_153835	GPR113	0.38	0.00	29	63	58	72
NM_032777	GPR124	0.05	-0.16	1568	1763	2529	2115
NM_001170880	GPR137	0.23	0.00	345	477	821	869
NM_207370	GPR153	0.36	0.00	59	110	299	340
NM_018969	GPR173	0.13	0.00	45	76	204	176
NM_005281	GPR3	0.21	0.00	67	111	81	57
NM_001508	GPR39	0.32	0.00	332	490	85	113
NM_001097613	GPR89A	0.18	0.00	210	293	383	401
NM_016235	GPRC5B	0.08	0.00	70	106	77	105
NM_212492	GPS1	0.53	0.00	1473	2300	4053	4270
NM_004489	GPS2	0.45	0.00	213	356	476	499
NM_001145638	GPSM1	0.20	0.00	645	835	1154	1061
NM_001276501	GPSM3	0.23	-0.02	80	130	243	192
NM_201397	GPX1	0.03	-0.18	1172	1315	3188	2656
NM_001039847	GPX4	0.22	0.00	2486	3091	7584	7837
NM_015696	GPX7	0.47	-0.07	677	1050	1373	1192
NM_013372	GREM1	0.14	-0.22	183659	203725	239474	204292
NM_012203	GRHPR	0.25	-0.13	1219	1581	3575	3078
NM_005308	GRK5	0.25	-0.07	394	546	499	407
NM_001130006	GSPT1	0.20	0.00	3743	4532	4760	4930
NM_000637	GSR	0.36	0.00	966	1365	1890	2018
NM_001143679	GSTK1	0.81	-0.19	767	1488	3488	2889

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_000848	GSTM2	0.05	0.00	171	224	805	776
NM_000850	GSTM4	0.02	0.00	88	123	428	403
NM_004832	GSTO1	0.06	-0.03	1983	2217	5045	4699
NM_000853	GSTT1	0.35	0.00	220	342	670	640
NM_145870	GSTZ1	0.24	0.00	90	145	335	327
NM_002096	GTF2F1	0.19	0.00	1527	1884	2373	2512
NM_004128	GTF2F2	0.06	0.00	249	315	410	416
NM_001521	GTF3C2	0.25	0.00	1050	1375	1888	1815
NM_012086	GTF3C3	0.08	0.00	678	810	1098	1041
NM_001122823	GTF3C5	0.31	-0.09	1065	1449	2051	1786
NM_001284251	GUCD1	0.40	0.00	2120	2998	4222	4309
NM_177925	H2AFJ	0.18	-0.45	1315	1622	2263	1532
NM_138635	H2AFV	0.34	-0.05	873	1228	1414	1244
NM_002105	H2AFX	0.42	-0.26	946	1397	980	728
NM_018649	H2AFY2	0.59	-0.01	112	220	410	344
NM_002106	H2AFZ	0.28	-0.53	1961	2558	2263	1445
NM_014282	HABP4	0.27	0.00	986	1309	1807	1699
NM_001184705	HADH	0.45	0.00	442	695	1044	1078
NM_002109	HARS	0.16	0.00	1532	1858	3159	3126
NM_012208	HARS2	0.11	-0.01	309	398	824	726
NM_005328	HAS2	0.30	-0.13	4581	5898	11051	9784
NM_003642	HAT1	0.19	0.00	564	734	794	871
NM_138443	HAUS1	0.43	-0.03	133	231	227	176
NM_018097	HAUS2	0.14	0.00	340	444	786	773
NM_001166269	HAUS4	0.19	-0.03	177	254	468	390
NM_017645	HAUS6	0.11	0.00	591	727	761	745
NM_017518	HAUS7	0.62	0.00	373	668	690	636
NM_001945	HBEGF	0.27	0.00	203	303	541	591
NM_006620	HBS1L	0.15	0.00	1205	1460	2493	2521
NM_005334	HCFC1	0.11	0.00	3594	4085	4839	5087
NM_004964	HDAC1	0.75	0.00	568	1074	2032	1891
NM_032019	HDAC10	0.12	0.00	159	220	474	538
NM_178423	HDAC9	0.51	-0.08	165	295	620	510
NM_016063	HDDC2	0.17	0.00	274	370	643	665
NM_004494	HDGF	0.52	0.00	2886	4378	4700	4473
NM_001001520	HDGFRP2	0.24	0.00	869	1139	1670	1577
NM_001135565	HDHD1	0.05	0.00	491	587	559	488
NM_031219	HDHD3	0.31	0.00	84	143	183	172
NM_018072	HEATR1	0.15	0.00	1584	1906	2862	2830

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_017802	HEATR2	0.19	0.00	642	830	1183	1094
NM_024602	HECTD3	0.02	-0.04	1182	1315	2425	2198
NM_020760	HECW2	0.05	-0.09	672	784	1331	1137
NM_001289067	HELLS	0.07	-0.07	335	416	195	144
NM_133636	HELQ	0.17	0.00	124	183	308	274
NM_003922	HERC1	0.06	0.00	2713	3001	5763	5924
NM_022079	HERC4	0.13	-0.04	3367	3880	6079	5663
NM_001165967	HES7	2.24	-0.39	35	249	225	133
NM_016458	HGH1	0.22	0.00	471	631	705	645
NM_004712	HGS	0.25	0.00	3183	4013	5852	6109
NM_022475	HHIP	0.10	0.00	3852	4357	1127	1179
NM_032558	HIATL1	0.35	0.00	1374	1903	3275	3353
NM_014362	HIBCH	0.26	0.00	88	144	339	342
NM_001098202	HIC1	0.35	0.00	425	628	788	708
NM_015094	HIC2	0.03	0.00	169	219	164	185
NM_001530	HIF1A	0.15	0.00	15128	17280	27056	26902
NM_138820	HIGD2A	0.06	-0.02	556	662	1333	1198
NM_005322	HIST1H1B	0.07	-0.68	7478	8154	3354	1956
NM_003513	HIST1H2AB	0.08	-0.13	513	622	297	220
NM_003512	HIST1H2AC	0.36	-0.06	2031	2792	3369	3055
NM_021064	HIST1H2AG	0.52	-0.25	1398	2168	665	486
NM_080596	HIST1H2AH	0.12	-0.06	1096	1309	476	390
NM_003510	HIST1H2AK	0.67	0.00	487	882	412	359
NM_021062	HIST1H2BB	0.25	-0.52	874	1156	545	323
NM_003526	HIST1H2BC	0.10	-0.09	4518	5091	4074	3634
NM_138720	HIST1H2BD	0.03	0.00	3040	3280	1689	1634
NM_003522	HIST1H2BF	0.25	0.00	868	1144	412	372
NM_003518	HIST1H2BG	0.40	-0.09	1290	1848	703	580
NM_003524	HIST1H2BH	0.12	0.00	1008	1213	64	74
NM_003525	HIST1H2BI	0.36	-0.47	1494	2076	784	494
NM_021058	HIST1H2BJ	0.05	0.00	4017	4381	2130	1987
NM_003519	HIST1H2BL	0.91	-0.01	334	730	320	262
NM_003521	HIST1H2BM	0.16	-0.22	1063	1306	410	294
NM_003520	HIST1H2BN	0.22	-0.37	1498	1886	1468	1031
NM_003537	HIST1H3B	0.11	-0.54	6097	6875	2897	1859
NM_003531	HIST1H3C	0.08	-0.52	4759	5271	2009	1286
NM_003534	HIST1H3G	0.33	0.00	1843	2490	651	588
NM_003536	HIST1H3H	0.16	-0.51	1688	2035	915	566
NM_003538	HIST1H4A	0.74	0.00	395	761	220	203

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_003542	HIST1H4C	0.29	-0.15	1357	1801	1050	848
NM_175065	HIST2H2AB	0.22	-0.27	458	617	406	281
NM_001024599	HIST2H2BF	0.18	0.00	1377	1698	836	863
NM_001005464	HIST2H3A	0.80	-0.61	3293	6017	2466	1501
NM_021059	HIST2H3C	0.80	-0.61	3293	6017	2466	1501
NM_001123375	HIST2H3D	0.28	-0.54	659	902	266	144
NM_001127714	HIVEP3	0.06	0.00	475	572	1127	1152
NM_018410	HJURP	0.22	-0.76	757	987	562	281
NM_002121	HLA-DPB1	0.19	0.00	124	185	108	87
NM_001098479	HLA-F	1.22	0.00	49	166	233	248
NM_003071	HLTF	0.28	0.00	749	1015	1630	1571
NM_000190	HMBS	0.21	-0.17	545	719	1092	876
NM_145901	HMGA1	0.31	-0.31	11513	14723	23733	18724
NM_000191	HMGCL	0.27	0.00	439	612	1346	1375
NM_031157	HNRNPA1	0.18	-0.20	1272	1569	2144	1726
NM_031243	HNRNPA2B 1	0.17	-0.08	6298	7396	7674	6968
NM_194247	HNRNPA3	0.05	0.00	760	882	1017	1103
NM_001013631	HNRNPCL1	1.53	0.00	28	130	150	126
NM_031370	HNRNPD	0.03	-0.08	933	1056	695	575
NM_001098206	HNRNPF	0.38	-0.06	4775	6489	5786	5309
NM_001257293	HNRNPH1	0.04	0.00	2240	2465	2936	2915
NM_001032393	HNRNPH2	0.01	0.00	1291	1424	2479	2414
NM_002140	HNRNPK	0.06	-0.03	2537	2822	4536	4220
NM_001533	HNRNPL	0.26	-0.10	1383	1794	2633	2303
NM_005968	HNRNPM	0.03	-0.23	1954	2151	3130	2505
NM_007040	HNRNPUL1	0.19	0.00	4705	5639	6753	6815
NM_018951	HOXA10	0.32	0.00	255	385	576	575
NM_002145	HOXB2	0.52	0.00	263	453	957	874
NM_002146	HOXB3	0.28	0.00	190	286	641	697
NM_014212	HOXC11	0.43	-0.29	37	79	347	233
NM_014620	HOXC4	0.31	0.00	191	294	385	407
NM_153693	HOXC6	0.15	0.00	595	749	1029	1139
NM_022658	HOXC8	0.27	-0.07	545	751	1227	1057
NM_000195	HPS1	0.06	-0.10	1026	1182	3644	3209
NM_001009931	HRNR	0.11	0.00	113	162	289	274
NM_005836	HRSP12	0.06	0.00	69	103	256	214
NM_022460	HS1BP3	0.28	-0.22	452	632	1986	1580
NM_004807	HS6ST1	0.06	0.00	939	1087	611	671
NM_001537	HSBP1	0.28	0.00	829	1123	2371	2466

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001206741	HSD11B1	0.65	0.00	1	12	189	179
NM_001037811	HSD17B10	0.06	-0.40	517	617	1054	712
NM_016245	HSD17B11	0.06	0.00	133	181	428	388
NM_001199291	HSD17B4	0.45	0.00	406	642	1316	1268
NM_025193	HSD3B7	0.24	0.00	1092	1420	2302	2429
NM_005348	HSP90AA1	0.29	0.00	11822	14867	16598	16161
NM_001271969	HSP90AB1	0.47	-0.08	10026	14303	20597	19000
NM_002154	HSPA4	0.32	0.01	2589	3430	5064	5323
NM_001541	HSPB2	0.36	-0.28	427	635	753	543
NM_001130106	HSPBP1	0.06	-0.32	391	479	838	593
NM_002156	HSPD1	0.15	-0.13	2386	2826	3288	2824
NM_002157	HSPE1	0.35	0.00	206	322	430	431
NM_001202485	HSPE1-MOB4	0.07	0.00	561	673	942	1031
NM_000870	HTR4	1.16	0.00	12	58	50	35
NM_053044	HTRA3	0.14	0.00	49	82	46	41
NM_001040107	HVCN1	0.03	0.00	40	65	279	327
NM_033158	HYAL2	0.15	-0.46	910	1119	2830	1919
NM_001243526	HYI	0.13	-0.25	1583	1880	1148	871
NM_001134793	HYLS1	0.61	-0.15	167	318	310	229
NM_001039613	IAH1	0.08	0.00	853	1004	1599	1617
NM_013417	IARS	0.19	0.00	4327	5196	12781	13149
NM_002167	ID3	0.84	0.00	4478	8364	7682	7859
NM_004969	IDE	0.16	0.00	627	791	1179	1107
NM_002168	IDH2	0.09	0.00	1063	1243	1044	989
NM_033261	IDI2	0.32	0.00	31	64	96	120
NM_016097	IER3IP1	0.25	0.00	693	925	1187	1207
NM_016545	IER5	0.20	-0.03	1035	1306	1343	1196
NM_005531	IFI16	0.01	0.00	1667	1821	2358	2364
NM_032036	IFI27L2	0.10	-0.01	420	525	1169	1048
NM_005533	IFI35	0.17	-0.42	231	317	774	506
NM_001547	IFIT2	0.26	0.00	46	84	112	113
NM_003641	IFITM1	0.18	-0.47	294	399	277	159
NM_006435	IFITM2	0.58	-0.53	1733	2790	2548	1640
NM_021034	IFITM3	0.36	-0.52	4256	5736	5401	3591
NM_006764	IFRD2	0.12	0.00	1188	1413	1370	1283
NM_016004	IFT52	0.41	0.00	170	282	557	519
NM_001099223	IFT74	0.60	0.00	37	88	189	216
NM_001190241	IFT80	0.22	0.00	120	184	582	664
NM_001551	IGBP1	0.15	0.00	497	635	1308	1268

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_006546	IGF2BP1	0.57	0.00	221	399	75	76
NM_003640	IKBKAP	0.02	-0.11	957	1075	2258	1941
NM_014002	IKBKE	0.22	-0.09	287	401	584	475
NM_000628	IL10RB	0.18	0.00	323	435	792	874
NM_000882	IL12A	0.29	0.00	14	36	94	91
NM_001167928	IL1RAP	0.25	0.00	210	307	235	214
NM_033439	IL33	0.03	0.00	55	84	220	198
NM_002185	IL7R	0.04	-0.02	831	954	634	545
NM_001267809	ILF2	0.43	-0.13	1344	1961	1878	1580
NM_001014795	ILK	0.11	-0.03	5437	6108	8647	8164
NM_006844	ILVBL	0.19	-0.04	902	1144	1811	1630
NM_001100169	IMMT	0.38	0.00	1096	1558	2456	2503
NM_018285	IMP3	0.33	0.00	494	712	668	726
NM_033416	IMP4	0.28	-0.07	1156	1539	1788	1573
NM_000884	IMPDH2	0.18	-0.23	3398	4069	5087	4142
NM_001040694	INCENP	0.14	0.00	846	1038	1009	919
NM_001127582	ING4	0.35	0.00	169	270	699	789
NM_002193	INHBB	0.40	0.00	51	100	212	181
NM_001098817	INO80C	0.23	0.00	288	403	595	553
NM_173618	INO80E	0.51	0.00	433	709	767	706
NM_005539	INPP5A	0.28	0.00	1631	2131	2111	2116
NM_005540	INPP5B	0.31	0.00	226	342	335	392
NM_019892	INPP5E	0.17	-0.16	332	442	730	575
NM_020395	INTS12	0.13	-0.03	378	485	842	734
NM_023015	INTS3	0.27	0.00	766	1031	2562	2691
NM_030628	INTS5	0.15	0.00	859	1058	1553	1645
NM_018250	INTS9	0.34	0.00	174	275	460	418
NM_015693	INTU	0.23	0.00	61	104	193	165
NM_001005909	IP6K2	0.01	0.00	659	753	1221	1268
NM_014652	IPO13	0.43	0.00	1050	1550	2943	2944
NM_024658	IPO4	0.39	0.00	746	1095	1915	1834
NM_006391	IPO7	0.07	0.00	3259	3607	4943	4920
NM_022755	IPPK	0.14	0.00	404	521	967	911
NM_001031715	IQCH	0.56	0.00	4	23	85	70
NM_153208	IQCK	0.21	0.00	34	64	202	203
NM_178229	IQGAP3	0.13	-0.96	1625	1927	1994	933
NM_001569	IRAK1	0.17	0.00	5587	6539	9009	9094
NM_007199	IRAK3	0.43	-0.13	181	304	613	488
NM_004136	IREB2	0.10	0.00	877	1045	1158	1187

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_015649	IRF2BP1	0.07	0.00	419	512	641	647
NM_006084	IRF9	0.06	0.00	413	504	1023	1017
NM_024337	IRX1	0.28	0.00	72	123	96	87
NM_033267	IRX2	0.25	0.00	68	115	56	67
NM_194279	ISCA2	0.20	0.00	89	140	198	155
NM_014301	ISCU	0.14	0.00	828	1019	2414	2249
NM_030980	ISG20L2	0.20	0.00	478	633	720	710
NM_016048	ISOC1	0.36	0.00	104	178	104	135
NM_024710	ISOC2	0.66	-0.03	527	944	1331	1190
NM_001199469	ISY1	0.10	0.00	558	684	846	800
NM_016368	ISYNA1	0.19	0.00	285	389	277	311
NM_018463	ITFG2	0.18	-0.01	252	347	551	473
NM_003637	ITGA10	0.41	0.00	285	450	832	841
NM_001291494	ITGA8	0.10	0.00	27	50	79	68
NM_002214	ITGB8	0.25	0.00	25	52	42	30
NM_001287241	ITM2C	0.13	0.00	734	904	790	791
NM_033453	ITPA	0.17	-0.30	340	453	994	721
NM_014216	ITPK1	0.43	0.00	846	1264	1312	1368
NM_002224	ITPR3	0.05	0.00	2835	3117	9429	9536
NM_001034841	ITPRIPL2	0.09	0.00	2686	3037	7119	7275
NM_000214	JAG1	0.16	0.00	688	866	534	482
NM_175061	JAZF1	0.37	0.00	308	473	813	815
NM_023007	JMJD4	0.38	0.00	369	561	994	924
NM_002230	JUP	0.29	0.00	47	87	69	83
NM_153186	KANK1	0.16	0.00	2463	2938	4440	4571
NM_001130089	KARS	0.16	-0.12	1917	2303	3065	2656
NM_006388	KAT5	0.23	0.00	848	1107	1605	1699
NM_007067	KAT7	0.45	0.00	529	823	1242	1209
NM_014867	KBTBD11	0.32	0.00	36	72	25	33
NM_016506	KBTBD4	0.09	0.00	505	619	950	996
NM_032505	KBTBD8	0.23	0.00	177	261	96	122
NM_013348	KCNJ14	0.06	0.00	49	78	102	105
NM_004982	KCNJ8	0.24	0.00	402	552	539	508
NM_001017424	KCNK2	0.07	-0.34	2934	3257	3970	2965
NM_031954	KCTD10	0.20	0.00	2066	2548	5010	5242
NM_001282684	KCTD17	0.28	0.00	283	410	886	824
NM_173562	KCTD20	0.08	-0.12	5345	5895	9446	8412
NM_016121	KCTD3	0.12	0.00	1083	1291	1761	1628
NM_153705	KDELC2	0.46	-0.17	892	1360	1329	1074

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_024773	KDM8	1.45	0.00	25	113	119	111
NM_006558	KHDRBS3	0.14	0.00	345	449	214	187
NM_003685	KHSRP	0.08	-0.19	1516	1738	1874	1519
NM_001145642	KIAA0226	0.06	0.00	1223	1401	1895	1782
NM_014734	KIAA0247	0.21	0.00	852	1093	1225	1275
NM_014732	KIAA0513	0.13	0.00	656	811	1522	1590
NM_001244189	KIAA0586	0.10	0.00	323	412	528	457
NM_001100425	KIAA0895	0.19	-0.42	118	177	135	72
NM_015634	KIAA1279	0.35	0.00	849	1198	1957	2094
NM_015496	KIAA1429	0.28	0.00	1089	1456	2637	2780
NM_020844	KIAA1456	0.86	0.00	17	58	4	13
NM_020890	KIAA1524	0.15	-0.61	297	394	403	218
NM_001105568	KIF13A	0.08	0.00	3630	4039	6129	6399
NM_020242	KIF15	0.43	-0.60	131	228	179	87
NM_001264573	KIF18B	0.14	-1.16	719	891	520	192
NM_005733	KIF20A	0.10	-1.28	1309	1528	1258	458
NM_001256269	KIF22	0.15	-0.48	963	1183	986	630
NM_138555	KIF23	0.05	-0.54	1094	1251	1013	619
NM_006845	KIF2C	0.22	-0.59	734	959	913	536
NM_002263	KIFC1	0.10	-0.36	1217	1429	643	434
NM_001130100	KIFC3	0.12	-0.16	2078	2414	3321	2800
NM_032531	KIRREL3	0.08	0.00	2876	3236	1660	1715
NM_000222	KIT	0.30	-1.55	34	68	77	13
NM_000899	KITLG	0.24	-0.45	1768	2247	3831	2645
NM_016270	KLF2	0.14	0.00	667	831	223	192
NM_016531	KLF3	0.11	0.00	708	862	1069	1113
NM_001206	KLF9	0.28	0.01	592	813	1876	2033
NM_173546	KLHDC8B	0.23	-0.18	529	711	1464	1176
NM_021633	KLHL12	0.74	0.00	243	487	928	832
NM_001007075	KLHL5	0.18	0.00	420	553	1046	1026
NM_018847	KLHL9	0.24	0.00	869	1141	1601	1647
NM_014708	KNTC1	0.02	-0.38	633	729	786	530
NM_002266	KPNA2	0.31	-0.53	1865	2491	2932	1891
NM_002265	KPNB1	0.19	0.00	6752	8002	9013	9246
NM_016618	KRCC1	0.16	0.00	285	382	603	673
NM_199187	KRT18	0.63	0.00	2353	3873	980	1067
NM_002277	KRT31	0.81	-0.45	46	120	403	244
NM_002279	KRT33B	0.13	0.00	62	99	250	246
NM_021013	KRT34	0.47	-0.05	1517	2268	7254	6743

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_030967	KRTAP1-1	1.04	-0.01	2	21	742	651
NM_031957	KRTAP1-5	0.14	-0.26	328	430	2514	1956
NM_173852	KRTCAP2	0.39	0.00	362	554	1368	1484
NM_014238	KSR1	0.71	0.00	81	180	239	233
NM_138417	KTI12	0.56	0.00	474	799	736	791
NM_001171948	KXD1	0.51	-0.01	1479	2270	4207	3969
NM_144581	L3HYPDH	0.35	0.00	304	461	293	349
NM_031488	L3MBTL2	0.46	0.00	594	921	1385	1309
NM_001105207	LAMA4	0.13	-0.90	1519	1805	7836	4002
NM_002291	LAMB1	0.02	-0.20	5680	6023	17211	14556
NM_017907	LAMTOR1	0.33	-0.23	1354	1855	3768	3030
NM_001243736	LAMTOR3	0.24	0.00	192	281	512	577
NM_001008395	LAMTOR4	0.14	0.00	693	859	1736	1678
NM_006402	LAMTOR5	0.40	0.00	505	760	1262	1384
NM_015907	LAP3	0.08	-0.25	422	518	1215	921
NM_004737	LARGE	0.13	0.00	844	1030	1955	2018
NM_018078	LARP1B	0.14	0.00	285	376	272	240
NM_052879	LARP4	0.34	0.00	1078	1499	1506	1512
NM_015155	LARP4B	0.13	0.00	2281	2662	2743	2874
NM_031206	LAS1L	0.33	-0.01	441	638	1034	924
NM_001258390	LAYN	0.18	-0.66	629	807	2171	1268
NM_002296	LBR	0.27	0.00	543	744	439	394
NM_001009812	LBX2	0.63	0.00	19	54	116	116
NM_014793	LCMT2	0.36	0.00	306	465	430	464
NM_001170765	LCOR	0.21	-0.04	536	706	776	669
NM_153686	LCORL	0.21	-0.11	175	255	152	105
NM_001174097	LDHB	0.20	-0.18	2524	3087	5261	4423
NM_174902	LDLRAD3	0.28	0.00	167	255	393	410
NM_012318	LETM1	0.22	0.00	2328	2888	3635	3693
NM_001243689	LETMD1	0.11	0.00	333	425	657	688
NM_005567	LGALS3BP	0.34	-0.18	4250	5634	5890	4970
NM_006859	LIAS	0.80	0.00	25	74	110	102
NM_013975	LIG3	0.10	0.00	702	848	1117	1076
NM_001113547	LIMA1	0.37	0.00	10458	13954	12813	12793
NM_001024674	LIN52	0.12	0.00	165	227	129	131
NM_005357	LIPE	0.30	0.00	68	119	42	39
NM_170707	LMNA	0.24	-0.22	22240	26812	49065	41411
NM_005573	LMNB1	0.02	-0.55	816	927	283	153
NM_012134	LMOD1	0.40	-0.40	198	322	1522	1052

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001146181	LOC649330	1.53	0.00	28	130	150	126
NM_001199053	LOC81691	0.79	-0.07	63	154	160	115
NM_153613	LPCAT4	0.12	0.00	1208	1442	1535	1486
NM_001164213	LRCH1	0.03	0.00	606	702	1100	1092
NM_153377	LRIG3	0.22	-0.23	120	183	225	150
NM_002333	LRP3	0.59	0.00	180	335	1250	1244
NM_182492	LRP5L	0.19	0.00	43	76	56	76
NM_133259	LRPPRC	0.27	0.00	1598	2087	3361	3220
NM_024512	LRRC2	0.19	-0.47	288	393	208	115
NM_001278211	LRRC20	0.78	-0.09	198	414	354	277
NM_001143757	LRRC27	2.14	0.00	9	104	189	227
NM_001010847	LRRC38	0.26	0.00	121	190	8	4
NM_017768	LRRC40	0.31	0.00	225	340	464	405
NM_001256409	LRRC42	0.48	0.00	684	1066	1316	1314
NM_018509	LRRC59	0.13	-0.02	11496	12994	10752	10279
NM_001113567	LRRC75A	0.16	0.00	193	269	252	262
NM_001127244	LRRC8A	0.12	-0.02	3710	4256	6709	6370
NM_138361	LRSAM1	0.05	0.00	348	425	701	793
NM_152892	LRWD1	0.22	0.00	352	483	697	619
NM_002338	LSAMP	0.27	0.00	51	92	127	144
NM_018385	LSG1	0.14	0.00	751	926	1256	1244
NM_032881	LSM10	0.19	0.00	718	919	1198	1146
NM_152344	LSM12	0.05	0.00	763	889	888	983
NM_021177	LSM2	0.26	-0.53	225	330	435	250
NM_014463	LSM3	0.82	0.00	63	157	212	190
NM_016199	LSM7	0.89	-0.17	224	500	678	525
NM_001260489	LSR	0.46	0.00	31	70	75	68
NM_002342	LTBR	0.12	-0.01	2724	3155	5584	5288
NM_001127213	LY6E	0.39	0.00	1764	2491	3899	3939
NM_021221	LY6G5B	0.22	0.00	37	69	116	150
NM_144586	LYPD1	0.32	0.00	425	613	89	100
NM_001279358	LYPLA1	0.14	0.00	251	336	318	364
NM_138794	LYPLAL1	0.29	0.00	70	121	264	277
NM_020424	LYRM1	0.07	0.00	121	167	343	318
NM_001076680	LYRM9	0.33	0.00	46	88	262	248
NM_002355	M6PR	0.09	0.00	1658	1908	2828	2688
NM_014067	MACROD1	0.33	0.00	163	258	537	492
NM_001013836	MAD1L1	0.01	0.00	981	1096	975	887
NM_002358	MAD2L1	0.35	-0.43	166	267	208	118

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_006341	MAD2L2	0.36	0.00	393	586	1061	1070
NM_001031804	MAF	0.46	0.00	22	54	44	44
NM_005461	MAFB	0.93	0.00	79	204	455	390
NM_002360	MAFK	0.05	0.00	2105	2335	1354	1423
NM_201222	MAGED2	0.06	0.00	3885	4253	6574	6828
NM_001272061	MAGED4	0.34	-0.08	635	904	730	606
NM_001242362	MAGED4B	0.34	-0.08	635	904	730	606
NM_005491	MAMLD1	0.21	0.00	391	529	439	397
NM_001256494	MAN2C1	0.04	0.00	864	991	1907	1946
NM_022077	MANBAL	0.44	0.00	926	1384	2277	2207
NM_019090	MAP10	1.07	0.00	12	55	27	31
NM_002419	MAP3K11	0.11	0.00	852	1024	1323	1405
NM_003954	MAP3K14	0.55	-0.08	275	480	607	499
NM_004672	MAP3K6	0.04	0.00	1036	1179	2204	2347
NM_144578	MAPK1IP1L	0.17	0.00	2404	2877	3606	3763
NM_001006617	MAPKAP1	0.17	-0.17	2344	2822	6879	5863
NM_004759	MAPKAPK2	0.07	-0.04	3669	4067	4309	3976
NM_001243925	MAPKAPK3	0.31	-0.02	455	648	1705	1555
NM_012325	MAPRE1	0.40	0.00	1761	2491	3814	3782
NM_014268	MAPRE2	0.36	-0.02	526	772	1520	1375
NM_017824	MARCH5	0.45	0.00	667	1022	1040	1052
NM_002356	MARCKS	0.07	0.00	3042	3389	4563	4499
NM_138395	MARS2	0.04	0.00	204	261	237	220
NM_031484	MARVELD1	0.48	0.00	1661	2486	2884	2791
NM_001042539	MAZ	0.37	-0.24	3022	4128	3492	2784
NM_178496	MB21D2	0.03	-0.66	506	596	632	342
NM_001144891	MBIP	0.36	0.00	147	241	264	257
NM_203406	MBLAC2	0.40	-0.10	156	261	206	150
NM_001080480	MBOAT1	0.08	0.00	37	63	21	31
NM_022132	MCCC2	0.20	-0.02	347	469	857	754
NM_032601	MCEE	0.07	0.00	103	146	135	174
NM_018518	MCM10	0.51	-0.75	474	772	193	85
NM_004526	MCM2	0.11	-0.20	1864	2170	1389	1098
NM_002388	MCM3	0.30	-0.33	2355	3087	1622	1177
NM_005914	MCM4	0.53	-0.22	2312	3545	2685	2157
NM_006739	MCM5	0.08	-0.16	2710	3050	1868	1538
NM_005915	MCM6	0.17	0.00	1615	1969	1562	1471
NM_001278595	MCM7	0.02	-0.31	3999	4282	2398	1795
NM_001281520	MCM8	0.36	-0.01	279	427	362	299

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_006337	MCRS1	0.41	0.00	1044	1526	1984	1922
NM_014641	MDC1	0.38	0.00	943	1357	1358	1364
NM_005918	MDH2	0.22	-0.16	3961	4841	8106	6983
NM_001199822	MDP1	0.02	0.00	124	166	183	229
NM_001161586	ME3	0.36	0.00	142	234	568	603
NM_001024732	MECR	0.01	0.00	269	329	678	638
NM_005120	MED12	0.01	0.00	1095	1216	2132	2074
NM_015335	MED13L	0.05	-0.03	3484	3802	5991	5623
NM_005481	MED16	0.26	-0.19	994	1311	2308	1885
NM_004268	MED17	0.24	0.00	411	564	609	673
NM_153450	MED19	0.26	0.00	235	342	564	627
NM_004830	MED23	0.14	0.00	722	894	1077	1181
NM_014815	MED24	0.05	0.00	1735	1944	2972	2823
NM_030973	MED25	0.27	0.00	387	546	846	830
NM_016060	MED31	0.46	0.00	209	351	410	455
NM_002398	MEIS1	0.07	-0.17	252	322	944	749
NM_014791	MELK	0.10	-0.20	647	783	593	445
NM_015955	MEMO1	0.11	0.00	135	189	318	311
NM_002402	MEST	0.81	-0.27	182	393	195	124
NM_015143	METAP1	0.14	0.00	1393	1669	2608	2525
NM_199227	METAP1D	0.21	0.00	16	37	110	100
NM_024042	METRN	0.13	-0.01	271	358	900	797
NM_015935	METTL13	0.06	-0.02	916	1064	1524	1383
NM_020961	METTL14	0.33	0.00	245	372	464	458
NM_024109	METTL22	0.22	0.00	485	649	1054	1129
NM_001206983	METTL23	0.04	0.00	260	324	443	381
NM_019852	METTL3	0.25	-0.10	1047	1369	1655	1420
NM_014168	METTL5	0.25	0.00	287	408	489	436
NM_024770	METTL8	0.07	0.00	234	300	566	567
NM_001077180	METTL9	0.21	0.00	1203	1527	3795	3922
NM_001174118	MEX3D	0.06	-0.18	529	634	855	667
NM_005926	MFAP1	0.12	0.00	410	519	572	599
NM_001135248	MFAP2	0.17	0.00	821	1032	1408	1534
NM_033540	MFN1	0.05	0.00	523	622	948	961
NM_014874	MFN2	0.19	0.00	2687	3253	6000	6035
NM_001242534	MFSD11	0.56	0.00	370	637	1123	1174
NM_174983	MFSD12	0.02	0.00	580	672	1250	1347
NM_001136493	MFSD2A	0.48	0.00	130	233	154	189
NM_001170790	MFSD5	0.11	0.00	732	889	1231	1251

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_052865	MGME1	0.60	0.00	195	363	420	488
NM_001260512	MGST1	0.08	0.00	2082	2366	4717	4741
NM_001204366	MGST2	0.47	0.00	33	74	139	142
NM_001286613	MICAL1	0.08	0.00	758	896	1730	1595
NM_033386	MICALL1	0.23	0.00	3082	3833	2884	2924
NM_182924	MICALL2	0.35	0.00	231	357	630	567
NM_001289160	MICB	0.30	0.00	514	725	632	604
NM_001195518	MICU1	0.09	0.00	1203	1406	3404	3571
NM_152726	MICU2	0.44	0.00	212	352	736	712
NM_139162	MIEF2	0.28	0.00	263	385	526	556
NM_032339	MIEN1	0.17	-0.09	733	923	1522	1312
NM_021933	MIIP	0.18	0.00	198	279	399	408
NM_019005	MIOS	0.21	0.00	308	425	574	519
NM_138798	MITD1	0.09	0.00	192	255	358	336
NM_017777	MKS1	0.02	0.00	172	221	333	275
NM_001242702	MKX	0.57	0.00	31	75	229	211
NM_001130157	MLF1	0.85	0.00	30	88	202	165
NM_000249	MLH1	0.16	0.00	502	646	984	1020
NM_005937	MLLT6	0.10	0.00	1278	1494	2003	2085
NM_170607	MLX	0.24	-0.12	1716	2180	3198	2763
NM_002421	MMP1	0.50	-0.04	11316	16457	6268	5830
NM_002425	MMP10	0.51	0.00	21	54	114	104
NM_002426	MMP12	0.05	-0.23	14	31	98	57
NM_002428	MMP15	0.02	0.00	214	268	551	582
NM_005941	MMP16	0.24	0.00	172	256	374	322
NM_002422	MMP3	0.15	-0.04	4384	5116	17523	16658
NM_022362	MMS19	0.22	0.00	1704	2139	3124	3298
NM_002430	MN1	0.42	0.00	326	513	998	1037
NM_018221	MOB1A	0.13	0.00	741	911	1393	1403
NM_130807	MOB3A	0.04	0.00	1554	1730	3213	3410
NM_014226	MOK	0.14	0.00	2765	3236	1385	1318
NM_014940	MON1B	0.03	0.00	678	781	973	1013
NM_024657	MORC4	0.09	0.00	439	541	1038	1037
NM_206839	MORF4L1	0.80	0.00	887	1699	1884	2033
NM_001286072	MOV10	0.07	-0.09	809	947	2161	1889
NM_002434	MPG	0.54	-0.04	617	1013	1460	1301
NM_022782	MPHOSPH9	0.09	0.00	340	429	480	455
NM_002435	MPI	0.29	0.00	606	837	1368	1434
NM_001130517	MPST	0.32	0.00	315	466	520	455

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_002437	MPV17	0.07	0.00	675	801	1429	1388
NM_005590	MRE11A	0.37	-0.24	162	264	389	274
NM_001272054	MRFAP1	0.02	-0.12	5828	6145	9279	8268
NM_001098515	MRGPRF	0.46	-0.20	249	412	638	482
NM_001031727	MRI1	0.12	0.00	508	634	1121	1150
NM_032450	MROH1	0.46	0.00	655	1012	1992	2091
NM_020236	MRPL1	0.24	0.00	112	175	231	242
NM_002949	MRPL12	0.19	-0.30	858	1089	1410	1042
NM_017840	MRPL16	0.05	-0.43	420	507	1044	693
NM_014161	MRPL18	0.16	0.00	989	1222	1734	1654
NM_017971	MRPL20	0.45	-0.03	451	710	1204	1067
NM_181514	MRPL21	0.03	-0.11	587	684	932	773
NM_014180	MRPL22	0.11	0.00	285	370	562	510
NM_021134	MRPL23	0.54	-0.15	490	815	1129	919
NM_007208	MRPL3	0.11	0.00	579	713	796	824
NM_004891	MRPL33	0.05	-0.27	475	570	747	542
NM_016622	MRPL35	0.48	0.00	347	566	830	823
NM_032479	MRPL36	0.12	-0.04	647	793	1140	1002
NM_003776	MRPL40	0.31	-0.31	214	326	786	556
NM_032477	MRPL41	0.13	-0.17	463	585	1381	1118
NM_020409	MRPL47	0.40	-0.01	259	412	562	484
NM_016497	MRPL51	0.14	-0.05	974	1189	1770	1579
NM_181304	MRPL52	0.15	-0.14	650	816	1616	1342
NM_181462	MRPL55	0.53	-0.14	245	427	848	682
NM_024026	MRPL57	0.44	-0.31	302	485	890	636
NM_022839	MRPS11	0.29	-0.28	512	715	1239	924
NM_033363	MRPS12	0.38	-0.15	483	719	932	749
NM_031280	MRPS15	0.08	-0.04	976	1140	2225	2015
NM_015969	MRPS17	0.38	0.00	203	326	391	333
NM_018135	MRPS18A	0.34	-0.14	387	572	838	673
NM_016070	MRPS23	0.08	0.00	499	608	1129	1102
NM_032014	MRPS24	0.24	-0.01	1109	1439	1633	1495
NM_030811	MRPS26	0.06	0.00	425	515	570	536
NM_005830	MRPS31	0.20	0.00	161	235	327	355
NM_016071	MRPS33	0.48	0.00	112	205	347	312
NM_023936	MRPS34	0.08	-0.22	964	1131	1934	1534
NM_001286264	MRS2	0.52	0.00	170	305	482	462
NM_016183	MRTO4	0.03	-0.20	718	824	1185	932
NM_130385	MRVI1	0.05	-0.99	657	768	3103	1455

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_024631	MSANTD2	0.72	0.00	24	68	85	102
NM_032424	MSANTD4	0.16	0.00	433	561	695	656
NM_000251	MSH2	0.43	0.00	381	599	449	518
NM_078629	MSL3	0.51	0.00	134	245	414	442
NM_001193460	MSRB3	0.41	0.00	1555	2237	3275	3307
NM_001256532	MSTO1	0.65	-0.15	255	480	903	723
NM_004739	MTA2	0.01	0.00	2380	2563	2679	2856
NM_002451	MTAP	0.03	0.00	696	799	1316	1381
NM_014342	MTCH2	0.02	0.00	952	1068	1772	1723
NM_001018025	MTCP1	0.46	0.00	35	77	143	135
NM_001164391	MTF2	0.11	0.00	168	229	181	194
NM_139242	MTFMT	0.32	0.00	173	270	399	425
NM_014637	MTFR1	0.07	0.00	583	699	911	1013
NM_001099625	MTFR1L	0.35	-0.03	833	1177	2535	2320
NM_015666	MTG2	0.03	0.00	486	571	699	693
NM_005956	MTHFD1	0.16	-0.29	1020	1258	1957	1475
NM_001005369	MTIF2	0.36	0.00	352	529	861	793
NM_017762	MTMR10	0.21	0.00	904	1159	1225	1211
NM_001243571	MTMR2	0.12	0.00	1706	2003	2504	2617
NM_004687	MTMR4	0.34	0.00	783	1105	1343	1408
NM_004685	MTMR6	0.13	0.00	729	896	1381	1462
NM_004294	MTRF1	1.28	0.00	14	67	79	109
NM_019041	MTRF1L	0.14	0.00	252	336	505	494
NM_001190708	MTRNR2L10	1.48	0.00	132	464	2026	2159
NM_001190487	MTRNR2L6	2.14	-0.03	56	344	1701	1536
NM_152793	MTURN	0.27	0.00	287	415	1146	1259
NM_002455	MTX1	0.03	0.00	524	616	988	911
NM_025128	MUS81	0.64	-0.04	571	1003	1215	1074
NM_000255	MUT	0.31	0.00	386	559	767	776
NM_138401	MVB12A	0.08	0.00	359	446	736	717
NM_002461	MVD	0.46	-0.16	276	453	824	654
NM_001144925	MX1	0.63	0.00	37	90	62	83
NM_001142935	MXD3	0.55	0.00	772	1259	2086	1972
NM_032348	MXRA8	0.26	0.00	5628	7036	10088	10194
NM_014520	MYBBP1A	0.20	0.01	2029	2492	3369	3586
NM_002466	MYBL2	0.48	-1.15	958	1471	327	115
NM_002467	MYC	0.25	0.00	2140	2715	3305	3377
NM_012333	MYCBP	0.28	0.00	150	232	410	442
NM_001172567	MYD88	0.21	0.00	693	901	1481	1479

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_002473	MYH9	0.19	0.00	29788	34631	57483	58380
NM_021019	MYL6	0.44	-0.08	10866	15214	22801	21125
NM_006097	MYL9	0.83	-0.21	10584	19391	38407	32665
NM_001185118	MYNN	0.43	0.00	180	302	362	370
NM_078471	MYO18A	0.29	0.00	871	1178	4059	4151
NM_001163735	MYO19	0.18	-0.25	1563	1921	1988	1543
NM_004998	MYO1E	0.18	-0.13	2962	3547	8920	7887
NM_001080527	MYO7B	0.04	0.00	171	223	54	41
NM_001146312	MYOCD	0.10	0.00	691	836	4	13
NM_013451	MYOF	0.11	-0.13	16695	18456	32033	28645
NM_001012643	MYPOP	0.61	0.00	82	171	223	201
NM_001071775	MZT1	0.14	0.00	241	323	275	316
NM_001256120	NAA10	0.19	0.00	1145	1432	2221	2259
NM_024635	NAA35	0.31	0.00	325	475	803	900
NM_025146	NAA50	0.12	0.00	2337	2712	3217	3274
NM_005468	NAALADL1	0.14	0.00	170	237	366	359
NM_024068	NABP2	0.02	0.00	436	514	782	762
NM_199290	NACA2	0.04	-0.20	1980	2190	3529	2900
NM_001146334	NACAD	0.54	0.00	78	156	243	296
NM_052876	NACC1	0.05	0.00	3329	3642	5792	5863
NM_144653	NACC2	0.05	-0.06	1557	1744	2776	2493
NM_018161	NADSYN1	0.31	0.00	807	1114	2059	2129
NM_138386	NAF1	0.68	0.00	112	234	189	213
NM_000262	NAGA	0.12	0.00	994	1197	2441	2379
NM_197956	NAIF1	0.48	0.00	118	214	314	296
NM_018946	NANS	0.20	-0.33	2987	3623	3030	2264
NM_005969	NAP1L4	0.20	-0.08	1768	2187	3635	3248
NM_003827	NAPA	0.49	-0.07	1716	2597	4852	4392
NM_022493	NARFL	0.65	0.00	277	516	821	800
NM_001256281	NARR	0.34	-0.05	290	437	757	647
NM_024678	NARS2	0.27	-0.35	250	365	403	264
NM_002482	NASP	0.35	-0.29	578	835	564	396
NM_001160170	NAT1	0.18	0.00	39	70	150	161
NM_024662	NAT10	0.24	-0.03	1273	1642	1716	1545
NM_001200016	NAT6	0.40	0.00	154	258	345	294
NM_015654	NAT9	0.02	0.00	533	621	982	1055
NM_014865	NCAPD2	0.33	-0.50	1673	2269	2612	1717
NM_015261	NCAPD3	0.05	-0.17	1334	1506	1429	1161
NM_022346	NCAPG	0.13	-0.86	696	855	846	405

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001281932	NCAPG2	0.04	-0.72	1148	1294	1323	721
NM_001185011	NCAPH2	0.17	0.00	1459	1783	2473	2333
NM_002486	NCBP1	0.10	-0.23	681	826	1680	1312
NM_007362	NCBP2	0.22	0.00	936	1207	1689	1828
NM_001146276	NCEH1	0.04	0.00	2579	2823	2691	2715
NM_003581	NCK2	0.22	0.00	533	708	857	906
NM_001145260	NCOA4	0.45	0.01	2385	3458	6322	6617
NM_020967	NCOA5	0.32	0.00	571	809	855	902
NM_014286	NCS1	0.08	-0.09	4139	4613	10953	9972
NM_001143979	NDE1	0.08	0.00	687	820	634	715
NM_024574	NDNF	0.33	0.00	124	203	218	251
NM_138704	NDNL2	0.48	0.00	372	604	780	815
NM_001242835	NDRG4	1.38	-0.11	24	105	162	113
NM_004544	NDUFA10	0.05	-0.02	1363	1542	2968	2749
NM_014222	NDUFA8	0.25	-0.01	827	1095	2046	1893
NM_005002	NDUFA9	0.25	0.00	416	575	1083	980
NM_005003	NDUFAB1	0.03	-0.25	564	658	1017	765
NM_174889	NDUFAF2	0.24	0.00	184	272	507	451
NM_199069	NDUFAF3	0.13	0.00	919	1114	2541	2586
NM_004545	NDUFB1	0.03	0.00	121	163	306	305
NM_004546	NDUFB2	0.55	0.00	556	920	1996	1998
NM_004146	NDUFB7	0.23	-0.11	824	1075	2019	1732
NM_005006	NDUFS1	0.14	0.00	1635	1949	3005	3163
NM_001184979	NDUFS5	0.34	0.00	500	726	1398	1407
NM_024407	NDUFS7	0.15	0.00	478	611	794	834
NM_002496	NDUFS8	0.20	-0.33	1361	1705	3783	2848
NM_022351	NECAB1	0.50	0.00	64	129	112	100
NM_015509	NECAP1	0.11	0.00	472	588	817	747
NM_018090	NECAP2	0.29	0.00	2176	2849	3839	3630
NM_001144966	NEDD4L	0.41	-0.14	517	782	455	349
NM_006156	NEDD8	0.18	-0.17	977	1224	2460	2039
NM_001199823	NEDD8-MDP1	0.46	0.00	272	447	591	579
NM_006403	NEDD9	0.15	-0.01	2617	3093	2123	1956
NM_001199397	NEK1	0.01	0.00	326	391	742	789
NM_003157	NEK4	0.33	0.00	241	367	562	547
NM_001166171	NEK6	0.23	-0.38	1956	2469	6370	4682
NM_033116	NEK9	0.29	0.00	993	1337	3232	3373
NM_005663	NELFA	0.04	0.00	412	495	410	460
NM_002904	NELFE	0.16	0.00	1154	1416	3278	3094

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001201477	NETO2	1.15	0.00	53	169	220	216
NM_006656	NEU3	0.24	0.00	112	175	250	270
NM_001142651	NEURL1B	0.02	-0.96	115	155	116	39
NM_181832	NF2	0.01	-0.15	6567	6905	7713	6671
NM_001278669	NFATC1	0.22	0.00	123	188	343	384
NM_032815	NFATC2IP	0.03	0.00	665	769	1040	1037
NM_020529	NFKBIA	0.09	0.00	770	918	769	689
NM_004556	NFKBIE	0.36	0.00	81	143	139	148
NM_001142588	NFYC	0.30	0.00	528	743	848	828
NM_002507	NGFR	0.49	0.00	7	31	81	111
NM_206915	NGFRAP1	0.06	-0.04	1257	1438	4527	4177
NM_024782	NHEJ1	0.22	0.00	185	269	322	344
NM_005008	NHP2L1	0.21	0.00	1447	1818	2512	2490
NM_001144060	NHSL1	0.06	0.00	781	909	1940	1887
NM_002508	NID1	0.10	0.00	4300	4853	3452	3427
NM_021824	NIF3L1	0.37	0.00	291	448	426	484
NM_004148	NINJ1	0.06	0.00	299	373	957	902
NM_025176	NINL	0.02	0.00	170	218	306	349
NM_003634	NIPSNAP1	0.09	-0.11	517	631	1435	1214
NM_020202	NIT2	0.06	0.00	341	420	928	937
NM_001144929	NKIRAS2	0.19	0.00	1236	1539	1863	1996
NM_001014445	NLE1	0.58	-0.17	275	489	611	471
NM_020726	NLN	0.02	0.00	921	1041	1649	1654
NM_032206	NLRC5	0.09	0.00	745	893	2034	1959
NM_021077	NMB	0.23	-0.14	79	129	3752	3216
NM_002512	NME2	0.38	-0.21	2409	3329	5715	4713
NM_001286438	NME4	0.16	-0.21	1706	2056	4852	3985
NM_005793	NME6	0.03	0.00	292	358	354	370
NM_020677	NMRAL1	0.68	0.00	388	718	1133	1028
NM_021079	NMT1	0.21	0.00	3401	4163	7004	7061
NM_005386	NNAT	0.40	0.00	25	57	56	37
NM_006169	NNMT	0.47	0.00	1726	2574	3814	3706
NM_032313	NOA1	0.43	0.00	250	406	724	662
NM_014062	NOB1	0.47	0.00	680	1058	1244	1353
NM_015658	NOC2L	0.47	-0.16	1143	1730	2408	2006
NM_015462	NOL11	0.53	-0.20	205	363	416	305
NM_022917	NOL6	0.19	-0.40	1820	2227	2803	1985
NM_001284388	NOLC1	0.31	0.00	2062	2743	2090	2120
NM_001145408	NONO	0.44	-0.12	2593	3736	5299	4662

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_016391	NOP16	0.04	-0.29	713	826	1179	869
NM_001033714	NOP2	0.04	-0.01	1240	1396	1318	1194
NM_174913	NOP9	0.16	0.00	1572	1904	2693	2741
NM_000603	NOS3	0.19	0.00	48	83	137	142
NM_002514	NOV	0.43	-0.19	457	710	216	148
NM_001291926	NOX4	0.57	-0.12	22	58	166	115
NM_002519	NPAT	0.29	0.00	365	522	568	540
NM_017921	NPLOC4	0.22	0.00	4577	5567	7996	8283
NM_006993	NPM3	0.26	-0.47	270	388	730	458
NM_000903	NQO1	0.63	-0.08	5148	8328	15747	14464
NM_001290221	NQO2	0.03	0.00	558	651	992	1098
NM_007121	NR1H2	0.10	0.00	1800	2086	3448	3347
NM_021005	NR2F2	0.13	-0.14	2093	2448	3047	2590
NM_005234	NR2F6	0.42	0.00	313	494	753	747
NM_000901	NR3C2	0.50	-0.15	612	974	1996	1664
NM_198465	NRK	0.27	-0.46	98	159	385	231
NM_024958	NRSN2	0.43	0.00	575	877	2683	2684
NM_014886	NSA2	0.02	0.00	319	385	595	556
NM_022455	NSD1	0.22	-0.01	3201	3934	4633	4390
NM_001206736	NSFL1C	0.15	0.00	1194	1452	2562	2599
NM_001287763	NSG1	1.10	0.00	19	73	75	83
NM_001042549	NSL1	0.24	0.00	238	341	534	545
NM_145080	NSMCE1	0.49	0.00	378	619	1589	1469
NM_173685	NSMCE2	0.39	0.00	153	254	354	375
NM_001199104	NT5C1B-RDH14	0.13	0.00	241	321	516	545
NM_012229	NT5C2	0.11	0.00	997	1191	1722	1824
NM_006179	NTF4	0.11	0.00	34	60	54	44
NM_002528	NTHL1	0.41	0.00	108	190	337	368
NM_001286798	NTMT1	0.18	-0.05	1671	2042	2113	1893
NM_030952	NUAK2	0.14	-0.90	477	607	443	194
NM_002484	NUBP1	0.14	0.00	302	397	476	438
NM_025152	NUBPL	0.43	-0.25	42	87	239	159
NM_022731	NUCKS1	0.02	0.00	4521	4815	6599	6800
NM_006600	NUDC	0.49	0.00	502	803	1079	1024
NM_032869	NUDCD1	0.10	0.00	636	772	570	508
NM_198948	NUDT1	0.28	0.00	279	407	466	399
NM_031438	NUDT12	0.70	0.00	58	135	247	226
NM_001105570	NUDT19	0.17	0.00	291	393	447	410
NM_001161	NUDT2	0.44	0.00	196	328	641	662

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_145697	NUF2	0.19	-0.84	215	302	254	109
NM_012345	NUFIP1	0.02	0.00	67	98	139	166
NM_018230	NUP133	0.65	-0.07	508	904	1275	1105
NM_004298	NUP155	0.16	-0.18	879	1091	1433	1152
NM_015231	NUP160	0.16	0.00	773	964	1025	1085
NM_015354	NUP188	0.29	-0.27	3261	4208	5817	4597
NM_015135	NUP205	0.27	0.00	1503	1956	2365	2251
NM_198887	NUP43	0.28	0.00	541	750	973	1076
NM_007172	NUP50	0.21	0.00	766	988	1381	1383
NM_017426	NUP54	0.41	0.00	436	670	680	750
NM_024844	NUP85	0.63	-0.12	635	1103	1144	950
NM_014669	NUP93	0.37	-0.06	1342	1885	2206	1965
NM_016320	NUP98	0.18	0.00	3468	4143	5586	5358
NM_001045477	NUTM2G	1.25	0.00	8	54	60	44
NM_002533	NVL	0.26	0.00	266	383	566	529
NM_022463	NXN	0.03	-0.02	1270	1418	1400	1266
NM_013248	NXT1	0.36	-0.01	262	404	406	340
NM_178507	OAF	0.10	-0.13	2203	2531	4962	4310
NM_006187	OAS3	0.01	-0.27	144	188	162	100
NM_000274	OAT	0.02	-0.20	2509	2712	4908	4072
NM_002540	ODF2	0.36	-0.03	1086	1529	2003	1815
NM_003611	OFD1	0.21	0.00	150	221	270	322
NM_002541	OGDH	0.14	0.00	5119	5883	9822	9516
NM_007346	OGFR	0.13	0.00	377	483	772	738
NM_024576	OGFRL1	0.32	0.00	463	665	674	752
NM_016828	OGG1	0.02	0.00	293	357	796	706
NM_001011708	OLA1	0.32	0.00	189	293	566	501
NM_015441	OLFML2B	0.05	-0.73	299	372	772	405
NM_001286352	OLFML3	0.06	-0.13	1102	1261	3444	2969
NM_130837	OPA1	0.24	0.00	962	1253	1938	1798
NM_182647	OPRL1	0.13	0.00	7	25	94	65
NM_001004462	OR10G4	0.80	0.00	41	109	131	128
NM_001190818	ORC1	0.49	0.00	337	555	154	120
NM_012381	ORC3	0.06	-0.26	167	221	501	355
NM_016467	ORMDL1	0.34	0.00	348	516	624	671
NM_001201480	OSBPL6	0.24	0.00	394	544	622	636
NM_145798	OSBPL7	0.07	0.00	85	124	164	152
NM_017807	OSGEP	0.26	-0.36	263	380	732	497
NM_182981	OSGIN1	0.04	0.00	681	791	416	455

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_005015	OXA1L	0.03	0.00	1703	1880	3433	3516
NM_000436	OXCT1	0.16	-0.17	473	609	1169	939
NM_001198533	OXR1	0.27	0.00	404	568	1279	1231
NM_000916	OXTR	0.07	-1.20	13965	15094	10394	4346
NM_006191	PA2G4	0.35	-0.50	1583	2177	2375	1555
NM_001267803	PAAF1	0.76	0.00	55	135	327	316
NM_004643	PABPN1	0.14	0.00	957	1169	1547	1508
NM_001100913	PACS2	0.13	0.00	1191	1429	3727	3673
NM_019088	PAF1	0.21	-0.05	756	977	1368	1209
NM_000430	PAFAH1B1	0.37	0.00	2101	2902	4274	4286
NM_002573	PAFAH1B3	0.07	-0.08	314	392	830	697
NM_006451	PAIP1	0.54	0.00	218	386	458	488
NM_001128620	PAK1	0.26	0.00	1024	1347	2668	2845
NM_002577	PAK2	0.33	0.00	1666	2255	2641	2763
NM_007203	PALM2-AKAP2	0.22	-0.15	8867	10707	24263	21369
NM_016069	PAM16	0.04	0.00	197	253	399	373
NM_148977	PANK1	0.19	0.00	77	123	121	137
NM_024594	PANK3	0.05	0.00	472	564	811	860
NM_152911	PAOX	0.39	0.00	52	101	127	139
NM_001040284	PAPD5	0.29	0.00	445	628	589	608
NM_173462	PAPLN	0.99	0.00	11	51	160	146
NM_022894	PAPOLG	0.08	0.01	276	352	406	477
NM_002581	PAPPA	0.09	0.00	1798	2060	10906	10872
NM_133367	PAQR8	0.17	0.00	26	51	143	163
NM_198504	PAQR9	1.49	0.00	18	91	29	46
NM_001184785	PARD3	0.66	0.00	336	620	1291	1364
NM_018622	PARL	0.27	0.00	146	225	458	477
NM_001618	PARP1	0.24	-0.36	1308	1681	1682	1201
NM_022750	PARP12	0.34	0.00	1094	1523	1023	970
NM_017554	PARP14	0.07	0.00	624	745	828	847
NM_001042618	PARP2	0.32	0.00	372	542	487	555
NM_006437	PARP4	0.21	0.00	1502	1882	3766	3954
NM_031458	PARP9	0.46	-0.14	146	256	520	405
NM_001252120	PASK	0.19	0.00	182	259	318	351
NM_152716	PATL1	0.19	0.00	1136	1424	1379	1325
NM_006195	PBX3	0.40	0.00	716	1058	1751	1660
NM_001040716	PC	0.31	0.00	608	850	1231	1325
NM_000532	PCCB	0.31	0.00	445	636	950	978
NM_019035	PCDH18	0.49	-0.39	1973	2962	6738	4915

Table 6A: Differentially Upregulated Genes in SR + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001173523	PCDH7	0.10	0.00	265	344	374	347
NM_022760	PCED1A	0.21	0.00	276	384	566	593
NM_002592	PCNA	0.40	-0.21	1467	2090	1543	1222
NM_032223	PCNXL3	0.15	0.00	2228	2651	3870	3835
NM_002593	PCOLCE	0.10	-0.23	1538	1782	3084	2462
NM_004716	PCSK7	0.40	-0.21	2203	3109	4952	4072
NM_001184917	PCYT2	0.05	-0.05	448	538	1678	1492
NM_001199462	PDCD2	0.23	0.00	243	345	499	458
NM_032346	PDCD2L	0.30	0.00	88	148	125	120
NM_182612	PDDC1	0.06	0.00	877	1015	2458	2384
NM_177966	PDE12	0.37	0.00	753	1085	1229	1172
NM_000921	PDE3A	0.09	0.00	664	796	796	741
NM_001111308	PDE4A	0.31	0.00	476	678	1077	1161
NM_002607	PDGFA	0.32	-0.04	612	866	790	682
NM_006206	PDGFRA	0.15	-0.63	3877	4533	5085	3109
NM_001173454	PDHA1	0.18	-0.03	1069	1328	1770	1604
NM_006457	PDLIM5	0.06	0.00	7107	7674	8695	8976
NM_001161779	PDP1	0.30	0.00	839	1145	1845	1808
NM_006474	PDPN	0.11	0.00	97	142	40	55
NM_014317	PDSS1	0.17	0.00	24	48	77	76
NM_020381	PDSS2	0.27	0.00	330	470	836	898
NM_016484	PDZD11	0.56	0.00	203	367	928	994
NM_001080471	PEAR1	0.21	-1.16	1926	2387	510	187
NM_001040152	PEG10	0.14	-0.32	1116	1351	616	425
NM_001135690	PENK	0.60	-1.15	4042	6409	3625	1525
NM_000285	PEPD	0.42	-0.23	1234	1795	2797	2238
NM_001243225	PES1	0.05	0.00	1792	2005	2469	2368
NM_001164811	PET117	0.25	0.00	212	310	347	383
NM_000466	PEX1	0.18	0.00	173	247	430	457
NM_003846	PEX11B	0.19	0.00	249	344	794	887
NM_004565	PEX14	0.29	0.00	240	356	414	451
NM_000318	PEX2	0.75	0.00	254	509	630	643
NM_012393	PFAS	0.36	-0.47	716	1026	1198	778
NM_002622	PFDN1	0.68	-0.15	484	884	1651	1366
NM_053024	PFN2	0.13	0.00	2363	2751	5906	5865
NM_001170543	PGAM5	0.28	0.00	1065	1425	1373	1312
NM_033419	PGAP3	0.10	-0.08	118	167	528	431
NM_152595	PGBD4	0.52	0.00	24	60	56	59
NM_002631	PGD	0.33	0.00	985	1367	4920	4845

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_005023	PGGT1B	0.37	0.00	95	165	229	237
NM_012088	PGLS	0.17	0.00	983	1222	2464	2445
NM_018290	PGM2	0.02	0.00	928	1045	1840	1872
NM_024419	PGS1	0.06	0.00	473	570	1023	1041
NM_001048183	PHACTR4	0.08	-0.06	620	743	859	732
NM_001281496	PHB	0.05	-0.21	1356	1529	2793	2257
NM_001144831	PHB2	0.13	-0.25	2884	3352	5103	4100
NM_004426	PHC1	0.11	0.00	485	604	948	874
NM_015651	PHF19	0.33	-0.03	1010	1397	1291	1152
NM_005392	PHF2	0.18	-0.02	1074	1334	1778	1614
NM_032458	PHF6	0.10	0.00	461	572	713	660
NM_000292	PHKA2	0.25	0.00	439	604	834	835
NM_000294	PHKG2	0.41	0.00	410	630	803	738
NM_001134438	PHLDB2	0.31	-0.13	783	1079	2263	1928
NM_015020	PHLPP2	0.07	0.00	679	807	873	970
NM_006214	PHYH	0.40	-0.01	251	398	1019	913
NM_001100876	PHYHD1	0.48	-0.50	39	85	239	131
NM_018323	PI4K2B	0.02	0.00	359	429	643	617
NM_058004	PI4KA	0.17	-0.08	2111	2551	6416	5828
NM_080476	PIGU	0.39	-0.13	231	367	580	460
NM_001042616	PIGY	0.09	0.00	555	675	834	896
NM_014602	PIK3R4	0.26	0.00	627	851	1163	1131
NM_001193621	PINLYP	0.07	-0.24	38	64	89	50
NM_017884	PINX1	0.17	0.00	251	343	314	285
NM_005028	PIP4K2A	0.24	0.00	1236	1599	2597	2445
NM_001135638	PIP5K1A	0.31	-0.13	1294	1751	1531	1277
NM_014338	PISD	0.10	-0.13	728	875	1321	1100
NM_001284278	PITPNB	0.07	0.00	1291	1484	1913	1989
NM_138370	PKDCC	0.13	0.00	207	281	183	179
NM_181805	PKIG	0.25	-0.17	599	809	1275	1028
NM_007069	PLA2G16	0.38	0.00	155	255	275	327
NM_003560	PLA2G6	0.69	0.00	31	81	175	194
NM_001012973	PLAC9	0.93	0.00	128	310	277	274
NM_000932	PLCB3	0.18	0.00	1655	2030	3302	3353
NM_001243108	PLD2	0.15	0.00	428	551	1281	1207
NM_024310	PLEKHF1	0.42	0.00	87	159	208	233
NM_024613	PLEKHF2	0.56	0.00	78	158	191	233
NM_022835	PLEKHG2	0.46	-0.51	431	683	1470	939
NM_015432	PLEKHG4	0.22	-0.41	528	704	1414	963

Table 6A: Differentially Upregulated Genes in SR + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_172069	PLEKHH2	0.51	-0.08	48	102	364	287
NM_018049	PLEKHJ1	0.06	0.00	502	602	838	791
NM_015164	PLEKHM2	0.18	0.00	5242	6193	9103	9425
NM_016274	PLEKHO1	0.12	0.00	1454	1717	2708	2769
NM_025201	PLEKHO2	0.14	0.00	1008	1228	2427	2521
NM_001164189	PLIN3	0.14	-0.04	7305	8341	16793	15924
NM_005030	PLK1	0.39	-1.00	957	1382	1177	521
NM_002669	PLRG1	0.10	0.00	1048	1238	2086	2128
NM_021105	PLSCR1	0.32	0.00	208	320	381	410
NM_021127	PMAIP1	0.43	-0.26	200	332	204	131
NM_001199653	PMF1	0.01	-0.24	412	486	934	702
NM_033238	PML	0.16	0.00	1114	1365	2236	2377
NM_002676	PMM1	0.43	-0.06	732	1104	2978	2688
NM_000303	PMM2	0.13	0.00	1167	1403	1599	1490
NM_001281455	PMP22	0.20	0.00	1867	2309	3192	3152
NM_001282946	PMPCA	0.03	-0.08	1069	1207	2352	2079
NM_000535	PMS2	0.29	0.00	191	290	516	462
NM_006556	PMVK	0.03	-0.08	370	444	973	824
NM_001077399	PNKD	0.65	-0.37	83	177	487	318
NM_020143	PNO1	0.18	0.00	293	396	410	445
NM_018129	PNPO	0.13	0.00	344	444	1160	1055
NM_001199781	POC1B-GALNT4	0.11	0.00	255	334	566	610
NM_001099271	POC5	0.18	0.00	82	129	137	118
NM_017542	POGK	0.06	0.00	1187	1355	1466	1349
NM_002689	POLA2	0.62	-0.14	547	950	728	579
NM_001256879	POLD2	0.02	0.00	940	1058	2213	2079
NM_015584	POLDIP2	0.26	-0.01	1667	2158	3858	3639
NM_001278657	POLDIP3	0.10	0.00	1431	1672	2531	2545
NM_001278255	POLE3	0.53	-0.02	782	1257	1229	1100
NM_006502	POLH	0.13	-0.08	1379	1641	2244	1978
NM_015425	POLR1A	0.18	-0.12	1411	1739	3067	2660
NM_004805	POLR2D	0.50	0.00	465	756	761	830
NM_002696	POLR2G	0.43	0.00	547	836	1329	1338
NM_006233	POLR2I	0.48	0.00	444	713	905	924
NM_006234	POLR2J	0.07	0.00	493	598	919	830
NM_021128	POLR2L	0.40	-0.45	2046	2889	5698	3989
NM_006467	POLR3G	0.21	0.00	63	105	135	135
NM_032305	POLR3GL	0.90	0.00	61	161	320	342
NM_001018050	POLR3H	0.31	0.00	1275	1725	3001	3030

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_005035	POLRMT	0.34	0.00	391	576	865	854
NM_015932	POMP	0.10	0.00	1162	1366	2352	2516
NM_013382	POMT2	0.23	0.00	355	490	1264	1344
NM_012230	POMZP3	0.11	0.00	296	383	491	518
NM_006627	POP4	0.42	0.00	420	652	930	941
NM_000941	POR	0.19	0.00	1425	1763	3192	3340
NM_001277406	POTEI	0.69	0.00	550	1006	478	551
NM_021129	PPA1	0.54	0.00	237	416	468	429
NM_176869	PPA2	0.71	-0.22	182	368	1079	834
NM_003713	PPAP2B	0.48	-0.45	1703	2546	2327	1579
NM_203453	PPAPDC2	0.64	-0.17	58	130	260	185
NM_024299	PPDPF	0.22	0.00	2125	2641	4344	4429
NM_006112	PPIE	0.35	0.00	567	819	1242	1270
NM_005729	PPIF	0.01	0.00	3731	3965	2138	2155
NM_006347	PPIH	0.39	-0.19	84	151	252	176
NM_014337	PPIL2	0.17	0.00	806	1012	1504	1627
NM_014634	PPM1F	0.23	-0.11	1853	2335	3575	3139
NM_177983	PPM1G	0.10	0.00	2059	2360	2441	2549
NM_001122764	PPOX	0.16	0.00	169	239	534	530
NM_002710	PPP1CC	0.28	0.00	1316	1734	1514	1457
NM_002714	PPP1R10	0.11	0.00	2033	2347	2456	2495
NM_021959	PPP1R11	0.30	-0.01	676	936	2075	1913
NM_002480	PPP1R12A	0.30	0.00	2181	2869	3635	3503
NM_001271618	PPP1R12C	0.10	0.00	987	1170	1938	2024
NM_138689	PPP1R14B	0.15	-0.22	782	971	1585	1250
NM_014811	PPP1R26	0.22	0.00	344	471	809	847
NM_145030	PPP1R35	0.03	-0.09	207	262	302	231
NM_006242	PPP1R3D	0.16	0.00	239	325	256	229
NM_001276318	PPP1R3E	0.29	0.00	52	95	114	131
NM_014225	PPP2R1A	0.55	0.00	5745	8742	18057	17800
NM_002717	PPP2R2A	0.14	0.00	652	810	880	969
NM_002718	PPP2R3A	0.37	0.00	773	1112	1252	1285
NM_013239	PPP2R3B	0.56	0.00	183	334	420	475
NM_017917	PPP2R3C	0.10	0.00	270	349	624	686
NM_178001	PPP2R4	0.48	-0.15	1780	2666	5669	4867
NM_006247	PPP5C	0.10	0.00	1822	2107	2728	2553
NM_001123355	PPP6C	0.15	0.00	621	780	986	956
NM_001242898	PPP6R2	0.18	0.00	1142	1419	2548	2710
NM_015062	PPRC1	0.04	0.00	2162	2379	2498	2643

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_000310	PPT1	0.18	-0.01	1067	1330	2017	1854
NM_001278926	PPWD1	0.16	0.00	276	371	497	560
NM_025078	PQLC1	0.14	0.00	859	1056	1370	1492
NM_001040125	PQLC2	0.02	0.00	619	715	867	896
NM_007213	PRAF2	0.05	0.00	885	1017	1940	1978
NM_003981	PRC1	0.03	-0.98	2695	2934	2502	1170
NM_199418	PRCP	0.04	0.00	948	1082	1759	1706
NM_001282934	PRDM15	0.10	0.01	344	437	489	567
NM_006793	PRDX3	0.02	0.00	1190	1325	2662	2573
NM_013388	PREB	0.30	0.00	1521	2030	1895	1824
NM_013237	PRELID1	0.49	-0.06	1259	1927	3151	2850
NM_006150	PRICKLE3	0.07	0.00	168	224	258	224
NM_000946	PRIM1	0.04	0.00	106	146	58	50
NM_000947	PRIM2	0.37	-0.14	362	549	460	355
NM_206907	PRKAA1	0.07	-0.02	994	1156	2136	1957
NM_002732	PRKACG	0.14	0.00	133	190	381	444
NM_001206710	PRKAG1	0.06	0.00	1255	1432	2350	2216
NM_001040633	PRKAG2	0.10	0.00	679	819	967	991
NM_001164760	PRKAR1B	0.04	0.00	204	260	397	377
NM_145040	PRKCDBP	0.05	-0.27	975	1117	2261	1743
NM_005400	PRKCE	0.07	0.00	316	396	534	527
NM_006255	PRKCH	0.91	0.00	13	51	85	78
NM_002742	PRKD1	0.04	0.00	1354	1515	2042	2061
NM_006904	PRKDC	0.05	-0.04	6452	6943	13025	12318
NM_005788	PRMT3	0.09	0.00	197	261	354	311
NM_001039619	PRMT5	0.31	0.00	1286	1740	1913	1815
NM_018137	PRMT6	0.12	0.00	230	306	302	279
NM_153256	PROSER2	0.32	0.00	186	288	141	172
NM_014502	PRPF19	0.02	-0.04	2027	2207	2051	1858
NM_015629	PRPF31	0.21	0.00	982	1256	1680	1632
NM_017922	PRPF39	0.18	0.00	255	349	356	388
NM_001244926	PRPF4	0.21	0.00	903	1155	1605	1510
NM_017892	PRPF40A	0.09	0.00	1577	1813	2525	2638
NM_006445	PRPF8	0.32	0.00	10139	13025	18796	19088
NM_002764	PRPS1	0.38	-0.37	2762	3797	4731	3486
NM_002766	PRPSAP1	0.36	0.00	452	667	1125	1207
NM_020719	PRR12	0.25	0.00	664	888	747	688
NM_018457	PRR13	0.33	-0.09	395	577	1553	1338
NM_024031	PRR14	0.23	0.00	422	573	574	610

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_173566	PRR14L	0.15	0.00	1221	1487	1843	1933
NM_016644	PRR16	0.18	-0.21	413	545	424	309
NM_199285	PRR19	0.07	0.00	58	90	227	203
NM_025263	PRR3	0.34	0.00	89	153	177	157
NM_004638	PRRC2A	0.18	-0.12	8554	10007	12164	10817
NM_013318	PRRC2B	0.05	0.01	6737	7247	11648	12055
NM_001173489	PRRG1	0.19	0.00	306	415	374	372
NM_016307	PRRX2	0.10	-0.27	482	597	776	566
NM_172341	PSENEN	0.29	0.00	254	375	799	787
NM_001184825	PSG1	0.36	-0.04	110	187	204	155
NM_031246	PSG2	0.16	0.00	209	289	299	287
NM_002780	PSG4	0.34	-0.07	1589	2168	3350	3018
NM_001130167	PSG8	0.16	0.00	52	87	108	140
NM_006742	PSKH1	0.21	0.00	1274	1609	2868	2950
NM_002786	PSMA1	0.23	0.00	1402	1782	2159	2026
NM_002787	PSMA2	0.85	0.00	353	741	747	669
NM_002790	PSMA5	0.23	-0.19	1051	1360	1915	1547
NM_001282232	PSMA6	0.34	-0.07	730	1034	1458	1268
NM_002792	PSMA7	0.10	-0.11	3420	3876	6549	5802
NM_002793	PSMB1	0.57	0.00	1808	2887	4767	4935
NM_002794	PSMB2	0.24	0.00	1859	2361	3161	3240
NM_002795	PSMB3	0.19	-0.10	1288	1607	3259	2872
NM_002796	PSMB4	0.08	0.00	3718	4146	6961	6780
NM_001144932	PSMB5	0.37	-0.06	3103	4225	6906	6342
NM_001270481	PSMB6	0.13	-0.05	2176	2554	4586	4218
NM_004159	PSMB8	0.17	-0.19	420	549	861	669
NM_002803	PSMC2	0.10	-0.12	880	1046	2063	1760
NM_002804	PSMC3	0.22	-0.21	1655	2085	4143	3397
NM_006503	PSMC4	0.22	0.00	1804	2260	3280	3371
NM_002807	PSMD1	0.16	-0.01	2277	2720	5162	4882
NM_001270482	PSMD11	0.29	-0.01	2736	3551	4349	4118
NM_002817	PSMD13	0.41	-0.05	2208	3125	4723	4344
NM_002810	PSMD4	0.27	0.00	571	783	1435	1388
NM_005047	PSMD5	0.06	-0.06	911	1056	2073	1845
NM_001271779	PSMD6	0.15	0.00	1102	1340	1870	1800
NM_002811	PSMD7	0.59	0.00	624	1053	1308	1240
NM_002813	PSMD9	0.06	-0.09	1517	1712	2795	2460
NM_002818	PSME2	0.46	-0.17	131	232	430	322
NM_001267045	PSME3	0.30	-0.05	2495	3266	4166	3811

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_006814	PSMF1	0.14	0.00	1791	2124	3569	3697
NM_001261824	PSMG1	0.39	0.00	429	650	857	773
NM_020232	PSMG2	0.15	0.00	436	563	722	780
NM_032302	PSMG3	0.30	-0.37	315	460	510	336
NM_001128592	PSMG4	0.17	-0.01	129	189	212	165
NM_001032291	PSRC1	0.78	-0.66	138	300	304	153
NM_024430	PSTPIP2	0.41	-0.09	237	382	428	340
NM_002819	PTBP1	0.12	-0.04	4837	5496	5499	5122
NM_001163788	PTBP3	0.19	0.00	991	1252	1477	1566
NM_017952	PTCD3	0.11	0.00	515	637	830	850
NM_001166292	PTCH2	1.39	-0.50	1767	4937	3298	2185
NM_025072	PTGES2	0.33	0.00	521	746	1778	1699
NM_001136042	PTGES3L-AARSD1	0.33	-0.04	259	391	532	445
NM_000960	PTGIR	0.33	0.00	282	424	732	717
NM_012212	PTGR1	0.30	0.00	518	731	1680	1734
NM_152444	PTGR2	0.15	0.00	35	63	139	116
NM_002824	PTMS	1.00	-0.05	2432	5150	3406	3107
NM_001253830	PTPDC1	0.02	0.00	308	373	630	717
NM_014241	PTPLA	0.24	0.00	228	328	437	396
NM_002834	PTPN11	0.26	0.00	3195	4054	6097	6270
NM_014369	PTPN18	0.18	0.00	701	893	801	752
NM_015466	PTPN23	0.36	0.00	1835	2523	3074	3018
NM_002833	PTPN9	0.27	0.00	1019	1354	1986	2085
NM_002837	PTPRB	0.09	0.00	1488	1715	2427	2440
NM_002842	PTPRH	0.04	0.00	94	132	54	67
NM_001291981	PTPRK	0.28	0.00	2721	3504	4095	4155
NM_000317	PTS	0.01	0.00	337	403	609	643
NM_001282382	PTTG1	0.27	-1.35	389	548	595	192
NM_002852	PTX3	0.51	-0.41	8141	11999	2774	1952
NM_001271098	PUF60	0.03	0.00	3073	3315	4353	4279
NM_019042	PUS7	0.17	0.00	345	458	507	499
NM_153339	PUSL1	0.35	0.00	183	291	322	287
NM_002855	PVRL1	0.62	0.01	195	368	378	447
NM_002856	PVRL2	0.15	0.00	1510	1822	2290	2405
NM_001243286	PVRL3	0.33	0.00	596	846	1098	1176
NM_005049	PWP2	0.15	0.00	931	1146	1133	1074
NM_007238	PXMP4	0.25	0.00	217	316	597	597
NM_138300	PYGO2	0.10	0.00	502	618	942	865
NM_032906	PYURF	0.09	0.00	555	675	834	896

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_018292	QRSL1	0.03	-0.22	174	224	393	281
NM_031209	QTRT1	0.05	0.00	356	436	709	682
NM_024638	QTRTD1	0.10	0.00	408	511	485	497
NM_138774	R3HDM4	0.13	0.00	725	894	1194	1142
NM_016322	RAB14	0.04	0.00	1942	2150	3479	3553
NM_016277	RAB23	0.33	0.00	730	1028	1568	1676
NM_004163	RAB27B	0.02	0.00	22	41	1059	1087
NM_006834	RAB32	0.85	-0.08	1109	2178	2263	1987
NM_001144942	RAB34	0.28	0.00	1770	2312	3893	3991
NM_013401	RAB3IL1	0.15	-0.05	256	343	1073	932
NM_201434	RAB5C	0.48	0.00	3380	4951	6567	6523
NM_012197	RABGAP1	0.17	0.00	1061	1311	2365	2285
NM_014857	RABGAP1L	0.46	0.00	222	372	992	991
NM_004581	RABGGTA	0.67	0.00	789	1396	1886	1920
NM_002871	RABIF	0.10	0.00	415	519	663	671
NM_002853	RAD1	0.33	0.00	329	488	395	453
NM_006265	RAD21	0.01	0.00	2135	2307	2539	2384
NM_001270362	RAD23A	0.06	-0.18	3990	4387	6726	5700
NM_002874	RAD23B	0.29	0.00	2683	3483	5006	5041
NM_002875	RAD51	0.07	-0.44	380	469	297	176
NM_003610	RAE1	0.45	0.00	532	826	876	885
NM_001001788	RAET1G	1.70	0.00	2	32	94	67
NM_002880	RAF1	0.47	0.00	1945	2894	3858	4015
NM_016732	RALY	0.33	0.00	2075	2782	4163	4055
NM_001278639	RANBP1	0.34	-0.21	347	517	624	468
NM_020850	RANBP10	0.04	0.00	368	447	792	885
NM_003624	RANBP3	0.17	0.00	1260	1550	2086	1959
NM_012294	RAPGEF5	0.87	0.00	19	63	31	24
NM_001042728	RARG	0.18	0.00	930	1169	1493	1577
NM_002887	RARS	0.44	0.00	1354	1996	2473	2421
NM_007368	RASA3	0.23	0.00	3051	3785	5563	5562
NM_017805	RASIP1	0.29	-0.90	334	482	863	401
NM_170713	RASSF1	0.16	0.00	1440	1753	1614	1497
NM_178169	RASSF3	0.20	-0.43	903	1148	2117	1449
NM_133452	RAVER1	0.04	0.00	1284	1446	1144	1129
NM_006606	RBBP9	0.76	0.00	191	397	821	745
NM_006047	RBM12	0.06	-0.20	2660	2953	2425	1974
NM_006328	RBM14	0.04	-0.06	1616	1800	1778	1571
NM_001291780	RBM38	0.30	0.00	116	188	162	207

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_002896	RBM4	0.10	0.00	1401	1636	2485	2632
NM_024321	RBM42	0.05	0.00	1455	1635	1832	1741
NM_005777	RBM6	0.15	0.00	895	1100	1385	1309
NM_005105	RBM8A	0.19	0.00	459	605	724	795
NM_001251974	RCAN2	0.06	0.00	87	125	152	118
NM_001268	RCBTB2	0.07	0.00	75	111	285	329
NM_002901	RCN1	0.26	0.00	3097	3931	6362	6102
NM_020905	RDH14	0.31	0.00	216	328	482	527
NM_001048205	REC8	0.49	0.00	23	57	77	100
NM_004260	RECQL4	0.02	0.00	370	443	443	381
NM_004259	RECQL5	0.17	0.00	167	238	293	342
NM_025232	REEP4	0.04	-0.21	478	569	616	462
NM_005045	RELN	0.17	-0.29	2490	2989	925	671
NM_002910	RENBP	0.04	0.00	78	113	285	251
NM_013400	REPIN1	0.12	0.00	721	878	984	933
NM_001278791	RFC2	0.21	-0.03	457	611	493	414
NM_002916	RFC4	0.07	-0.17	422	516	318	231
NM_018339	RFK	0.23	-0.02	374	513	788	688
NM_015150	RFTN1	0.32	0.00	1639	2210	4062	3974
NM_022457	RFWD2	0.11	0.00	249	326	489	484
NM_018124	RFWD3	0.11	-0.18	1265	1495	1346	1081
NM_000449	RFX5	0.23	0.00	414	565	1140	1166
NM_003721	RFXANK	0.32	-0.26	606	853	1395	1057
NM_001012761	RGMB	0.44	-0.12	6096	8610	9602	8534
NM_001282848	RGN	0.39	-0.49	31	67	195	105
NM_002926	RGS12	0.18	0.00	369	489	697	750
NM_006480	RGS14	0.73	0.00	68	158	206	174
NM_001282773	RGS7	0.37	0.00	52	100	33	31
NM_001242359	RHOBTB1	0.57	0.00	297	521	799	736
NM_014578	RHOD	0.41	-0.21	193	317	670	505
NM_001665	RHOG	0.21	0.00	1659	2070	2188	2264
NM_138769	RHOT2	0.10	0.00	1041	1231	1364	1423
NM_033103	RHPN2	0.49	0.00	37	82	19	33
NM_021932	RIC8A	0.25	0.00	5016	6222	8539	8504
NM_018157	RIC8B	0.19	0.01	291	397	510	591
NM_018151	RIF1	0.09	0.00	1405	1632	1649	1784
NM_145058	RILPL2	0.21	0.00	192	277	198	205
NM_004292	RIN1	0.36	0.00	245	381	480	551
NM_024832	RIN3	0.08	0.00	963	1130	1774	1867

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_018343	RIOK2	0.07	0.00	439	537	634	710
NM_016033	RMDN1	0.72	0.00	180	365	790	841
NM_152308	RMI2	0.01	0.00	74	106	73	70
NM_032193	RNASEH2C	0.66	0.00	515	926	1470	1590
NM_022064	RNF123	0.05	0.00	1076	1231	2215	2379
NM_001184992	RNF135	0.14	0.00	287	379	584	647
NM_016422	RNF141	0.18	0.00	463	607	1046	1035
NM_001242844	RNF146	0.37	0.00	263	409	722	708
NM_016494	RNF181	0.57	0.00	331	575	1242	1227
NM_001256071	RNF213	0.12	0.00	6897	7790	17419	17770
NM_024546	RNF219	0.17	0.00	270	365	343	362
NM_022453	RNF25	0.13	0.00	376	484	932	850
NM_002938	RNF4	0.51	0.00	859	1357	1834	1957
NM_001207033	RNF40	0.41	0.00	2057	2925	4484	4628
NM_006913	RNF5	0.04	0.00	345	421	510	564
NM_203387	RNH1	0.25	-0.01	5557	6898	14959	14456
NM_001286625	RNPS1	0.43	0.00	1377	2012	2209	2116
NM_022370	ROBO3	0.51	0.00	72	143	110	124
NM_002945	RPA1	0.32	0.00	1625	2182	2523	2569
NM_001286076	RPA2	0.23	-0.06	400	547	532	440
NM_002947	RPA3	1.09	0.00	18	70	79	68
NM_001033002	RPAIN	0.26	0.00	590	803	905	948
NM_015540	RPAP1	0.46	0.00	538	842	1233	1320
NM_001278283	RPE	0.26	0.00	258	374	755	684
NM_006013	RPL10	0.15	-0.08	4357	5056	9288	8468
NM_007104	RPL10A	0.27	-0.39	1480	1938	3232	2307
NM_000975	RPL11	0.07	-0.12	4723	5204	8961	7965
NM_000976	RPL12	1.00	-0.11	317	741	1013	843
NM_033251	RPL13	0.41	-0.38	4442	6194	10648	7885
NM_012423	RPL13A	0.44	-0.22	2671	3849	5987	4915
NM_001253382	RPL15	0.26	-0.24	6011	7518	14955	12327
NM_000985	RPL17	1.05	0.00	996	2258	2716	2896
NM_001199356	RPL17-C18orf32	0.43	0.00	562	861	1291	1416
NM_000979	RPL18	0.11	-0.29	4194	4757	7699	6039
NM_000980	RPL18A	0.49	-0.41	1354	2065	3525	2503
NM_000981	RPL19	0.64	-0.23	1380	2332	3506	2817
NM_000982	RPL21	0.51	0.00	93	178	177	148
NM_000983	RPL22	0.19	-0.01	1208	1507	2658	2466
NM_000984	RPL23A	0.24	-0.12	1690	2158	3078	2671

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_000986	RPL24	1.00	-0.16	345	801	980	784
NM_000987	RPL26	0.31	-0.09	1272	1720	3084	2725
NM_000990	RPL27A	0.12	-0.03	2132	2480	3388	3122
NM_001136134	RPL28	0.69	-0.02	4317	7259	9013	8553
NM_000967	RPL3	0.45	-0.28	6338	8994	11900	9482
NM_000989	RPL30	0.04	0.00	4147	4492	5987	5970
NM_001099693	RPL31	0.43	-0.13	380	597	1027	843
NM_001007074	RPL32	0.97	-0.46	3916	8037	68665	49312
NM_033625	RPL34	0.33	-0.20	374	548	772	593
NM_007209	RPL35	0.07	-0.22	2140	2415	5538	4532
NM_033643	RPL36	0.80	-0.35	822	1579	2196	1593
NM_021029	RPL36A	0.13	-0.52	69	108	166	85
NM_001199973	RPL36A-HNRNPH2	0.09	0.00	1240	1441	2543	2377
NM_001001	RPL36AL	0.18	0.00	1475	1817	2217	2327
NM_052969	RPL39L	1.09	-0.17	82	234	302	218
NM_000968	RPL4	0.31	-0.31	4844	6298	10964	8527
NM_000969	RPL5	0.22	-0.12	2280	2836	5160	4514
NM_000971	RPL7	0.39	-0.16	506	757	1111	893
NM_000972	RPL7A	0.36	-0.45	2918	3971	7740	5431
NM_001024921	RPL9	1.18	-0.12	389	1013	1096	906
NM_053275	RPLP0	0.31	-0.17	10422	13300	18261	15881
NM_001003	RPLP1	0.70	-0.34	1964	3408	3157	2338
NM_001004	RPLP2	1.11	-0.03	1117	2624	2797	2577
NM_148179	RPP25L	0.42	0.00	144	246	383	421
NM_183005	RPP38	0.13	0.00	302	395	420	431
NM_021215	RPRD1B	0.38	0.00	558	824	1108	1172
NM_001203245	RPS10	0.40	0.00	753	1108	1425	1353
NM_001202470	RPS10-NUDT3	0.38	0.00	998	1430	1903	1991
NM_001015	RPS11	0.68	0.00	3469	5838	8223	7904
NM_001016	RPS12	0.44	0.00	1065	1584	1911	1810
NM_001017	RPS13	0.04	-0.17	752	870	1281	1035
NM_001025070	RPS14	0.87	-0.48	1170	2319	4280	2911
NM_001018	RPS15	0.38	-0.55	1636	2301	4648	3017
NM_001019	RPS15A	0.79	0.00	314	638	703	684
NM_001020	RPS16	0.46	-0.24	2732	3995	5147	4159
NM_022551	RPS18	0.90	-0.26	517	1090	1845	1416
NM_194326	RPS19BP1	0.08	0.00	859	1012	1391	1357
NM_002952	RPS2	0.18	-0.35	4327	5142	7042	5303

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001023	RPS20	0.37	0.00	2165	2985	3625	3506
NM_001024	RPS21	0.21	0.00	273	380	605	593
NM_001025	RPS23	0.60	-0.38	1525	2500	3660	2652
NM_001030	RPS27	0.19	0.00	93	144	256	235
NM_015920	RPS27L	0.16	-0.13	1071	1313	3228	2773
NM_001032	RPS29	1.27	0.00	116	359	495	529
NM_001260506	RPS3	0.23	-0.35	5032	6168	8541	6445
NM_001007	RPS4X	0.20	-0.17	3478	4204	6929	5928
NM_001009	RPS5	0.54	-0.29	1682	2634	3764	2915
NM_001010	RPS6	0.22	-0.25	9254	11144	18727	15381
NM_021135	RPS6KA2	0.19	-0.20	4011	4813	7445	6236
NM_001006944	RPS6KA4	0.26	-0.32	994	1311	1805	1327
NM_001011	RPS7	0.53	-0.62	972	1548	2452	1477
NM_001012	RPS8	0.24	-0.28	5557	6843	12336	9848
NM_032795	RPUSD4	0.15	-0.22	615	775	977	749
NM_001271634	RQCD1	0.16	-0.26	1830	2205	2227	1728
NM_016656	RRAGB	0.03	0.00	150	197	225	266
NM_012250	RRAS2	0.17	0.00	587	751	1135	1190
NM_001033	RRM1	0.28	-0.11	1840	2399	2573	2224
NM_015997	RRNAD1	0.16	0.00	236	321	291	333
NM_016052	RRP15	0.06	-0.03	356	439	451	375
NM_033112	RRP36	0.68	-0.15	522	950	1720	1427
NM_015703	RRP7A	0.25	-0.08	892	1180	1539	1338
NM_004704	RRP9	0.35	-0.12	505	734	690	558
NM_018364	RSBN1	0.07	0.00	314	393	381	416
NM_001130841	RTCA	0.22	0.00	467	625	1341	1366
NM_014306	RTCB	0.17	0.00	2224	2682	3248	3447
NM_001283035	RTFDC1	0.19	0.00	1564	1931	3427	3495
NM_032730	RTN4IP1	0.33	-0.10	35	71	135	92
NM_173630	RTTN	0.21	0.00	454	605	537	490
NM_001037442	RUFY3	0.14	0.00	96	144	331	305
NM_001105203	RUSC1	0.10	-0.05	970	1148	1809	1614
NM_006666	RUVBL2	0.37	-0.23	1628	2263	2928	2342
NM_016104	RWDD1	0.25	-0.06	443	610	973	839
NM_016940	RWDD2B	0.29	0.00	264	388	489	564
NM_001278248	RWDD3	1.42	0.00	37	151	177	150
NM_001005861	RYK	0.29	0.00	496	693	1250	1213
NM_002960	S100A3	0.28	-0.11	50	91	162	113
NM_014624	S100A6	0.52	0.00	7410	10971	22491	22164

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001400	S1PR1	0.05	-0.14	1060	1212	799	641
NM_004230	S1PR2	0.14	0.00	615	769	717	799
NM_013299	SAC3D1	0.61	0.00	74	156	125	118
NM_005500	SAE1	0.38	-0.20	1853	2596	3022	2466
NM_138352	SAMD1	0.30	0.00	249	372	312	368
NM_017827	SARS2	0.68	-0.24	168	334	553	403
NM_015278	SASH1	0.18	0.00	2596	3123	4754	4811
NM_133491	SAT2	0.30	-0.28	639	890	1325	989
NM_001195470	SATB1	0.07	0.00	118	164	584	632
NM_018322	SAYSD1	0.39	0.00	82	148	345	331
NM_014963	SBNO2	0.18	0.00	1577	1933	1932	2026
NM_005698	SCAMP3	0.22	-0.14	1598	2012	3818	3286
NM_012235	SCAP	0.15	0.00	1395	1680	2034	1896
NM_153334	SCARF2	0.05	0.00	1973	2191	2835	2976
NM_016106	SCFD1	0.12	0.00	824	998	1714	1739
NM_152540	SCFD2	0.18	-0.56	1264	1559	3440	2189
NM_016510	SCLY	0.09	0.00	126	176	247	227
NM_001172218	SCMH1	0.07	0.00	669	791	1052	1057
NM_001037	SCN1B	0.03	0.00	67	99	331	307
NM_001204856	SCNM1	0.33	0.00	312	466	668	677
NM_001169111	SCO2	0.02	0.00	687	788	1377	1466
NM_002979	SCP2	0.26	0.00	976	1287	2350	2397
NM_007281	SCRG1	0.52	-0.14	77	153	44	22
NM_001288984	SDAD1	0.22	0.00	344	472	684	725
NM_002999	SDC4	0.29	-0.08	2244	2921	3165	2823
NM_006923	SDF2	0.37	0.00	685	992	1466	1516
NM_022044	SDF2L1	0.02	0.00	282	344	399	434
NM_017841	SDHAF2	0.14	0.00	439	561	846	902
NM_003000	SDHB	0.39	0.00	922	1333	2142	2225
NM_003001	SDHC	0.07	0.00	605	720	1722	1691
NM_001276506	SDHD	0.12	0.00	399	506	707	719
NM_001136026	SEC13	0.08	0.00	5442	5997	5634	5462
NM_014866	SEC16A	0.22	0.01	4629	5653	8462	8802
NM_001172746	SEC23B	0.14	0.00	1617	1927	2125	2244
NM_007190	SEC23IP	0.22	0.00	1236	1576	1965	2017
NM_004922	SEC24C	0.08	0.00	4174	4647	6630	6647
NM_006808	SEC61B	0.91	-0.21	318	701	1125	876
NM_001282688	SECISBP2	0.05	0.00	395	478	923	845
NM_003004	SECTM1	0.04	0.00	57	87	48	28

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_031216	SEH1L	0.04	0.00	866	994	1204	1311
NM_001258289	SELENBP1	0.19	-0.77	36	66	204	89
NM_016275	SELT	0.08	0.00	836	985	1730	1835
NM_006080	SEMA3A	0.21	0.00	228	323	308	261
NM_017893	SEMA4G	0.06	0.00	107	150	189	231
NM_153617	SEMA6D	0.16	-0.29	234	320	58	28
NM_015670	SENP3	0.05	0.00	1874	2086	2699	2806
NM_012247	SEPHS1	0.14	0.00	517	653	720	652
NM_020451	SEPN1	0.18	0.00	2972	3576	6002	6281
NM_003009	SEPW1	0.56	0.00	328	569	1689	1680
NM_004155	SERPINB9	0.24	-0.74	217	315	258	120
NM_002615	SERPINF1	0.34	-0.56	229	353	1210	734
NM_001207014	SERPINH1	0.28	-0.06	8513	10678	10523	9763
NM_003011	SET	0.52	0.00	1750	2687	3696	3560
NM_001160305	SETD6	0.17	0.00	142	206	293	333
NM_020382	SETD8	0.18	0.00	646	829	1258	1262
NM_001145415	SETDB1	0.18	0.00	550	711	772	858
NM_001287737	SETSIP	0.67	0.00	104	218	223	220
NM_007165	SF3A2	0.38	0.00	697	1014	586	628
NM_006802	SF3A3	0.32	0.00	616	869	925	882
NM_012426	SF3B3	0.31	-0.12	3833	4988	6451	5689
NM_005850	SF3B4	0.10	-0.07	1271	1488	1522	1325
NM_031287	SF3B5	0.21	-0.02	1359	1706	2859	2654
NM_016047	SF3B6	0.26	0.00	634	860	1431	1420
NM_005066	SFPQ	0.33	-0.05	2459	3294	2512	2274
NM_001261411	SFSWAP	0.28	-0.17	602	829	952	754
NM_030971	SFXN3	0.34	0.00	1235	1701	2595	2664
NM_213649	SFXN4	0.28	0.00	109	175	204	205
NM_144579	SFXN5	0.20	0.00	186	267	616	654
NM_005627	SGK1	0.05	-0.06	8304	8922	3589	3244
NM_147156	SGMS1	0.22	0.00	681	894	917	976
NM_015705	SGSM3	0.10	0.00	1076	1266	2236	2187
NM_001103161	SH2D5	0.08	-0.50	729	869	738	453
NM_031469	SH3BGRL2	2.14	0.00	1	31	77	83
NM_018957	SH3BP1	0.83	0.00	52	135	112	137
NM_014521	SH3BP4	0.28	-0.06	4207	5375	6443	5944
NM_001009555	SH3D19	0.17	0.00	1624	1971	2970	3066
NM_003025	SH3GL1	0.05	0.00	3189	3500	3802	3719
NM_020870	SH3RF1	0.27	0.00	3964	5024	4773	4810

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_024745	SHCBP1	0.05	-0.64	929	1066	782	436
NM_138356	SHF	1.28	-2.03	243	699	524	100
NM_001272067	SHISA5	0.12	-0.29	2286	2655	4887	3789
NM_004169	SHMT1	0.39	0.00	252	399	285	253
NM_013276	SHPK	0.42	0.00	397	615	736	776
NM_018130	SHQ1	0.25	0.00	302	428	412	447
NM_020859	SHROOM3	0.25	-0.21	1335	1723	2408	1939
NM_001199922	SIAE	0.13	0.00	173	239	749	760
NM_198567	SIMC1	0.71	0.00	105	226	125	129
NM_015073	SIPA1L3	0.07	0.00	5341	5852	4359	4264
NM_012237	SIRT2	0.11	-0.06	862	1036	2057	1837
NM_012241	SIRT5	0.04	-0.32	183	237	489	331
NM_016539	SIRT6	0.43	-0.11	207	341	532	423
NM_006427	SIVA1	0.31	-0.20	410	591	674	512
NM_005982	SIX1	0.22	0.00	209	301	532	593
NM_182620	SKA2	0.17	-0.02	338	448	485	410
NM_005983	SKP2	0.07	-0.45	390	480	539	336
NM_005072	SLC12A4	0.04	0.00	3320	3620	5682	5896
NM_012450	SLC13A4	0.10	0.00	40	68	141	150
NM_004172	SLC1A3	0.27	0.00	224	330	279	309
NM_006749	SLC20A2	0.20	0.00	2527	3093	6457	6471
NM_003562	SLC25A11	0.38	0.00	1106	1578	2063	2116
NM_001160210	SLC25A13	0.12	0.00	263	345	464	433
NM_014252	SLC25A15	0.22	0.00	171	251	343	298
NM_021734	SLC25A19	0.67	0.00	119	246	293	268
NM_000387	SLC25A20	0.11	0.00	197	265	684	738
NM_024698	SLC25A22	0.29	-0.07	665	918	898	763
NM_013386	SLC25A24	0.14	-0.01	984	1196	1714	1569
NM_213611	SLC25A3	0.24	-0.22	5866	7201	10822	8978
NM_032315	SLC25A33	0.75	0.00	40	103	96	87
NM_017875	SLC25A38	0.20	0.00	395	531	709	706
NM_018843	SLC25A40	0.22	-0.03	173	254	287	229
NM_145305	SLC25A43	0.32	0.00	453	650	1198	1198
NM_001286184	SLC25A44	0.54	0.00	573	944	1183	1170
NM_001152	SLC25A5	0.25	-0.46	2798	3536	4390	3018
NM_001166347	SLC26A11	0.15	0.00	203	279	497	444
NM_005094	SLC27A4	0.08	-0.19	934	1093	2874	2357
NM_012254	SLC27A5	0.05	-0.22	34	58	79	44
NM_001174098	SLC29A3	0.26	0.00	123	193	275	333

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_020062	SLC2A4RG	0.22	0.00	889	1149	1886	1859
NM_021194	SLC30A1	0.25	0.00	348	488	534	556
NM_080670	SLC35A4	0.07	-0.22	1472	1678	2512	2018
NM_015139	SLC35D1	0.23	0.00	439	594	1092	1144
NM_001164277	SLC37A4	0.04	0.00	384	462	618	566
NM_173514	SLC38A9	0.09	0.00	100	144	247	283
NM_001271957	SLC39A1	0.44	-0.22	1202	1783	2593	2079
NM_001039960	SLC4A8	0.85	0.00	28	83	366	420
NM_003041	SLC5A2	0.07	0.00	448	545	720	726
NM_012244	SLC7A8	0.29	0.00	75	128	2556	2510
NM_001260491	SLC9A8	0.38	0.00	186	300	724	717
NM_001289009	SLFN12	0.12	0.00	133	188	262	262
NM_144682	SLFN13	0.30	0.00	121	195	87	113
NM_004787	SLIT2	0.22	-0.20	2629	3250	3479	2859
NM_001014999	SLX1A	0.34	0.00	639	912	672	603
NM_024044	SLX1B	0.34	0.00	639	912	672	603
NM_005900	SMAD1	0.74	0.00	125	269	401	381
NM_005902	SMAD3	0.42	-0.27	984	1446	2394	1852
NM_001031628	SMAGP	0.67	0.00	178	351	695	730
NM_022733	SMAP2	0.05	-0.44	1083	1234	2159	1475
NM_003069	SMARCA1	0.04	-0.31	765	885	1770	1312
NM_003076	SMARCD1	0.19	0.00	1179	1471	1583	1715
NM_001098426	SMARCD2	0.06	0.00	1363	1553	1853	1861
NM_003079	SMARCE1	0.51	0.00	673	1074	1470	1405
NM_015110	SMC5	0.19	0.00	696	892	1144	1037
NM_020179	SMCO4	0.35	0.00	149	241	121	133
NM_033318	SMDT1	0.37	0.00	226	355	497	464
NM_001124767	SMIM4	0.12	-0.27	132	187	597	427
NM_005871	SMNDC1	0.27	0.00	366	517	570	636
NM_018225	SMU1	0.22	0.00	462	621	859	932
NM_020197	SMYD2	0.43	0.00	618	942	1425	1549
NM_006062	SMYD5	0.59	0.00	591	1006	1221	1192
NM_003068	SNAI2	0.72	-0.20	777	1415	3885	3205
NM_053052	SNAP47	0.28	0.00	746	1015	1364	1455
NM_003082	SNAPC1	0.07	0.00	755	888	690	701
NM_012437	SNAPIN	0.06	0.00	270	340	747	811
NM_007241	SNF8	0.16	-0.03	516	659	1348	1203
NM_003498	SNN	0.10	0.00	325	414	799	884
NM_022717	SNRNP35	0.35	0.00	174	277	366	396

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_003090	SNRPA1	0.47	0.00	91	170	125	129
NM_003091	SNRPB	0.01	-0.19	5364	5663	5415	4543
NM_003093	SNRPC	0.19	-0.03	448	593	851	741
NM_177542	SNRPD2	0.10	-0.02	2155	2468	4706	4427
NM_006750	SNTB2	0.07	0.00	1911	2159	3463	3335
NM_005701	SNUPN	0.47	0.00	380	614	928	996
NM_001256188	SNX12	0.12	0.00	1524	1797	2647	2680
NM_013306	SNX15	0.10	0.00	383	480	487	542
NM_001102575	SNX18	0.03	0.00	689	796	1944	1821
NM_014758	SNX19	0.45	0.00	1816	2667	4739	4930
NM_001278199	SNX2	0.06	0.00	715	839	1753	1808
NM_014426	SNX5	0.63	0.00	300	549	676	638
NM_021249	SNX6	0.11	0.00	1178	1395	2789	2806
NM_015976	SNX7	0.22	0.00	287	399	842	900
NM_013321	SNX8	0.27	0.00	708	957	2003	1863
NM_003101	SOAT1	0.13	0.00	991	1196	1730	1671
NM_018013	SOBP	0.42	0.00	147	251	258	255
NM_014598	SOCS7	0.24	0.01	641	853	813	913
NM_005775	SORBS3	0.24	0.00	2230	2814	3367	3203
NM_006943	SOX12	0.40	0.00	288	452	699	712
NM_005686	SOX13	0.02	0.00	326	393	198	220
NM_001025436	SPAG16	0.53	0.00	55	116	171	159
NM_006461	SPAG5	0.19	-0.74	1406	1748	1310	706
NM_006038	SPATA2	0.48	0.00	200	343	302	362
NM_024063	SPATA5L1	0.50	0.00	100	188	235	214
NM_018418	SPATA7	0.64	0.00	41	98	137	133
NM_001100423	SPATS2L	0.06	0.00	2522	2798	5170	5007
NM_182513	SPC24	0.62	-0.83	97	199	235	100
NM_020675	SPC25	0.49	-0.65	87	166	133	59
NM_001004351	SPDYE3	0.65	0.00	24	65	96	76
NM_025137	SPG11	0.08	0.00	836	989	2498	2628
NM_016630	SPG21	0.29	0.00	967	1309	2277	2216
NM_003119	SPG7	0.17	0.00	1539	1877	3621	3739
NM_182965	SPHK1	0.01	-0.47	5455	5745	7699	5351
NM_001080394	SPIDR	0.07	-0.14	461	559	986	799
NM_001010862	SPIN3	0.78	0.00	38	101	181	214
NM_144569	SPOCD1	0.10	-0.54	830	995	3261	2103
NM_001007226	SPOP	0.16	0.00	728	910	1096	1037
NM_001077238	SPPL2B	0.04	0.00	535	632	1002	1091

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_207344	SPRYD4	0.32	0.00	138	221	260	279
NM_020456	SPRYD7	0.69	0.00	146	298	453	442
NM_001281303	SPTLC1	0.60	0.00	851	1424	2154	2174
NM_021199	SQRDL	0.34	0.00	684	973	2263	2227
NM_001047	SRD5A1	0.06	0.00	91	130	360	396
NM_001033117	SRGAP3	0.12	0.00	47	78	183	205
NM_003132	SRM	0.17	0.00	2324	2795	3034	3091
NM_001130440	SRP9	0.15	0.00	756	940	1318	1392
NM_003137	SRPK1	0.12	0.00	1360	1615	2693	2808
NM_182692	SRPK2	0.35	0.00	594	856	1252	1264
NM_005839	SRRM1	0.20	-0.07	1724	2133	2466	2201
NM_001078166	SRSF1	0.02	0.00	2911	3131	3510	3529
NM_001191005	SRSF10	0.08	0.00	533	644	784	811
NM_003016	SRSF2	0.23	0.00	2213	2780	2381	2316
NM_001031684	SRSF7	0.03	0.00	1723	1905	1655	1638
NM_001009998	SSBP4	0.02	0.00	118	159	281	270
NM_018984	SSH1	0.25	-0.09	5186	6444	7975	7198
NM_017857	SSH3	0.29	-0.10	153	238	780	641
NM_003731	SSNA1	0.57	-0.07	722	1197	1926	1693
NM_003145	SSR2	0.29	-0.08	3942	5062	6441	5854
NM_007107	SSR3	0.07	0.00	8407	9159	11186	11562
NM_003146	SSRP1	0.19	-0.05	2681	3257	3741	3414
NM_001278589	ST13	0.15	0.00	934	1151	2161	2022
NM_174963	ST3GAL3	0.02	0.00	693	792	1083	1129
NM_213618	ST5	0.17	-0.01	440	572	984	876
NM_173216	ST6GAL1	0.43	0.00	9	35	121	122
NM_175039	ST6GALNAC4	0.78	-0.20	396	782	1572	1251
NM_001286999	ST6GALNAC6	0.09	0.00	1482	1708	4756	4991
NM_021908	ST7	0.24	0.00	366	506	638	706
NM_015136	STAB1	0.69	-0.20	210	412	724	551
NM_005862	STAG1	0.05	0.00	1440	1623	1739	1837
NM_001013841	STAP2	0.23	-0.24	57	98	133	81
NM_178006	STARD13	0.12	0.00	618	760	917	952
NM_032016	STARD3NL	0.66	-0.08	347	641	1040	882
NM_001142503	STARD8	0.19	0.00	290	395	599	606
NM_007315	STAT1	0.42	-0.20	2776	3945	6961	5798
NM_207342	STEAP1B	0.21	-0.04	259	363	327	262
NM_182915	STEAP3	0.26	-0.23	849	1128	3350	2682

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001282936	STIL	0.02	-0.20	517	604	485	359
NM_006819	STIP1	0.13	0.00	2986	3456	3945	3869
NM_005990	STK10	0.15	0.00	2498	2947	3369	3538
NM_006281	STK3	0.02	0.00	370	442	584	623
NM_007271	STK38	0.23	0.00	1143	1470	2600	2726
NM_005563	STMN1	0.10	-0.54	2797	3175	3413	2203
NM_001199214	STMN2	0.54	-1.62	5	26	946	261
NM_004099	STOM	0.02	-0.50	4540	4816	6430	4331
NM_001256677	STOML1	0.24	0.00	293	412	828	924
NM_013442	STOML2	0.14	-0.37	1807	2150	4018	2932
NM_001271006	STRA13	0.23	-0.31	621	826	955	686
NM_007178	STRAP	0.18	0.00	1721	2097	2812	2939
NM_016930	STX18	0.29	-0.09	201	304	624	510
NM_052874	STX1B	0.06	0.00	27	49	241	231
NM_004853	STX8	0.28	0.00	349	497	928	1000
NM_178509	STXBP4	0.03	0.00	99	137	241	279
NM_018423	STYK1	0.13	0.00	40	69	71	92
NM_016086	STYXL1	0.40	0.00	152	254	549	505
NM_006713	SUB1	0.10	0.00	568	694	1190	1152
NM_003850	SUCLA2	0.09	0.00	329	416	645	641
NM_003849	SUCLG1	0.42	0.00	457	703	1256	1187
NM_003848	SUCLG2	0.15	-0.18	509	648	1065	847
NM_001193311	SUGCT	0.22	0.00	51	89	297	342
NM_001017392	SUGP2	0.21	-0.10	1536	1918	3361	2950
NM_001128205	SULF1	0.13	-0.12	6706	7605	21270	19087
NM_000456	SUOX	0.49	-0.36	211	362	641	433
NM_007192	SUPT16H	0.11	0.00	1709	1987	2450	2355
NM_001280787	SURF1	0.44	0.00	92	168	403	445
NM_001278942	SURF6	0.10	-0.08	463	574	693	577
NM_003173	SUV39H1	0.11	-0.32	353	448	391	261
NM_001193424	SUV39H2	0.04	0.00	161	211	210	196
NM_001040011	SWI5	0.03	0.00	453	537	1052	1044
NM_033025	SYDE1	0.31	-0.16	2110	2793	2691	2253
NM_030786	SYNC	0.11	-0.10	2376	2729	6052	5397
NM_001159677	SYNCRIP	0.19	-0.11	1592	1967	2518	2183
NM_003898	SYNJ2	0.02	0.00	4019	4294	9271	9325
NM_001242394	SYTL3	0.19	0.00	581	754	1115	1092
NM_001114600	SZRD1	0.37	-0.05	4090	5541	6802	6320
NM_015284	SZT2	0.13	0.00	2763	3218	3357	3248

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_006342	TACC3	0.25	-0.66	815	1078	821	455
NM_001488	TADA2A	0.22	0.00	194	280	345	298
NM_006354	TADA3	0.34	-0.05	1229	1697	3296	3005
NM_006284	TAF10	0.14	0.00	657	817	2146	2017
NM_153809	TAF1L	0.13	0.00	195	266	468	521
NM_014409	TAF5L	0.54	-0.10	370	627	653	532
NM_001190415	TAF6	0.47	-0.13	763	1179	1568	1311
NM_015975	TAF9B	0.28	0.00	139	217	225	264
NM_001001522	TAGLN	0.57	-0.44	34290	51712	62715	45611
NM_006755	TALDO1	0.09	-0.09	6037	6707	11030	10065
NM_001145909	TANC1	0.24	-0.04	1163	1505	3687	3403
NM_024562	TANGO6	0.57	-0.10	648	1079	1491	1275
NM_016151	TAOK2	0.16	0.00	1416	1715	2934	2900
NM_000116	TAZ	0.72	0.00	198	398	478	451
NM_001204240	TBC1D10A	0.51	0.00	285	484	682	734
NM_015527	TBC1D10B	0.21	0.00	1291	1629	2009	1983
NM_015188	TBC1D12	0.03	0.00	163	212	227	250
NM_018201	TBC1D13	0.28	0.00	1086	1447	2575	2673
NM_019020	TBC1D16	0.19	0.00	1250	1556	3488	3407
NM_016495	TBC1D7	0.59	0.00	368	644	965	985
NM_015130	TBC1D9	0.18	0.01	1294	1598	2323	2499
NM_004607	TBCA	0.41	0.00	180	297	364	384
NM_001079515	TBCE	0.27	0.00	419	585	1002	1044
NM_001163435	TBCK	0.23	0.00	225	323	838	787
NM_001139466	TBL1X	0.11	-0.04	715	870	1666	1494
NM_003194	TBP	0.97	0.00	197	469	478	497
NM_004865	TBPL1	0.58	0.00	87	176	204	192
NM_001261834	TBRG4	0.28	0.00	1437	1895	2338	2327
NM_001080508	TBX18	0.19	0.00	524	684	570	636
NM_153333	TCEAL8	0.07	-0.10	576	691	1304	1103
NM_007108	TCEB2	0.61	0.00	1166	1939	4860	4684
NM_007109	TCF19	0.09	-0.37	1654	1905	1316	921
NM_198392	TCF21	1.22	-1.91	17	73	69	6
NM_003200	TCF3	0.02	0.00	931	1048	1023	1116
NM_006602	TCFL5	0.55	0.00	168	308	655	593
NM_030752	TCP1	0.47	0.00	1439	2150	3103	2930
NM_022171	TCTA	0.08	0.00	585	705	1666	1536
NM_001146071	TDRD3	0.39	0.00	141	236	351	372
NM_001256661	TEAD2	0.16	-0.10	545	696	1065	895

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_003213	TEAD4	0.50	-0.39	384	632	233	139
NM_014844	TECPR2	0.08	0.00	878	1030	2333	2216
NM_138501	TECR	0.37	0.00	281	434	641	601
NM_024683	TEFM	0.29	0.00	106	172	237	268
NM_170754	TENC1	0.13	-0.08	597	744	1603	1388
NM_017746	TEX10	0.06	-0.16	532	637	1298	1054
NM_144582	TEX261	0.09	0.00	1652	1899	3369	3444
NM_001278195	TEX264	0.78	0.00	641	1233	1672	1739
NM_003201	TFAM	0.05	0.00	277	346	320	311
NM_022366	TFB2M	0.14	0.00	192	263	310	370
NM_007111	TFDP1	0.15	-0.01	1415	1708	1857	1702
NM_016521	TFDP3	0.76	0.00	30	83	96	76
NM_007162	TFEB	0.51	0.00	38	85	123	144
NM_015927	TGFB1I1	0.25	-0.16	1804	2303	3088	2590
NM_001199514	TGIF2	0.28	0.00	197	297	287	259
NM_001199535	TGIF2-C20orf24	0.64	0.00	598	1050	1564	1682
NM_004613	TGM2	0.13	0.00	2758	3199	4020	4135
NM_001083953	THADA	0.43	0.00	541	831	1535	1449
NM_018105	THAP1	0.29	0.00	192	291	395	442
NM_138350	THAP3	0.17	-0.20	485	629	844	651
NM_015963	THAP4	0.42	0.00	1020	1499	2477	2407
NM_144721	THAP6	0.05	0.00	111	153	243	287
NM_001008695	THAP7	0.24	0.00	209	305	316	294
NM_152658	THAP8	0.93	0.00	32	97	119	122
NM_000361	THBD	0.30	-0.06	381	547	2575	2307
NM_003247	THBS2	0.26	-0.03	13115	16124	32251	31038
NM_016647	THEM6	0.18	-0.01	147	214	239	190
NM_017872	THG1L	0.09	0.00	142	195	218	220
NM_024838	THNSL1	0.30	0.00	40	77	148	172
NM_032361	THOC3	0.16	0.00	371	487	541	584
NM_024339	THOC6	0.18	0.00	365	487	339	390
NM_003249	THOP1	0.08	-0.29	1244	1441	1965	1482
NM_001190919	THRA	0.30	0.00	657	911	1456	1381
NM_024817	THSD4	0.02	-0.53	790	897	1707	1081
NM_024328	THTPA	0.25	0.00	142	217	422	377
NM_017736	THUMPD1	0.02	0.00	461	540	668	712
NM_022173	TIA1	0.03	0.00	371	447	734	673
NM_004740	TIAF1	0.36	0.00	123	206	803	871
NM_012454	TIAM2	0.20	-0.31	456	607	1483	1091

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_182919	TICAM1	0.63	-0.38	443	786	961	658
NM_012456	TIMM10	0.46	0.00	264	435	551	534
NM_001167947	TIMM17B	0.32	-0.37	239	363	595	397
NM_014177	TIMM21	0.44	0.00	321	514	468	481
NM_013337	TIMM22	0.14	0.00	559	704	1177	1067
NM_004085	TIMM8A	0.24	0.00	139	212	208	205
NM_012460	TIMM9	0.28	0.00	158	243	293	246
NM_001146018	TJAP1	0.21	0.00	463	617	690	675
NM_003258	TK1	0.31	-0.43	1595	2129	1042	688
NM_001135055	TKT	0.06	-0.15	13833	14856	17057	14972
NM_005077	TLE1	0.08	0.00	332	417	853	945
NM_001282748	TLE4	0.01	-0.10	1903	2067	1104	930
NM_001284333	TLK2	0.12	0.00	249	328	476	499
NM_015059	TLN2	0.09	-0.10	2058	2352	4839	4309
NM_003266	TLR4	0.04	0.00	1633	1822	1639	1697
NM_078474	TM2D3	0.05	0.00	271	338	638	699
NM_014858	TMCC2	0.15	0.00	159	225	272	253
NM_181719	TMCO4	0.63	-0.34	323	586	537	362
NM_018502	TMCO6	0.34	0.00	106	178	191	205
NM_001143842	TMEM106C	0.48	0.00	380	618	1142	1142
NM_032354	TMEM107	1.49	-0.03	1693	5070	5099	4754
NM_007024	TMEM115	0.04	0.00	1570	1747	2570	2575
NM_001193531	TMEM116	0.41	0.00	5	24	77	107
NM_052932	TMEM123	0.06	0.00	2153	2406	2704	2869
NM_001127266	TMEM129	0.27	0.00	790	1059	2161	2322
NM_052907	TMEM132B	0.61	0.00	30	75	210	205
NM_001198670	TMEM136	0.15	0.00	144	206	318	353
NM_016464	TMEM138	0.16	0.00	457	592	890	813
NM_032928	TMEM141	0.47	-0.12	314	515	1210	1009
NM_001242597	TMEM147	0.53	0.00	824	1321	2514	2678
NM_024789	TMEM180	0.08	0.00	31	55	64	74
NM_138391	TMEM183A	0.47	0.00	224	378	526	510
NM_001079809	TMEM183B	0.33	0.00	222	341	499	481
NM_001097620	TMEM184A	0.25	0.00	167	251	148	135
NM_018279	TMEM19	0.24	0.00	276	391	761	830
NM_013390	TMEM2	0.05	0.00	1787	1996	2396	2377
NM_053045	TMEM203	0.17	-0.01	639	814	1414	1281
NM_024600	TMEM204	0.18	0.00	454	593	776	841
NM_198536	TMEM205	0.75	0.00	117	255	503	506

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001258245	TMEM218	0.05	0.00	79	115	289	311
NM_001083613	TMEM219	0.19	0.00	850	1080	2365	2401
NM_001009924	TMEM230	0.04	0.00	1036	1177	2286	2445
NM_019118	TMEM234	0.09	0.00	120	169	399	347
NM_001098621	TMEM251	0.11	0.00	119	170	166	205
NM_017799	TMEM260	0.27	0.00	104	168	435	492
NM_018112	TMEM38B	0.42	0.00	333	524	1000	1035
NM_018056	TMEM39B	0.36	-0.05	354	534	711	603
NM_024334	TMEM43	0.09	0.00	2900	3280	5139	5029
NM_001136218	TMEM51	0.49	0.00	94	177	351	388
NM_024587	TMEM53	0.38	-0.01	40	81	285	231
NM_018710	TMEM55A	0.51	0.00	232	400	622	636
NM_001199691	TMEM56-RWDD3	0.89	0.00	33	97	121	102
NM_194291	TMEM65	0.02	0.00	439	518	433	499
NM_001286657	TMEM68	0.40	0.00	142	239	279	335
NM_014573	TMEM97	0.40	-0.08	219	353	482	388
NM_015544	TMEM98	0.09	0.00	513	627	1872	1987
NM_014548	TMOD2	0.37	0.00	285	439	1988	1954
NM_001032283	TMPO	0.22	-0.50	619	815	539	323
NM_021109	TMSB4X	0.45	-0.08	10426	14703	30300	28081
NM_032813	TMTC4	0.71	-0.03	171	348	349	283
NM_002160	TNC	0.26	-1.03	3327	4199	13501	6370
NM_021137	TNFAIP1	0.24	-0.18	2185	2763	3569	2981
NM_006291	TNFAIP2	0.19	0.00	645	832	1553	1519
NM_152362	TNFAIP8L1	0.81	-0.10	54	137	185	133
NM_001204848	TNFAIP8L2-SCNM1	0.46	0.00	251	415	589	590
NM_002546	TNFRSF11B	0.01	-0.49	5506	5798	1795	1168
NM_016639	TNFRSF12A	0.05	-0.10	6207	6707	6863	6142
NM_001065	TNFRSF1A	0.10	0.00	3288	3732	6480	6456
NM_014452	TNFRSF21	0.16	0.00	244	331	636	616
NM_003823	TNFRSF6B	0.01	0.00	32	54	60	50
NM_001161560	TNIK	0.23	0.00	133	202	318	377
NM_022748	TNS3	0.24	0.00	293	412	1556	1590
NM_016272	TOB2	0.13	0.00	1232	1476	2082	1996
NM_020243	TOMM22	0.34	-0.34	731	1034	1884	1375
NM_001134484	TOMM5	0.45	-0.04	479	749	911	791
NM_001134493	TOMM6	0.03	-0.08	1043	1174	2389	2107
NM_013432	TONSL	0.04	0.00	270	335	266	255

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_007027	TOPBP1	0.17	0.00	940	1173	1027	998
NM_000113	TOR1A	0.27	0.01	1088	1437	2826	3017
NM_130459	TOR2A	0.42	0.00	77	143	158	135
NM_022371	TOR3A	0.31	0.00	273	405	539	617
NM_014729	TOX	0.13	0.00	57	92	52	44
NM_014828	TOX4	0.30	0.00	1187	1601	2321	2353
NM_001141979	TP53BP1	0.42	0.00	1016	1490	3442	3641
NM_001258320	TP53I11	0.24	0.00	1071	1387	543	580
NM_004881	TP53I3	0.50	-0.40	387	634	2269	1599
NM_033550	TP53RK	0.35	0.00	238	367	661	593
NM_033513	TPGS1	0.66	0.00	19	55	56	63
NM_213674	TPM2	0.18	-0.13	16559	19170	30082	26996
NM_001278189	TPM3	0.29	-0.04	4631	5922	9286	8747
NM_001145160	TPM4	0.19	-0.27	26570	30835	63316	51679
NM_000367	TPMT	0.64	0.00	114	231	331	281
NM_001136053	TPRA1	0.14	0.00	1416	1693	1766	1749
NM_001128228	TPRN	0.04	0.00	164	214	316	320
NM_003595	TPST2	0.38	0.00	961	1381	2263	2307
NM_012112	TPX2	0.41	-1.02	1714	2454	2354	1068
NM_001282759	TRA2A	0.18	0.00	534	693	1699	1621
NM_021138	TRAF2	0.09	-0.15	380	476	422	320
NM_032271	TRAF7	0.17	0.00	3201	3802	5499	5647
NM_005879	TRAIP	0.54	-0.24	91	178	189	122
NM_001042646	TRAK1	0.25	-0.02	2483	3133	2190	2007
NM_012288	TRAM2	0.02	0.00	15850	16507	14745	14369
NM_014831	TRANK1	0.13	0.00	457	579	1250	1137
NM_016292	TRAP1	0.25	0.00	1934	2464	3363	3200
NM_021210	TRAPPC1	0.50	0.00	1033	1607	2866	3054
NM_016030	TRAPPC12	0.15	0.00	1136	1388	2125	2262
NM_001011658	TRAPPC2	0.25	0.00	75	125	146	163
NM_001270896	TRAPPC3	0.18	0.00	1202	1494	2152	2296
NM_016146	TRAPPC4	0.03	0.00	949	1074	1362	1292
NM_001042461	TRAPPC5	0.09	0.00	556	674	1574	1664
NM_001160372	TRAPPC9	0.39	-0.01	409	623	1154	1039
NM_145214	TRIM11	0.35	0.00	427	629	480	444
NM_001037330	TRIM16L	0.24	0.00	88	142	345	394
NM_003141	TRIM21	0.31	-0.23	353	513	684	510
NM_001656	TRIM23	0.18	0.00	386	511	576	654
NM_003449	TRIM26	0.02	0.00	1071	1196	1716	1747

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_006510	TRIM27	0.30	0.00	1491	1994	2269	2290
NM_001003827	TRIM34	0.15	0.00	155	219	356	312
NM_171982	TRIM35	0.20	0.00	526	689	890	863
NM_033092	TRIM5	0.26	0.00	686	923	595	566
NM_001003819	TRIM6-TRIM34	0.08	-0.03	276	352	545	462
NM_173547	TRIM65	0.24	-0.02	410	563	497	421
NM_018073	TRIM68	0.06	-0.14	259	328	433	331
NM_003302	TRIP6	0.18	-0.42	1387	1710	2899	2020
NM_017819	TRMT10C	0.47	0.00	152	267	370	408
NM_001286082	TRMT112	0.38	-0.30	753	1097	1699	1270
NM_017956	TRMT12	0.23	0.00	156	233	285	303
NM_001257994	TRMT2A	0.43	-0.04	621	944	1300	1150
NM_152307	TRMT61A	0.10	0.00	279	359	439	453
NM_017910	TRMT61B	0.25	-0.23	149	226	308	214
NM_018006	TRMU	0.37	0.00	290	447	420	445
NM_001013642	TRNP1	0.19	0.00	345	464	1219	1146
NM_003306	TRPC4	0.30	-1.13	948	1285	1004	399
NM_016113	TRPV2	0.37	-0.33	2156	2966	9808	7508
NM_021625	TRPV4	0.30	0.00	130	207	437	486
NM_000368	TSC1	0.13	-0.08	1217	1458	3363	3009
NM_030935	TSC22D4	0.40	0.00	588	878	1034	963
NM_025265	TSEN2	0.45	0.00	58	115	210	201
NM_207346	TSEN54	0.05	-0.05	229	292	220	168
NM_020856	TSHZ3	0.20	0.00	1448	1801	2408	2377
NM_130783	TSPAN18	0.95	0.00	29	91	37	54
NM_021648	TSPYL4	0.14	0.00	554	697	1021	996
NM_003310	TSSC1	0.25	0.00	410	568	1065	1009
NM_005706	TSSC4	0.26	0.00	370	518	761	704
NM_052841	TSSK3	0.44	-0.08	24	57	48	26
NM_003313	TSTA3	0.03	-0.06	918	1041	1624	1434
NM_001282500	TTC1	0.27	-0.07	710	960	1583	1381
NM_017868	TTC12	0.54	0.00	18	49	162	142
NM_001288615	TTC23	0.03	0.00	378	454	593	678
NM_024926	TTC26	0.15	0.00	53	88	208	179
NM_017735	TTC27	0.07	0.00	374	463	576	547
NM_001145418	TTC28	0.22	0.00	798	1036	1736	1702
NM_001008237	TTC32	0.05	0.00	31	54	35	33
NM_001080494	TTC39A	2.49	0.00	1	39	133	146
NM_004623	TTC4	0.21	0.00	443	592	894	810

Table 6A: Differentially Upregulated Genes in SR + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_138376	TTC5	0.66	0.00	125	254	422	444
NM_173810	TTC9C	0.07	0.00	477	579	759	719
NM_003594	TTF2	0.08	-0.20	631	754	728	555
NM_014657	TTI1	0.11	0.00	520	645	736	817
NM_025115	TTI2	0.18	0.00	551	712	645	645
NM_001166691	TTK	0.15	-0.92	255	343	335	140
NM_015140	TTLL12	0.06	0.00	1332	1511	1957	1811
NM_014640	TTLL4	0.61	0.00	402	707	530	481
NM_025250	TTYH3	0.19	-0.32	2562	3105	3136	2364
NM_001270399	TUBA1A	0.67	-0.43	5700	9409	17311	12504
NM_006082	TUBA1B	0.49	-0.64	24029	34465	32484	20447
NM_032704	TUBA1C	0.39	-0.64	15529	20794	21822	13643
NM_178014	TUBB	0.48	-0.35	30537	43320	56651	43657
NM_001069	TUBB2A	0.27	-0.19	2069	2675	4157	3462
NM_178012	TUBB2B	0.56	-0.43	541	903	1657	1126
NM_006086	TUBB3	0.19	-0.39	1065	1341	8198	6004
NM_001289130	TUBB4A	1.77	-0.90	13	89	116	41
NM_006088	TUBB4B	0.30	-0.52	12969	16445	15350	10364
NM_032525	TUBB6	0.42	-0.36	17083	23402	33459	25606
NM_001070	TUBG1	0.75	-0.17	964	1778	2236	1850
NM_052903	TUBGCP5	0.08	0.00	598	717	832	880
NM_001004125	TUSC1	0.65	0.00	154	304	262	288
NM_022830	TUT1	0.13	0.00	320	417	439	442
NM_007284	TWF2	0.03	0.00	1467	1625	2795	2813
NM_001271893	TWIST2	0.51	0.00	407	671	998	978
NM_001002926	TWISTNB	0.10	-0.01	310	396	568	488
NM_012473	TXN2	0.23	-0.06	642	853	1587	1401
NM_001160047	TXNDC16	0.15	0.00	56	92	152	133
NM_005783	TXNDC9	0.10	0.00	308	393	668	747
NM_017853	TXNL4B	0.21	0.00	138	206	210	207
NM_006293	TYRO3	0.03	0.00	302	369	890	948
NM_001145440	TYW1B	0.23	0.00	52	91	106	128
NM_001012478	U2AF2	0.10	0.00	2784	3175	5555	5506
NM_207309	UAP1L1	0.21	0.00	844	1086	2410	2257
NM_016172	UBAC1	0.30	-0.05	715	985	1994	1786
NM_018449	UBAP2	0.20	-0.04	1613	2004	2304	2092
NM_014847	UBAP2L	0.08	-0.03	4869	5372	7433	6989
NM_032873	UBASH3B	0.05	-0.01	1408	1585	1501	1368
NM_018955	UBB	0.85	0.00	4272	8061	21607	21136

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_181838	UBE2D2	0.32	0.00	746	1041	1514	1584
NM_181886	UBE2D3	0.20	0.00	2310	2834	4839	4909
NM_015983	UBE2D4	0.11	-0.05	186	252	622	523
NM_194458	UBE2J2	0.01	0.00	737	836	903	867
NM_003969	UBE2M	0.24	0.00	424	579	688	699
NM_003348	UBE2N	0.54	0.00	743	1208	1526	1495
NM_001012989	UBE2NL	0.80	0.00	66	161	204	240
NM_014501	UBE2S	0.37	-0.50	597	871	761	468
NM_014176	UBE2T	0.18	-0.41	255	350	297	179
NM_001204077	UBE4A	0.12	0.00	1268	1510	2924	3030
NM_001267584	UBOX5	0.29	0.00	230	342	489	471
NM_175748	UBR7	0.51	0.00	494	801	913	821
NM_015853	UBXN1	0.38	0.00	742	1079	1872	1954
NM_183008	UBXN11	0.42	0.00	120	209	264	226
NM_014607	UBXN4	0.03	0.00	1176	1319	1932	2042
NM_006002	UCHL3	0.33	0.00	327	484	830	889
NM_001261450	UCK1	0.10	-0.06	461	572	977	843
NM_012474	UCK2	0.25	0.00	1534	1973	1938	2022
NM_001040697	UEVLD	0.32	0.00	195	301	520	534
NM_001048201	UHRF1	0.15	-0.71	1218	1481	547	283
NM_017754	UHRF1BP1	0.34	0.01	470	686	680	773
NM_001199297	UIMC1	0.05	0.00	436	523	455	447
NM_001039675	UNC45A	0.08	0.00	2434	2751	5430	5419
NM_001080419	UNK	0.66	-0.21	225	430	672	506
NM_001114403	UPK3BL	0.13	0.00	118	170	285	287
NM_001003684	UQCR10	0.10	-0.29	792	952	1955	1471
NM_006830	UQCR11	0.25	0.00	769	1023	1811	1856
NM_003365	UQCRC1	0.20	0.00	2817	3437	6975	6798
NM_003366	UQCRC2	0.22	-0.01	1675	2101	3250	3039
NM_006003	UQCRFS1	0.51	0.00	900	1411	1840	1817
NM_006004	UQCRH	0.53	0.00	458	760	1056	1122
NM_014402	UQCRQ	0.50	0.00	949	1477	2365	2495
NM_001077663	URGCP	0.02	0.00	1186	1321	1562	1532
NM_001204871	URGCP-MRPS24	0.24	0.00	1171	1512	1685	1567
NM_001265582	URM1	0.33	-0.36	925	1282	2562	1863
NM_024598	USB1	0.10	0.00	855	1024	1206	1139
NM_001272075	USP10	0.03	-0.01	1256	1401	2250	2081
NM_004651	USP11	0.24	0.00	1374	1767	2290	2233
NM_001252078	USP15	0.08	0.00	625	748	1248	1305

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001014443	USP21	0.13	0.00	295	386	399	394
NM_020886	USP28	0.10	0.00	399	499	661	627
NM_020718	USP31	0.08	0.00	1300	1498	1215	1296
NM_025090	USP36	0.10	0.00	1651	1919	2556	2586
NM_001290326	USP38	0.22	0.00	767	998	1314	1327
NM_018218	USP40	0.05	-0.10	483	577	1510	1294
NM_032236	USP48	0.12	0.00	775	941	1310	1364
NM_001098536	USP5	0.25	0.00	2373	3009	6711	6870
NM_152586	USP54	0.32	0.00	101	169	399	420
NM_001128610	USP8	0.16	0.00	710	890	1200	1209
NM_006649	UTP14A	0.34	-0.25	273	415	526	379
NM_032175	UTP15	0.11	-0.15	320	410	534	412
NM_016001	UTP18	0.35	-0.16	171	274	416	314
NM_014503	UTP20	0.03	-0.16	862	978	1356	1107
NM_018428	UTP6	0.26	0.00	452	623	794	850
NM_003369	UVRAG	0.63	0.00	357	643	986	893
NM_153477	UXT	0.32	0.00	559	792	1233	1281
NM_018052	VAC14	0.33	0.00	2101	2826	6308	6305
NM_199245	VAMP1	0.59	0.00	89	181	235	237
NM_001185127	VAMP4	0.56	0.00	140	263	428	482
NM_001172411	VANGL1	0.04	0.00	1244	1405	1637	1680
NM_006295	VARS	0.20	0.00	2673	3256	5255	5464
NM_001167734	VARS2	0.26	0.00	443	613	774	832
NM_003370	VASP	0.47	-0.20	1454	2178	3876	3200
NM_001134398	VAV2	0.13	0.00	994	1200	1913	1859
NM_016206	VGLL3	0.06	0.00	6394	6947	5734	5865
NM_001128219	VGLL4	0.24	0.00	1072	1394	1379	1482
NM_001193314	VIPAS39	0.32	0.00	273	408	715	747
NM_001017921	VMAC	0.15	0.00	13	32	79	61
NM_017684	VPS13C	0.01	0.00	1315	1450	3918	3871
NM_015378	VPS13D	0.14	0.00	1884	2226	4571	4724
NM_020857	VPS18	0.39	-0.01	1586	2238	3702	3492
NM_016208	VPS28	0.13	0.00	1166	1398	2901	2880
NM_001282168	VPS36	0.14	0.00	439	560	1031	946
NM_152415	VPS37A	0.64	0.00	566	994	1158	1211
NM_007259	VPS45	0.18	0.00	476	623	1273	1196
NM_013265	VPS51	0.11	0.00	774	938	1381	1423
NM_001271087	VPS72	0.07	-0.28	892	1042	1352	1011
NM_016440	VRK3	0.39	-0.14	439	664	1029	839

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_019086	VSIG10	0.23	0.00	359	493	655	728
NM_016485	VTA1	0.18	0.00	912	1142	1520	1399
NM_015058	VWA8	0.04	0.00	368	445	1217	1183
NM_003931	WASF1	0.02	0.00	338	406	476	464
NM_016312	WBP11	0.09	0.00	1241	1446	1379	1266
NM_001083913	WBP1L	0.35	0.00	1202	1670	2527	2656
NM_152559	WBSCR27	0.15	-0.47	62	100	164	87
NM_020830	WDFY1	0.16	-0.16	2012	2405	3664	3098
NM_052950	WDFY2	0.64	0.00	609	1067	1393	1420
NM_015910	WDPCP	0.80	0.00	55	138	189	216
NM_024100	WDR18	0.18	-0.40	293	397	626	410
NM_018383	WDR33	0.15	0.00	973	1192	1402	1442
NM_052844	WDR34	0.48	-0.43	276	459	969	641
NM_001260474	WDR4	0.22	-0.14	445	598	510	396
NM_001029896	WDR45	0.16	0.00	310	412	894	900
NM_017588	WDR5	0.14	-0.20	616	769	994	776
NM_001083961	WDR62	0.49	-0.16	439	710	462	351
NM_001178003	WDR66	0.13	0.00	318	413	110	129
NM_015285	WDR7	0.04	0.00	722	835	1348	1440
NM_032856	WDR73	0.09	0.00	174	233	453	518
NM_032168	WDR75	0.33	0.00	547	783	892	911
NM_024102	WDR77	0.33	-0.06	746	1049	1911	1702
NM_001099737	WDR83	0.23	0.00	409	559	1044	1091
NM_001258272	WDR89	0.05	0.00	115	158	127	155
NM_133330	WHSC1	0.10	-0.26	4227	4755	3920	3096
NM_001077269	WIPF1	0.14	0.00	1912	2268	3045	3168
NM_003882	WISP1	0.87	0.00	38	107	175	146
NM_032387	WNK4	0.12	-0.18	3386	3883	2441	2007
NM_017818	WRAP73	0.24	0.00	293	413	505	473
NM_001080436	WTIP	0.45	-0.04	684	1050	821	710
NM_015691	WWC3	0.03	0.00	1602	1771	1406	1433
NM_020196	XAB2	0.12	0.00	1500	1764	1909	1994
NM_004628	XPC	0.23	0.00	921	1200	1678	1678
NM_022459	XPO4	0.25	0.00	457	628	984	945
NM_006297	XRCC1	0.15	0.00	535	680	828	738
NM_021141	XRCC5	0.06	-0.13	5681	6182	9774	8660
NM_001288976	XRCC6	0.15	0.00	3089	3626	5241	5074
NM_022167	XYLT2	0.24	-0.03	1661	2111	2818	2588
NM_020192	YAE1D1	0.78	0.00	58	143	129	157

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001190979	YAF2	0.14	0.00	229	308	493	495
NM_003680	YARS	0.18	0.00	2791	3358	5796	6033
NM_001017964	YDJC	0.22	0.00	162	239	329	362
NM_020470	YIF1A	0.47	0.00	1473	2207	3228	3298
NM_019589	YLPM1	0.06	0.00	1861	2094	2808	2900
NM_024640	YRDC	0.35	0.00	437	645	557	481
NM_006761	YWHAE	0.34	-0.06	6442	8456	13305	12358
NM_175907	ZADH2	0.57	0.00	347	603	938	845
NM_001287603	ZBTB17	0.11	0.00	579	714	732	786
NM_006352	ZBTB18	0.13	0.00	572	713	772	769
NM_020861	ZBTB2	0.27	0.01	475	658	742	839
NM_020924	ZBTB26	0.97	0.00	22	75	89	111
NM_014830	ZBTB39	0.02	0.00	285	348	343	397
NM_006626	ZBTB6	0.28	0.00	187	282	310	336
NM_016010	ZC2HC1A	0.57	0.00	95	189	349	340
NM_033390	ZC3H12C	0.17	0.00	267	362	665	688
NM_001160103	ZC3H14	0.09	0.00	1181	1380	2360	2508
NM_015117	ZC3H3	0.35	0.00	319	482	740	652
NM_001282190	ZC3HC1	0.35	0.00	274	419	543	490
NM_017665	ZCCHC10	0.70	0.00	79	175	129	137
NM_024617	ZCCHC6	0.04	0.00	962	1093	1778	1778
NM_017612	ZCCHC8	0.10	0.00	320	407	391	384
NM_032280	ZCCHC9	0.37	0.00	171	276	299	259
NM_033114	ZCRB1	0.26	0.00	97	157	329	381
NM_024630	ZDHHC14	0.01	0.00	165	212	360	312
NM_032283	ZDHHC18	0.09	0.00	1202	1400	1194	1309
NM_207340	ZDHHC24	0.54	0.00	77	155	499	451
NM_001134387	ZDHHC4	0.35	0.00	354	528	913	932
NM_001170796	ZFAND1	0.38	0.00	149	247	241	288
NM_001282905	ZFAND4	0.49	0.00	61	123	135	139
NM_153688	ZFP1	0.62	0.00	52	117	212	218
NM_003407	ZFP36	0.01	-0.41	1190	1319	1102	745
NM_153813	ZFPM1	0.10	0.00	66	102	98	129
NM_001281734	ZFYVE1	0.13	0.00	651	807	1643	1671
NM_001105251	ZFYVE16	0.11	0.00	425	535	955	1026
NM_001077268	ZFYVE19	0.44	0.01	407	639	676	769
NM_015346	ZFYVE26	0.31	0.00	1428	1918	3049	3231
NM_001204180	ZHX1-C8orf76	0.16	0.00	241	327	416	414
NM_003412	ZIC1	0.29	-0.28	188	285	437	303

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001012981	ZKSCAN2	0.22	0.00	200	288	441	379
NM_001242894	ZKSCAN3	0.21	0.00	97	152	206	194
NM_005857	ZMPSTE24	0.17	0.00	769	971	1888	1981
NM_001289091	ZMYM1	0.52	0.00	171	305	435	440
NM_201599	ZMYM3	0.17	0.00	845	1058	1747	1778
NM_005095	ZMYM4	0.04	0.00	1062	1203	2419	2329
NM_173531	ZNF100	0.88	0.00	34	99	81	68
NM_016265	ZNF12	0.57	0.00	159	297	430	464
NM_003434	ZNF133	0.25	-0.23	244	351	510	372
NM_021030	ZNF14	0.25	0.00	27	55	98	109
NM_144680	ZNF18	0.28	0.00	106	171	266	287
NM_007149	ZNF184	0.24	0.00	94	151	185	189
NM_197977	ZNF189	0.04	0.00	171	223	503	569
NM_001242841	ZNF195	0.33	0.00	130	211	285	266
NM_001017396	ZNF2	0.47	0.00	66	130	225	185
NM_001203250	ZNF20	0.14	0.00	24	47	154	148
NM_001278158	ZNF205	0.17	0.00	141	205	225	209
NM_001098507	ZNF207	0.10	0.00	1814	2093	2747	2900
NM_013359	ZNF221	0.19	0.00	25	50	89	98
NM_013362	ZNF225	0.35	0.00	53	100	152	196
NM_001099282	ZNF239	0.37	-0.02	52	100	214	166
NM_001278677	ZNF254	0.58	0.00	64	136	191	226
NM_001265588	ZNF267	0.33	0.00	157	250	200	207
NM_152943	ZNF268	0.10	0.00	231	303	453	519
NM_152287	ZNF276	0.12	0.00	451	566	470	523
NM_001037813	ZNF284	0.03	0.00	56	85	87	87
NM_020653	ZNF287	0.03	0.00	129	173	341	340
NM_014347	ZNF324	0.02	0.00	156	203	312	349
NM_024620	ZNF329	0.10	0.00	162	221	428	466
NM_014487	ZNF330	0.26	-0.04	747	1003	990	863
NM_001286769	ZNF34	0.20	0.00	28	55	104	87
NM_001282933	ZNF341	0.33	-0.03	147	236	160	118
NM_001282497	ZNF343	0.51	0.00	201	351	468	458
NM_012279	ZNF346	0.25	0.00	207	304	439	388
NM_003420	ZNF35	0.07	0.00	156	209	229	242
NM_018083	ZNF358	0.09	0.00	626	754	1343	1359
NM_152493	ZNF362	0.34	0.00	245	375	493	494
NM_015481	ZNF385A	0.01	0.00	43	68	141	122
NM_020781	ZNF398	0.51	0.01	449	737	923	1030

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_024741	ZNF408	0.70	0.00	182	364	437	486
NM_001242924	ZNF410	0.21	0.00	856	1100	1452	1449
NM_015069	ZNF423	0.50	0.00	69	137	50	46
NM_024106	ZNF426	0.16	0.00	166	235	324	342
NM_001164276	ZNF44	0.07	0.00	83	121	160	185
NM_017908	ZNF446	0.29	0.00	55	99	297	255
NM_021224	ZNF462	0.19	-0.19	513	671	1410	1128
NM_001006656	ZNF473	0.19	-0.03	210	295	318	257
NM_020713	ZNF512B	0.16	0.00	313	416	684	675
NM_001278524	ZNF518A	0.31	0.00	147	233	254	255
NM_145287	ZNF519	0.52	0.00	23	58	29	30
NM_015461	ZNF521	0.05	0.00	52	81	256	240
NM_153219	ZNF524	0.36	0.00	59	110	119	144
NM_133444	ZNF526	0.13	-0.05	758	930	1183	1037
NM_020880	ZNF530	0.38	0.00	58	110	87	83
NM_001044387	ZNF557	0.37	0.00	153	250	287	344
NM_144693	ZNF558	0.94	0.00	65	174	314	336
NM_001042474	ZNF565	0.02	-0.49	75	108	173	91
NM_152484	ZNF569	0.23	0.00	43	78	166	183
NM_152360	ZNF573	0.35	0.00	32	67	92	74
NM_022752	ZNF574	0.41	-0.15	508	772	886	708
NM_152600	ZNF579	0.57	0.00	82	166	154	131
NM_016202	ZNF580	1.73	0.00	32	165	183	181
NM_001159860	ZNF583	0.40	0.00	25	57	162	183
NM_173548	ZNF584	0.61	0.00	106	213	320	366
NM_001204814	ZNF586	0.33	0.00	63	114	177	179
NM_015871	ZNF593	0.52	0.00	166	298	383	412
NM_001007248	ZNF599	0.41	0.00	31	68	121	94
NM_001031721	ZNF613	0.65	0.00	23	63	89	104
NM_133374	ZNF618	0.05	-0.03	1493	1678	2710	2484
NM_014789	ZNF623	0.24	0.00	285	402	605	593
NM_033113	ZNF628	0.18	0.00	85	133	181	179
NM_001080417	ZNF629	0.16	-0.07	833	1036	1788	1571
NM_014699	ZNF646	0.05	0.00	809	937	1025	1020
NM_001083956	ZNF655	0.23	0.00	372	512	745	691
NM_001204299	ZNF664-FAM101A	0.04	0.00	32	55	104	85
NM_024833	ZNF671	0.11	0.00	65	101	216	250
NM_182609	ZNF677	0.49	0.00	51	106	87	85
NM_021915	ZNF69	0.52	0.00	13	40	89	83

Table 6A: Differentially Upregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_030895	ZNF696	0.19	0.00	63	104	123	104
NM_025069	ZNF703	0.21	-0.16	285	396	433	327
NM_001267708	ZNF706	0.19	0.00	230	320	393	366
NM_023931	ZNF747	0.17	0.00	130	190	158	200
NM_153028	ZNF75A	0.21	0.00	72	118	237	253
NM_024671	ZNF768	0.13	0.00	748	915	986	950
NM_001201407	ZNF778	0.63	0.00	103	211	299	329
NM_001286697	ZNF79	0.46	0.00	94	174	324	301
NM_001013659	ZNF793	0.34	0.00	16	40	98	131
NM_178835	ZNF827	0.36	0.00	421	627	1242	1335
NM_001136501	ZNF844	0.21	0.00	70	115	179	222
NM_138374	ZNF845	0.23	0.00	128	196	216	264
NM_001195605	ZNF865	0.22	-0.02	185	269	283	227
NM_001145434	ZNF880	0.40	0.00	110	191	356	416
NM_001101338	ZNF883	0.50	0.00	10	37	121	126
NM_001277291	ZNF891	2.33	0.00	4	71	35	37
NM_001287533	ZNF92	0.06	0.00	76	112	85	65
NM_014205	ZNHIT2	0.96	-0.14	48	137	220	157
NM_147128	ZNRF2	0.54	0.00	56	118	85	105
NM_080603	ZSWIM1	0.10	0.00	255	331	478	523
NM_001287821	ZWILCH	0.26	-0.21	310	440	497	366
NM_032997	ZWINT	0.47	-0.53	607	947	819	497
NM_001010972	ZYX	0.20	0.00	7940	9431	14755	14447

Table 6B: Differentially Upregulated Genes in SEN + IL-2

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_005954	MT3	0.00	6.09	4	1	0	453
NM_000425	L1CAM	0.00	4.29	9	10	12	469
NM_199296	ISM2	0.00	4.24	2	8	10	433
NM_001216	CA9	0.00	3.88	22	26	12	355
NM_182762	MACC1	0.00	3.66	2	1	2	118
NM_198516	GALNT18	0.00	3.56	46	40	33	584
NM_006771	KRT38	0.00	3.51	0	5	2	107
NM_001039130	ALOX15B	0.00	3.33	1	6	4	139
NM_004112	FGF11	0.00	3.09	67	48	10	198
NM_001144994	C2orf72	0.00	3.07	25	10	4	116
NM_017413	APLN	0.00	2.97	277	249	83	845
NM_006426	DPYSL4	0.00	2.83	49	56	35	373
NM_003122	SPINK1	-0.01	2.70	8	1	6	116
NM_001958	EEF1A2	0.00	2.50	2	11	8	122
NM_019058	DDIT4	0.00	2.46	532	480	720	4338
NM_000230	LEP	0.00	2.41	76	83	56	412
NM_001128850	RRAD	-0.66	2.39	47	15	54	396
NM_002246	KCNK3	0.00	2.35	7	12	150	939
NM_004052	BNIP3	0.00	2.17	2262	2243	1083	5257
NM_004967	IBSP	0.00	2.14	2	2	21	157
NM_000201	ICAM1	0.00	2.14	295	325	487	2408
NM_181726	ANKRD37	-0.06	2.14	339	269	50	312
NM_006516	SLC2A1	-0.01	2.05	6356	6044	1329	5907
NM_022834	VWA1	0.00	2.04	22	33	23	157
NM_001142386	PDK3	0.00	2.02	191	157	270	1277
NM_005165	ALDOC	0.00	2.00	534	478	516	2316
NM_002820	PTHLH	0.00	1.98	46	38	52	290
NM_001002814	RAB11FIP1	0.00	1.98	42	60	6	72
NM_020311	ACKR3	0.00	1.96	40	39	27	168
NM_007036	ESM1	-0.34	1.94	2562	1887	1863	7612
NM_009590	AOC2	0.00	1.93	21	35	15	107
NM_032727	INA	0.00	1.89	17	31	21	133
NM_015053	PPFIA4	0.00	1.88	235	232	129	593
NM_001142617	STRA6	0.00	1.88	2	4	25	150
NM_019105	TNXB	0.00	1.81	2575	2620	129	567
NM_000316	PTH1R	0.00	1.79	0	4	21	124

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001025366	VEGFA	0.00	1.78	5690	5914	5781	20606
NM_206966	C5orf46	0.00	1.72	21	13	27	144
NM_000094	COL7A1	0.00	1.71	376	398	1416	4952
NM_021219	JAM2	0.00	1.68	37	26	48	222
NM_001145106	FIBCD1	0.00	1.68	352	369	69	301
NM_170744	UNC5B	0.00	1.68	1077	1011	1404	4828
NM_003391	WNT2	0.00	1.68	7	13	19	107
NM_016953	PDE11A	0.00	1.65	22	24	245	911
NM_001286485	RGS11	0.00	1.65	14	13	21	113
NM_016588	NRN1	0.00	1.64	455	447	37	174
NM_001282349	OSCAR	0.00	1.63	53	40	60	259
NM_001855	COL15A1	0.00	1.63	171	210	1196	4004
NM_000962	PTGS1	0.00	1.63	1202	1233	2595	8456
NM_000299	PKP1	-0.33	1.61	196	119	8	68
NM_001089	ABCA3	0.00	1.60	37	32	87	347
NM_005545	ISLR	0.00	1.59	1165	1067	2007	6429
NM_030949	PPP1R14C	0.00	1.58	25	33	27	131
NM_003278	CLEC3B	0.00	1.54	58	81	52	216
NM_001166222	CARNS1	0.00	1.54	8	24	21	105
NM_002023	FMOD	0.00	1.53	68	74	173	610
NM_001012706	C14orf182	0.00	1.51	10	15	42	177
NM_000291	PGK1	0.00	1.48	6933	7191	8146	23458
NM_001039570	KREMEN1	0.00	1.46	115	130	308	983
NM_001146079	CLDN14	-0.07	1.45	868	734	164	551
NM_001193582	NRCAM	0.00	1.44	24	25	37	153
NM_018192	LEPREL1	0.00	1.42	947	1050	1508	4338
NM_001185080	CLDN15	0.00	1.41	61	78	44	172
NM_148672	CCL28	-0.20	1.39	68	37	44	170
NM_000923	PDE4C	0.00	1.36	18	31	31	126
NM_001277307	MAGEB17	0.00	1.36	280	284	50	185
NM_014367	FAM162A	0.00	1.36	593	570	761	2148
NM_004997	MYBPH	0.00	1.34	27	26	204	623
NM_005562	LAMC2	0.00	1.33	360	327	470	1336
NM_001290294	SORBS1	0.00	1.33	23	27	69	237
NM_014936	ENPP4	0.00	1.30	2	6	29	115
NM_001199989	RASD1	0.00	1.30	58	48	69	233
NM_000441	SLC26A4	0.00	1.30	16	22	64	218

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_006813	PNRC1	0.00	1.29	572	634	759	2055
NM_001164507	NEB	0.00	1.29	60	48	123	383
NM_173354	SIK1	0.00	1.29	249	265	505	1392
NM_000636	SOD2	0.00	1.27	1297	1180	1483	3828
NM_001040619	ATF3	0.00	1.26	167	164	83	266
NM_134262	RORA	0.00	1.26	640	706	713	1887
NM_144717	IL20RB	0.00	1.24	27	24	35	128
NM_001012631	IL32	0.00	1.24	404	422	526	1397
NM_001099952	ITPR1	0.00	1.24	166	167	559	1479
NM_001838	CCR7	0.00	1.23	44	43	27	104
NM_004102	FABP3	0.00	1.22	98	72	310	845
NM_001040167	LFNG	0.00	1.22	117	153	67	216
NM_002317	LOX	0.00	1.22	42411	42652	50535	119408
NM_014650	ZNF432	0.00	1.22	88	62	164	471
NM_001195541	GS1-259H13.2	-0.37	1.22	66	31	35	126
NM_001164665	KIAA1549	0.00	1.22	60	81	200	562
NM_007037	ADAMTS8	0.00	1.19	16	25	29	107
NM_001082967	FAM19A5	-0.37	1.19	407	262	106	314
NM_003355	UCP2	0.00	1.19	84	77	77	237
NM_000888	ITGB6	0.00	1.18	1	1	37	129
NM_001253845	ADM2	0.00	1.18	142	165	185	512
NM_005962	MXI1	-0.08	1.17	598	491	778	1932
NM_004864	GDF15	0.00	1.16	4509	4526	2219	5268
NM_001166239	CGREF1	0.00	1.15	60	77	137	384
NM_080552	SLC32A1	0.00	1.15	11	24	29	104
NM_020125	SLAMF8	0.00	1.14	15	22	35	120
NM_001042784	CCDC158	0.00	1.14	2	3	31	109
NM_005704	PTPRU	0.00	1.14	109	108	318	817
NM_032148	SLC41A2	0.00	1.13	153	182	449	1122
NM_014399	TSPAN13	0.00	1.13	368	379	726	1765
NM_006167	NKX3-1	0.00	1.13	289	242	218	575
NM_006871	RIPK3	0.00	1.12	130	124	220	573
NM_139125	MASP1	0.00	1.11	1205	1205	229	593
NM_001161572	MAFF	0.00	1.11	1915	1861	1491	3460
NM_004115	FGF14	0.00	1.11	61	69	89	255
NM_030957	ADAMTS10	-0.50	1.11	139	70	87	250

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_032532	FNDC1	0.00	1.10	123	160	343	854
NM_024787	RNF122	0.00	1.10	115	141	54	166
NM_025107	MYCT1	0.00	1.10	260	270	6	41
NM_031866	FZD8	0.00	1.09	445	452	339	837
NM_152701	ABCA13	0.00	1.09	19	25	247	625
NM_001130026	FAM115C	0.00	1.09	115	105	44	139
NM_001946	DUSP6	0.00	1.08	133	144	1589	3606
NM_001161352	KCNMA1	0.00	1.08	252	251	2115	4750
NM_001243784	PDE2A	0.00	1.07	31	30	62	183
NM_022818	MAP1LC 3B	-0.01	1.07	2676	2492	2859	6325
NM_018004	TMEM45 A	0.00	1.07	437	380	441	1055
NM_001033045	GPR155	0.00	1.07	166	127	320	782
NM_144665	SESN3	0.00	1.06	212	192	378	911
NM_002245	KCNK1	-0.34	1.06	158	92	60	177
NM_020309	SLC17A7	-0.08	1.06	44	23	50	152
NM_016133	INSIG2	0.00	1.06	287	334	266	656
NM_004748	CCPG1	0.00	1.06	1702	1722	2731	5998
NM_033518	SLC38A5	0.00	1.06	1760	1793	1824	4048
NM_133494	NEK7	0.00	1.05	7431	7614	7711	16495
NM_198276	TMEM17	0.00	1.05	23	25	64	185
NM_001159643	MCTP2	0.00	1.04	2	6	114	303
NM_001282192	RNASE4	0.00	1.04	356	367	686	1571
NM_001004439	ITGA11	0.00	1.04	6800	6553	10423	22038
NM_002250	KCNN4	0.00	1.04	69	70	842	1904
NM_014331	SLC7A11	-0.07	1.04	854	722	1227	2728
NM_005202	COL8A2	0.00	1.03	353	400	900	2024
NM_013332	HILPDA	0.00	1.03	416	443	237	580
NM_002061	GCLM	0.00	1.03	1509	1517	1350	2981
NM_024896	ERMP1	0.00	1.03	331	301	580	1327
NM_001077619	UBXN2B	0.00	1.03	28	21	106	281
NM_012328	DNAJB9	-0.09	1.02	487	390	327	774
NM_020689	SLC24A3	0.00	1.02	498	528	156	394
NM_000093	COL5A1	-0.07	1.02	14317	13263	13133	27299
NM_001040084	ANXA8	0.00	1.01	131	161	58	166
NM_017817	RAB20	0.00	1.00	99	103	40	122
NM_001759	CCND2	0.00	1.00	122	126	1279	2771
NM_153360	APCDD1 L	-0.03	1.00	2412	2212	6576	13626
NM_006072	CCL26	0.00	1.00	108	131	154	384

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001081	CUBN	0.00	1.00	11	27	146	366
NM_005220	DLX3	0.00	1.00	19	19	35	109
NM_007325	GRIA3	-0.24	0.99	429	306	1040	2257
NM_001130987	DYSF	-0.20	0.99	695	530	2392	5033
NM_018000	MREG	-0.53	0.99	109	51	106	274
NM_181079	IL21R	0.00	0.99	71	64	19	68
NM_000392	ABCC2	0.00	0.98	37	55	37	113
NM_005211	CSF1R	-0.27	0.98	80	43	189	455
NM_001001794	DENND6B	0.00	0.98	24	20	79	211
NM_001039966	GPER1	0.00	0.98	302	336	247	580
NM_152666	PLD5	-0.36	0.98	49	21	54	153
NM_152772	TCP11L2	0.00	0.97	270	219	387	872
NM_001252100	KIF21B	0.00	0.97	103	88	35	107
NM_016577	RAB6B	0.00	0.96	61	75	279	643
NM_001199619	NCOA7	0.00	0.96	510	554	582	1275
NM_001098845	ANXA8L1	0.00	0.96	67	95	37	111
NM_002275	KRT15	-0.21	0.96	83	47	181	431
NM_001286423	GLB1L	0.00	0.96	347	342	1025	2170
NM_000379	XDH	0.00	0.95	58	84	52	146
NM_025218	ULBP1	0.00	0.95	280	263	385	858
NM_017694	MFSD6	0.00	0.95	96	105	243	560
NM_002658	PLAU	0.00	0.95	246	268	1709	3525
NM_194296	SPATA24	0.00	0.94	46	29	25	81
NM_021111	RECK	0.01	0.93	3270	3477	5422	10732
NM_153006	NAGS	0.00	0.92	79	58	67	177
NM_181481	LDLRAD4	0.00	0.92	21	15	100	248
NM_004598	SPOCK1	0.00	0.91	10414	10436	9246	17944
NM_001134338	RNF24	0.00	0.91	1086	1189	1422	2887
NM_152405	JMY	0.00	0.91	197	206	381	828
NM_004936	CDKN2B	0.00	0.91	81	99	287	636
NM_001042410	ANKZF1	0.00	0.91	380	372	316	695
NM_032623	MGARP	0.00	0.91	37	31	46	128
NM_022817	PER2	0.00	0.90	188	177	198	451
NM_007332	TRPA1	0.00	0.90	145	167	225	505
NM_001145115	PPP1R3G	0.00	0.89	142	132	106	257
NM_001785	CDA	-0.23	0.89	220	146	293	640
NM_001170820	IFITM10	0.00	0.89	110	108	418	889
NM_000451	SHOX	0.00	0.89	4	14	121	288

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001135219	PIP5KL1	0.00	0.89	18	29	75	190
NM_001001791	C10orf55	0.00	0.88	88	90	618	1275
NM_001136537	BTBD19	0.00	0.87	71	97	156	357
NM_015012	TMEM41B	0.00	0.87	609	592	892	1795
NM_001323	CST6	0.00	0.87	25	33	37	105
NM_006208	ENPP1	0.00	0.87	545	553	1406	2774
NM_022051	EGLN1	0.00	0.87	1466	1523	1217	2407
NM_004717	DGKI	0.00	0.86	1118	1195	688	1396
NM_003660	PPFIA3	0.00	0.86	64	82	62	159
NM_003486	SLC7A5	0.00	0.86	3975	4108	1884	3647
NM_000955	PTGER1	0.00	0.86	9	19	37	104
NM_031464	RPS6KL1	0.00	0.85	69	94	42	115
NM_001113498	MDGA2	0.00	0.85	2	8	139	318
NM_001206995	PPP2R2C	0.00	0.85	102	132	433	896
NM_012068	ATF5	0.00	0.85	903	922	1670	3225
NM_000202	IDS	0.00	0.84	2240	2352	4409	8259
NM_000640	IL13RA2	0.00	0.84	50	73	349	728
NM_001792	CDH2	0.00	0.84	12840	13233	12338	22695
NM_033656	BRWD1	0.00	0.84	730	734	948	1863
NM_001001891	ANO7	0.00	0.84	64	53	50	131
NM_178554	KY	0.00	0.84	102	91	177	390
NM_153610	CMYA5	0.00	0.84	31	25	166	368
NM_004978	KCNC4	0.00	0.83	352	347	2136	4050
NM_181712	KANK4	0.00	0.83	3	5	110	255
NM_005233	EPHA3	0.00	0.83	22	10	54	139
NM_002923	RGS2	0.00	0.83	144	126	233	497
NM_016599	MYOZ2	0.00	0.83	33	26	85	203
NM_013231	FLRT2	0.00	0.82	2909	2973	4702	8682
NM_001030273	ARNTL	0.00	0.82	335	335	297	619
NM_015482	SLC22A23	0.00	0.82	389	406	809	1580
NM_198390	CMIP	0.00	0.82	1503	1435	1289	2460
NM_001099773	CYP11A1	0.00	0.81	19	18	119	270
NM_018012	KIF26B	0.00	0.81	348	390	661	1298
NM_025225	PNPLA3	0.00	0.81	10	24	85	201
NM_001010858	RNF187	0.00	0.81	2966	3079	4421	8089
NM_017680	ASPN	0.00	0.81	28	41	114	259
NM_032812	PLXDC2	0.00	0.81	32	22	401	808
NM_024841	PRR5L	0.00	0.81	389	404	428	858

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_015193	ARC	-0.93	0.80	68	20	21	65
NM_030788	DCSTAMP	0.00	0.80	0	2	94	218
NM_005099	ADAMTS4	0.00	0.80	578	603	1135	2155
NM_015672	RIMBP3	0.00	0.80	37	59	25	74
NM_145648	SLC15A4	0.00	0.80	912	921	1163	2205
NM_001199383	RNF145	0.00	0.80	1750	1651	1337	2519
NM_001199723	CRABP2	0.00	0.80	79	90	206	436
NM_001195144	ANKRD44	-0.20	0.80	387	280	618	1205
NM_006520	DYNLT3	0.00	0.80	318	332	778	1497
NM_023016	SOWAHC	-0.04	0.79	445	368	428	852
NM_003979	GPRC5A	0.00	0.79	961	1002	351	706
NM_003897	IER3	-0.14	0.79	6943	6033	3138	5700
NM_144599	NIPA1	0.00	0.79	761	856	1061	1998
NM_001270764	CHST15	0.00	0.78	89	76	227	471
NM_181784	SPRED2	0.00	0.78	577	661	1031	1939
NM_014840	NUAK1	0.00	0.78	1562	1609	1379	2560
NM_001170330	C4orf3	-0.17	0.78	1159	932	1479	2737
NM_138371	PCED1B	0.00	0.78	180	197	156	335
NM_021999	ITM2B	0.00	0.77	2699	2733	3966	7100
NM_005069	SIM2	0.00	0.77	130	98	175	370
NM_005734	HIPK3	0.00	0.77	2724	2760	3621	6488
NM_000152	GAA	-0.40	0.77	591	384	1387	2556
NM_015444	TMEM158	0.00	0.77	325	291	2148	3898
NM_001204108	BCL2L11	-0.22	0.77	69	37	35	94
NM_005629	SLC6A8	-0.01	0.77	1157	1039	1462	2682
NM_001823	CKB	0.00	0.77	1022	1040	1383	2542
NM_003896	ST3GAL5	0.00	0.77	171	179	225	462
NM_005524	HES1	0.00	0.76	103	89	52	129
NM_030647	KDM7A	0.00	0.76	335	354	368	725
NM_001100912	BEND7	0.00	0.76	95	92	81	187
NM_005640	TAF4B	0.00	0.76	108	104	69	163
NM_020957	PCDHB16	0.00	0.76	13	14	40	104
NM_001731	BTG1	0.00	0.76	1170	1284	1250	2298
NM_015015	KDM4B	-0.12	0.76	1017	839	1138	2096
NM_012309	SHANK2	0.00	0.76	81	69	137	294
NM_003272	GPR137B	0.00	0.76	171	194	501	961
NM_007224	NXPH4	-0.30	0.75	147	87	73	170

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_004669	CLIC3	0.00	0.75	97	93	218	445
NM_003532	HIST1H3E	-0.65	0.75	794	440	52	128
NM_001178106	ZNF185	0.00	0.75	487	540	89	201
NM_001206951	SLC16A3	-0.06	0.75	9943	9200	11315	19558
NM_000290	PGAM2	0.00	0.75	28	29	77	177
NM_006636	MTHFD2	0.00	0.74	1635	1720	869	1606
NM_001161546	PROB1	0.00	0.74	133	137	58	139
NM_145658	SPESP1	0.00	0.74	76	78	58	139
NM_152680	TMEM154	0.00	0.74	89	91	283	560
NM_173208	TGIF1	0.00	0.74	863	948	834	1536
NM_002890	RASA1	0.00	0.74	1300	1342	2957	5196
NM_020777	SORCS2	0.00	0.74	335	291	1360	2449
NM_018964	SLC37A1	0.00	0.73	80	53	37	96
NM_153365	TAPT1	0.00	0.73	288	305	366	706
NM_001135216	ZSCAN31	0.00	0.73	10	14	40	102
NM_019050	USP53	0.00	0.73	1457	1427	1878	3333
NM_153487	MDGA1	0.00	0.73	332	380	921	1680
NM_001270691	SMOX	-0.10	0.73	664	540	549	1028
NM_017514	PLXNA3	-0.03	0.73	2184	1984	4999	8625
NM_198581	ZC3H6	0.00	0.73	400	347	343	662
NM_001172646	PLCB4	0.00	0.72	809	816	1506	2682
NM_001433	ERN1	0.00	0.72	257	306	462	871
NM_001135556	DYNC1I1	0.00	0.72	31	48	362	693
NM_001105244	PTPRM	0.01	0.72	3725	3953	5035	8628
NM_003183	ADAM17	0.00	0.72	747	786	703	1288
NM_005127	CLEC2B	0.00	0.71	208	190	177	359
NM_001128588	SLC14A1	0.00	0.71	75	68	385	730
NM_203394	E2F7	0.00	0.71	1629	1635	2914	5039
NM_020485	RHCE	0.00	0.71	47	59	60	140
NM_001098722	GNG4	0.00	0.71	27	35	60	140
NM_019107	C19orf10	0.00	0.71	6232	6065	8560	14429
NM_001130144	LTBP3	0.00	0.71	2082	1944	3101	5333
NM_024592	SRD5A3	0.00	0.70	115	142	403	758
NM_032530	ZNF594	0.00	0.70	43	52	52	124
NM_018227	UBA6	0.00	0.70	1163	1231	2250	3898
NM_001160148	DDHD1	0.00	0.70	526	563	745	1349
NM_001258379	SLC4A7	0.00	0.70	1922	1933	2674	4603
NM_012334	MYO10	0.01	0.70	5198	5465	6671	11249

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_181486	TBX5	0.00	0.70	86	89	37	94
NM_198159	MITF	0.00	0.70	167	167	206	408
NM_007350	PHLDA1	0.00	0.70	1860	1978	6904	11608
NM_001336	CTSZ	-0.02	0.70	6070	5747	10047	16785
NM_032642	WNT5B	0.00	0.70	5099	5198	10641	17759
NM_002840	PTPRF	0.00	0.70	13060	12751	11579	19301
NM_017649	CNNM2	0.00	0.70	97	124	183	366
NM_002632	PGF	0.00	0.69	471	471	842	1503
NM_004947	DOCK3	0.00	0.69	40	29	44	107
NM_015194	MYO1D	0.00	0.69	1674	1646	3841	6480
NM_178518	TMEM102	-0.24	0.69	211	139	85	185
NM_001204397	PITX2	0.00	0.68	128	142	466	856
NM_001012361	WDR31	0.00	0.68	10	6	83	181
NM_173200	NR4A3	0.00	0.68	161	184	75	166
NM_001145671	SORBS2	0.00	0.68	86	102	114	238
NM_018941	CLN8	0.00	0.68	1538	1657	1882	3229
NM_002517	NPAS1	0.00	0.68	116	154	168	335
NM_020975	RET	0.00	0.68	25	35	60	137
NM_014287	NOMO1	0.00	0.67	5419	5437	8036	13259
NM_017580	ZRANB1	0.00	0.67	1238	1329	944	1656
NM_024303	ZSCAN5A	0.00	0.67	48	63	58	133
NM_182487	OLFML2A	0.00	0.67	16	30	58	133
NM_000959	PTGFR	0.00	0.67	306	317	437	799
NM_019053	EXOC6	0.00	0.67	133	101	73	161
NM_001151	SLC25A4	-0.22	0.67	2057	1631	1237	2137
NM_001042496	SLC12A6	0.00	0.67	1214	1263	1996	3388
NM_005892	FMNL1	0.00	0.67	67	71	166	329
NM_005139	ANXA3	0.00	0.67	51	37	10	41
NM_017644	KLHL24	0.00	0.67	508	493	686	1216
NM_001031680	RUNX3	-0.20	0.67	188	125	69	153
NM_003749	IRS2	0.00	0.67	851	872	747	1318
NM_004457	ACSL3	0.00	0.66	955	974	1967	3322
NM_015419	MXRA5	0.00	0.66	273	296	1148	1978
NM_001077624	ZNF846	0.00	0.66	49	50	137	275
NM_031463	HSDL1	0.01	0.66	512	593	767	1342
NM_001242804	LOC100505549	0.00	0.65	88	110	81	174
NM_001142550	WDR47	0.00	0.65	601	540	697	1225

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001121	ADD3	0.00	0.65	1620	1573	2325	3887
NM_024006	VKORC1	0.01	0.65	1455	1590	3573	5902
NM_003395	WNT9A	0.00	0.65	34	55	85	181
NM_002210	ITGAV	0.01	0.65	6797	7110	10656	17227
NM_001714	BICD1	0.00	0.65	767	758	988	1702
NM_032409	PINK1	0.00	0.65	2952	3068	6759	10996
NM_030627	CPEB4	0.00	0.65	1268	1267	1069	1832
NM_005560	LAMA5	-0.23	0.65	347	243	129	259
NM_002556	OSBP	0.00	0.64	2109	2232	2313	3843
NM_148893	SVIP	0.00	0.64	81	91	127	255
NM_033254	BOC	0.00	0.64	460	498	745	1294
NM_017789	SEMA4C	0.00	0.64	472	477	374	677
NM_001258210	TSKU	0.00	0.64	977	971	838	1444
NM_001281731	CERS5	0.00	0.64	868	944	1522	2553
NM_006517	SLC16A2	0.00	0.64	1926	1872	2870	4715
NM_001178007	BBS12	0.00	0.64	74	49	135	268
NM_001278376	MPP2	0.00	0.64	215	254	277	512
NM_005493	RANBP9	0.00	0.64	1164	1240	1111	1885
NM_005149	TBX19	-0.63	0.64	74	29	56	126
NM_173552	C3orf58	0.00	0.63	336	399	208	394
NM_006091	CORO2B	0.00	0.63	436	470	1483	2481
NM_001200	BMP2	0.00	0.63	10	18	60	133
NM_001005291	SREBF1	0.00	0.63	1122	1091	1323	2220
NM_182752	TPRG1L	0.00	0.63	3275	3097	4968	8016
NM_012168	FBXO2	0.00	0.63	7	9	52	118
NM_016127	SARAF	0.00	0.63	1623	1546	4026	6521
NM_004093	EFNB2	0.00	0.63	106	82	29	74
NM_007214	SEC63	-0.01	0.63	526	451	747	1283
NM_198542	ZNF773	0.00	0.63	118	112	154	299
NM_152445	FAM161B	0.00	0.62	127	166	345	621
NM_001708	OPN1SW	0.00	0.62	225	261	133	262
NM_022763	FNDC3B	0.00	0.62	3339	3164	4392	7068
NM_001039548	KLHL35	0.00	0.62	69	91	87	181
NM_001025077	CELF2	0.00	0.62	249	304	339	610
NM_001104647	SLC25A36	0.00	0.62	754	795	948	1601
NM_001199039	SERINC2	0.01	0.62	2806	2994	6622	10540
NM_012317	LDOC1	0.00	0.62	252	308	166	318
NM_177552	SULT1A3	0.00	0.62	198	200	183	347
NM_001017390	SULT1A4	0.00	0.62	198	200	183	347

Table 6B: Differentially Upregulated Genes in SEN + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_003185	TAF4	0.00	0.62	245	197	162	311
NM_004415	DSP	0.00	0.62	24219	24316	29861	46568
NM_002047	GARS	0.00	0.61	6352	6573	8996	14209
NM_006219	PIK3CB	0.00	0.61	400	389	468	819
NM_005399	PRKAB2	0.00	0.61	442	500	1190	1981
NM_003956	CH25H	0.00	0.61	10	22	227	420
NM_002846	PTPRN	0.00	0.61	193	232	185	349
NM_030671	PTPRO	0.00	0.61	0	3	67	144
NM_182961	SYNE1	0.00	0.61	12665	12456	8828	13905
NM_017510	TMED9	-0.17	0.61	10691	9190	11866	18591
NM_001195202	LOC100129636	0.00	0.61	58	72	60	131
NM_001166050	APBB2	0.00	0.61	1688	1688	1892	3083
NM_001040667	HSF4	0.00	0.61	62	68	123	242
NM_001957	EDNRA	0.00	0.61	84	79	310	556
NM_058238	WNT7B	0.00	0.60	18	11	256	466
NM_016445	PLEK2	0.00	0.60	291	304	410	719
NM_004984	KIF5A	-0.43	0.60	36	11	46	105
NM_006472	TXNIP	0.00	0.60	832	819	3409	5444
NM_022465	IKZF4	0.00	0.60	151	193	181	340
NM_019112	ABCA7	0.00	0.60	35	50	283	510
NM_198181	GOLGA6L9	0.00	0.60	52	42	21	57
NM_201380	PLEC	-0.10	0.60	12686	11469	21412	33088
NM_031449	ZMIZ2	-0.21	0.60	1482	1171	1581	2575
NM_001201380	CNTNAP3B	0.00	0.60	94	118	110	218
NM_032134	QRICH2	0.00	0.59	133	146	212	390
NM_032801	JAM3	0.00	0.59	945	956	3045	4848
NM_032867	MICALCL	0.00	0.59	118	120	156	296
NM_152495	CNIH3	0.00	0.59	24	39	1512	2460
NM_152703	SAMD9L	0.00	0.59	271	261	774	1296
NM_031435	THAP2	0.00	0.59	112	134	100	200
NM_005098	MSC	0.00	0.59	757	818	649	1096
NM_025160	WDR26	0.00	0.59	2963	2876	3612	5712
NM_015061	KDM4C	0.00	0.59	561	593	701	1177
NM_015833	ADARB1	0.00	0.59	731	723	455	784
NM_001199771	RDH5	0.00	0.59	122	104	195	360
NM_001102603	ZNF160	0.00	0.59	366	422	507	867
NM_025081	NYNRIN	0.00	0.58	1139	1257	1714	2760

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001144903	TM6SF1	-0.44	0.58	96	47	60	129
NM_007257	PNMA2	0.00	0.58	480	554	216	394
NM_020801	ARRDC3	0.00	0.58	365	405	455	782
NM_004031	IRF7	0.00	0.58	94	119	73	152
NM_152527	SLC16A14	0.00	0.58	6	9	54	118
NM_001001713	SH3BGR	0.00	0.58	3	9	54	118
NM_001258205	TRPV3	-0.24	0.58	99	57	54	118
NM_015650	TRAF3IP1	0.00	0.58	234	261	283	503
NM_022374	ATL2	0.00	0.58	416	473	372	647
NM_015448	DPCD	0.00	0.58	156	189	345	603
NM_198935	SS18L1	-0.12	0.58	456	355	289	512
NM_203314	BDH1	0.00	0.58	70	56	35	83
NM_015513	CRELD1	0.00	0.58	1032	926	1951	3111
NM_004612	TGFBR1	0.00	0.58	2002	2082	3583	5612
NM_001118887	ANGPT2	-0.47	0.58	430	259	89	179
NM_006896	HOXA7	0.00	0.57	213	221	195	357
NM_030790	ITFG1	0.00	0.57	1067	1164	2398	3793
NM_002228	JUN	0.00	0.57	5158	5103	4862	7553
NM_001284341	FKBP9	0.00	0.57	5348	5604	8333	12809
NM_013309	SLC30A4	0.00	0.57	293	342	441	754
NM_004671	PIAS2	0.00	0.57	418	406	578	970
NM_174899	FBXO36	0.00	0.57	85	101	175	323
NM_017623	CNNM3	0.00	0.57	576	632	435	743
NM_001128303	LACC1	0.00	0.57	131	167	512	865
NM_022897	RANBP17	0.00	0.57	56	71	160	298
NM_145799	SEPT6	0.00	0.57	587	643	1321	2124
NM_000690	ALDH2	0.00	0.57	326	370	622	1037
NM_001013732	PTCHD4	0.00	0.57	10	8	116	224
NM_001004067	NOMO3	0.00	0.57	4823	4775	7054	10830
NM_006252	PRKAA2	0.00	0.57	92	89	175	322
NM_001042544	LTBP4	0.00	0.57	201	217	92	183
NM_001220488	CDH13	0.00	0.56	4350	4553	7104	10887
NM_178450	MARCH3	-0.01	0.56	369	307	154	287
NM_018590	CSGALNACT2	0.01	0.56	1369	1500	1233	1983
NM_001242828	ELOVL5	0.00	0.56	2034	2092	2437	3821
NM_014028	OSTM1	0.00	0.56	1259	1352	2335	3665
NM_005272	GNAT2	0.00	0.56	29	15	56	120
NM_001130858	PPIP5K1	0.00	0.56	250	205	903	1469

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_003337	UBE2B	0.00	0.56	466	481	693	1142
NM_000165	GJA1	0.00	0.56	5578	5681	5773	8845
NM_023071	SPATS2	-0.04	0.56	1173	1035	1352	2157
NM_198463	C3orf67	0.00	0.56	70	85	98	192
NM_001242801	ZNF790	0.00	0.56	40	63	98	192
NM_001146254	PODNL1	0.00	0.56	108	121	279	488
NM_001024807	APLP1	0.00	0.56	172	199	455	767
NM_030759	NRBF2	0.00	0.56	588	584	755	1235
NM_001282716	STAG3	0.00	0.56	94	121	166	305
NM_138448	ACYP2	-0.17	0.55	112	70	146	272
NM_001285878	CEBPB	-0.05	0.55	2040	1825	2240	3503
NM_015016	MAST3	0.00	0.55	305	271	497	832
NM_173614	NOMO2	0.00	0.55	5918	5975	8678	13144
NM_024615	PARP8	0.00	0.55	152	169	547	909
NM_001135036	TVP23C	0.00	0.55	205	183	243	429
NM_001083617	RB1CC1	0.00	0.55	1220	1285	1890	2965
NM_004040	RHOB	0.00	0.55	4756	4726	3720	5723
NM_003235	TG	0.00	0.55	27	16	48	105
NM_199054	MKNK2	0.00	0.55	1813	1878	1647	2591
NM_015052	HECW1	0.00	0.55	10	24	131	246
NM_080660	ZC3HAV1L	0.00	0.55	182	198	191	344
NM_000428	LTBP2	0.00	0.55	21013	20804	44866	66470
NM_001204478	TVP23C-CDRT4	0.00	0.55	190	202	252	442
NM_177924	ASAH1	0.00	0.55	565	629	2683	4148
NM_000875	IGF1R	0.00	0.54	2519	2666	3180	4891
NM_007266	GPN1	0.00	0.54	739	807	1025	1640
NM_001134878	KIF9	0.00	0.54	75	81	112	214
NM_015274	MAN2B2	0.00	0.54	1855	2002	3870	5922
NM_012139	SERGEF	0.00	0.54	140	156	220	390
NM_021244	RRAGD	0.00	0.54	43	45	356	606
NM_002332	LRP1	-0.08	0.54	60577	56575	116461	171215
NM_020702	KIAA1161	0.00	0.54	156	200	270	469
NM_001287491	TET3	0.00	0.54	34	52	29	70
NM_001080423	GRIP2	0.00	0.54	62	83	29	70
NM_001114634	PLAG1	0.00	0.54	91	80	141	261
NM_015407	ABHD14A	0.00	0.54	282	314	518	856
NM_001184940	FAM219	0.00	0.54	1318	1383	1360	2140

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
	A						
NM_001172223	MOB2	0.00	0.54	378	347	391	658
NM_001190274	FBXO11	0.00	0.54	973	876	809	1301
NM_003060	SLC22A5	0.00	0.53	61	67	171	309
NM_001172624	NEO1	0.00	0.53	910	983	2462	3787
NM_024501	HOXD1	0.00	0.53	144	114	541	889
NM_152402	TRAM1L 1	0.00	0.53	225	183	279	481
NM_001248008	SKIL	0.00	0.53	1951	1985	2410	3706
NM_024496	IRF2BPL	0.00	0.53	347	406	1048	1662
NM_001718	BMP6	0.00	0.53	1403	1344	977	1553
NM_014797	ZBTB24	0.00	0.53	363	315	358	604
NM_000577	IL1RN	0.00	0.53	28	23	79	157
NM_052868	IGSF8	0.00	0.53	267	288	591	963
NM_001214909	ZNF48	0.00	0.53	193	210	168	303
NM_001244808	FOXP1	0.00	0.53	3787	3900	4001	6052
NM_001013657	GDPGP1	0.00	0.53	63	48	46	100
NM_144629	RFTN2	0.00	0.53	144	131	141	259
NM_001288748	P4HA3	0.00	0.53	174	195	900	1431
NM_172016	TRIM39	0.00	0.53	411	422	376	630
NM_001286067	C11orf54	0.00	0.53	167	184	116	218
NM_033411	RWDD2A	0.00	0.52	101	106	104	198
NM_004186	SEMA3F	0.00	0.52	897	952	389	649
NM_018366	BLOC1S4	0.00	0.52	276	232	243	421
NM_001256267	MYPN	-0.03	0.52	603	514	630	1018
NM_001199861	KCNAB2	0.00	0.52	267	266	493	808
NM_025147	COQ10B	-0.11	0.52	1232	1037	1073	1684
NM_032875	FBXL20	0.00	0.52	582	554	1009	1586
NM_001627	ALCAM	0.00	0.52	9874	10091	13823	20299
NM_001114	ADCY7	0.00	0.52	2753	2901	4111	6166
NM_001130690	PDE10A	0.00	0.52	213	191	179	318
NM_021943	ZFAND3	0.00	0.52	1601	1734	1801	2762
NM_001030055	ARHGAP 5	0.00	0.51	1760	1725	2069	3157
NM_002149	HPCAL1	0.00	0.51	686	631	1701	2612
NM_173557	RNF152	0.00	0.51	354	322	314	529
NM_016472	GSKIP	0.00	0.51	302	342	611	983
NM_020354	ENTPD7	-0.07	0.51	1171	1008	1362	2107
NM_173074	PIGF	0.00	0.51	439	436	801	1268
NM_002731	PRKACB	0.00	0.51	344	358	643	1030

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_014960	ARSG	0.00	0.51	43	40	139	253
NM_001408	CELSR2	-0.18	0.51	88	52	27	65
NM_001145536	C17orf107	0.00	0.51	52	53	27	65
NM_002835	PTPN12	0.00	0.51	1499	1594	2431	3678
NM_000052	ATP7A	0.00	0.51	288	300	485	789
NM_005929	MFI2	0.00	0.51	279	332	316	530
NM_013399	CDIP1	0.00	0.51	951	970	1208	1871
NM_173174	PTK2B	0.00	0.51	275	256	191	335
NM_003255	TIMP2	0.00	0.51	23515	23998	28668	41461
NM_001130080	IFI27	0.00	0.51	187	150	1007	1571
NM_022164	TINAGL1	0.00	0.51	4555	4721	2271	3434
NM_006772	SYNGAP 1	0.00	0.51	379	362	557	896
NM_181093	SCYL3	0.00	0.50	176	205	229	394
NM_005402	RALA	0.00	0.50	1646	1781	2991	4482
NM_000203	IDUA	-0.38	0.50	329	206	559	898
NM_001282511	NPIPA8	0.00	0.50	370	341	389	640
NM_001282507	NPIPA7	0.00	0.50	370	341	389	640
NM_001025389	AMPD3	0.00	0.50	503	509	1258	1939
NM_007157	ZXDB	0.00	0.50	306	294	395	649
NM_001779	CD58	0.00	0.50	139	142	214	370
NM_198404	KCTD4	0.00	0.50	45	30	25	61
NM_004642	CDK2AP 1	0.00	0.50	2854	2983	3529	5255
NM_145257	CCSAP	0.00	0.50	329	301	227	390
NM_014498	GOLIM4	-0.08	0.50	1160	994	1595	2431
NM_000100	CSTB	-0.15	0.50	3010	2546	7004	10268
NM_152230	IPMK	0.00	0.50	127	141	114	211
NM_015626	WSB1	0.00	0.50	1027	1083	1266	1946
NM_001204	BMPR2	0.00	0.50	3312	3506	6528	9571
NM_022151	MOAP1	0.00	0.50	352	330	503	810
NM_001164496	CFAP44	0.00	0.50	70	89	143	257
NM_020651	PELI1	0.00	0.50	141	158	89	170
NM_139025	ADAMTS 13	-0.13	0.50	41	20	46	98
NM_018490	LGR4	0.00	0.49	445	499	980	1519
NM_173485	TSHZ2	0.00	0.49	13	10	214	368
NM_001198568	ADCY4	0.00	0.49	293	316	264	445
NM_173519	CLVS1	0.00	0.49	310	293	630	998
NM_000351	STS	0.00	0.49	858	951	1774	2680
NM_022740	HIPK2	0.00	0.49	6503	6325	11039	15965

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001710	CFB	0.00	0.49	69	53	64	128
NM_024686	TTLL7	0.00	0.49	41	40	166	292
NM_001145306	CDK6	0.00	0.49	2799	2933	2683	3991
NM_001039886	ZNF808	0.00	0.49	223	244	327	540
NM_015680	CNPPD1	0.00	0.49	1507	1493	2489	3710
NM_001037582	SCD5	-0.04	0.49	284	224	378	617
NM_001039703	NBPF10	-0.04	0.49	669	570	1042	1603
NM_001079526	IKZF2	0.00	0.49	73	64	44	94
NM_022365	DNAJC1	0.00	0.49	830	891	936	1447
NM_000514	GDNF	0.00	0.49	2980	3166	1782	2682
NM_153607	CREBRF	0.00	0.49	225	278	526	839
NM_002127	HLA-G	0.00	0.49	392	454	630	994
NM_005252	FOS	0.00	0.49	109	122	54	111
NM_001080424	KDM6B	0.00	0.49	448	425	358	586
NM_001136499	ZNF841	0.00	0.49	211	229	717	1122
NM_001278267	NBPF20	-0.23	0.49	834	631	1190	1817
NM_003437	ZNF136	0.00	0.49	135	120	114	209
NM_133466	ZFP82	0.00	0.49	171	136	143	255
NM_006547	IGF2BP3	0.00	0.48	22	34	200	344
NM_001103184	FMN1	0.00	0.48	755	738	873	1351
NM_144690	ZNF582	0.00	0.48	8	13	50	104
NM_005070	SLC4A3	0.00	0.48	93	65	260	436
NM_003287	TPD52L1	0.00	0.48	139	128	264	442
NM_000697	ALOX12	0.00	0.48	47	36	62	124
NM_080836	STK35	0.00	0.48	1060	1161	1431	2163
NM_001113482	MANEAL	-0.40	0.48	40	15	62	124
NM_001769	CD9	0.00	0.48	1309	1388	3637	5336
NM_032788	ZNF514	0.00	0.48	195	219	275	458
NM_002350	LYN	-0.03	0.48	223	172	312	514
NM_001014447	CPZ	0.00	0.48	6	17	81	155
NM_144736	NDUFAF 7	0.00	0.48	203	165	372	604
NM_021818	SAV1	0.00	0.48	675	704	609	957
NM_015348	TMEM13 1	0.00	0.48	1577	1708	3893	5691
NM_017918	CCDC109 B	0.00	0.48	261	270	304	501
NM_033429	CALML4	0.00	0.48	153	167	123	222
NM_001271441	C21orf2	0.00	0.48	183	206	200	342
NM_012413	QPCT	0.00	0.48	300	270	539	852
NM_024336	IRX3	0.00	0.48	228	223	297	490

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_032017	STK40	0.00	0.48	848	906	851	1311
NM_032854	CORO6	0.00	0.47	153	185	341	556
NM_007202	AKAP10	0.00	0.47	581	570	801	1237
NM_032383	HPS3	0.00	0.47	752	809	1025	1564
NM_001278740	TSPAN6	0.00	0.47	258	216	526	832
NM_007285	GABARAPL2	0.00	0.47	513	546	903	1386
NM_004183	BEST1	-0.03	0.47	165	123	424	680
NM_016032	ZDHHC9	0.00	0.47	1352	1460	2820	4146
NM_198335	GANAB	0.00	0.47	14444	14592	20102	28519
NM_001172655	ZNF701	0.00	0.47	93	120	150	264
NM_005013	NUCB2	0.00	0.47	1298	1218	1429	2146
NM_003999	OSMR	0.00	0.47	4665	4563	4334	6286
NM_030768	ILKAP	0.00	0.47	420	396	393	632
NM_001008401	ZNF761	0.00	0.47	220	220	254	423
NM_017659	QPCTL	0.00	0.47	532	555	1017	1547
NM_203371	FIBIN	0.00	0.47	57	64	345	560
NM_032927	TMEM128	0.00	0.47	203	201	218	368
NM_004272	HOMER1	0.00	0.47	203	244	218	368
NM_020123	TM9SF3	0.00	0.47	4186	4396	5561	8015
NM_015044	GGA2	0.00	0.47	1200	1265	1701	2532
NM_004714	DYRK1B	0.00	0.47	183	167	289	475
NM_012110	CHIC2	0.00	0.47	419	462	435	693
NM_024848	MORN1	0.00	0.47	39	35	67	131
NM_021255	PELI2	0.00	0.47	119	125	131	233
NM_012142	CCNDBP1	0.00	0.47	1075	974	1718	2551
NM_001024845	SLC6A9	0.00	0.47	611	587	308	503
NM_001289125	IFNAR2	0.00	0.47	344	333	381	612
NM_001282116	RFX3	0.00	0.46	103	78	46	96
NM_178140	PDZD2	0.00	0.46	54	41	46	96
NM_145276	ZNF563	0.00	0.46	35	45	58	116
NM_001099434	DCDC2B	0.00	0.46	36	28	58	116
NM_172037	RDH10	0.00	0.46	573	613	543	850
NM_080491	GAB2	0.00	0.46	1265	1338	1818	2686
NM_020699	GATAD2B	0.00	0.46	1123	1082	1215	1823
NM_176814	ZNF800	0.00	0.46	568	621	724	1113
NM_001284274	HECTD2	0.00	0.46	82	73	158	274
NM_016085	ATRAID	0.00	0.46	1220	1326	2186	3207

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001271928	KIF27	0.00	0.46	38	21	54	109
NM_001195608	PLEKHA1	0.00	0.46	716	676	713	1096
NM_018842	BAIAP2L1	-0.15	0.46	588	457	595	924
NM_001001664	SPOPL	0.00	0.46	357	356	329	532
NM_006565	CTCF	0.00	0.46	972	902	859	1307
NM_000527	LDLR	0.00	0.46	2516	2501	4045	5828
NM_001040457	RHBDD2	0.00	0.46	979	942	2649	3858
NM_005957	MTHFR	-0.01	0.46	680	594	821	1251
NM_001291860	HSPG2	-0.13	0.46	26212	23496	31269	43654
NM_145021	MARCH8	0.00	0.46	511	552	1015	1530
NM_030777	SLC2A10	0.00	0.46	1958	1892	2154	3152
NM_002312	LIG4	0.00	0.45	184	216	272	445
NM_014636	RALGPS1	0.00	0.45	30	20	89	165
NM_021089	ZNF8	0.00	0.45	187	235	295	479
NM_001005404	YPEL2	0.00	0.45	159	196	559	867
NM_016498	MTFP1	0.00	0.45	180	218	58	115
NM_172027	ABTB1	0.00	0.45	235	279	586	906
NM_001195263	PDZD7	-0.42	0.45	223	129	231	383
NM_001009955	SSBP3	0.00	0.45	373	373	530	824
NM_001167856	SBNO1	0.00	0.45	1973	2010	2283	3322
NM_006260	DNAJC3	0.00	0.45	2248	2403	2872	4146
NM_006045	ATP9A	0.00	0.45	1685	1807	5043	7177
NM_001276435	KCNJ15	0.00	0.44	38	46	150	259
NM_001204883	RAB43	0.00	0.44	779	754	838	1264
NM_004261	SEP15	0.00	0.44	1539	1644	2227	3229
NM_004538	NAP1L3	0.00	0.44	11	14	48	98
NM_001134707	SARDH	-0.72	0.44	199	90	19	48
NM_002917	RFNG	0.00	0.44	964	1019	1075	1601
NM_004388	CTBS	-0.09	0.44	389	307	591	908
NM_018462	BRK1	0.00	0.44	1676	1595	2618	3774
NM_001101802	PHF21A	0.00	0.44	478	512	930	1394
NM_181333	PRR5	0.00	0.44	54	35	64	124
NM_000629	IFNAR1	-0.07	0.44	1096	942	1778	2593
NM_007218	RNF139	0.00	0.44	553	577	566	871
NM_014232	VAMP2	0.00	0.44	879	840	888	1333
NM_001166345	MDFIC	0.00	0.44	1120	1138	2236	3235
NM_052888	LRRC37B	0.00	0.44	112	143	185	311
NM_020310	MNT	0.00	0.44	600	668	919	1375

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_012330	KAT6B	0.00	0.44	761	764	1111	1647
NM_181453	GCC2	0.00	0.44	622	601	1004	1495
NM_018023	YEATS2	0.00	0.44	2162	2291	2225	3211
NM_207333	ZNF320	0.00	0.44	167	189	293	471
NM_033280	SEC11C	0.00	0.44	165	141	287	462
NM_030665	RAI1	0.00	0.44	791	829	1152	1702
NM_001291415	KDM6A	0.01	0.43	551	635	572	876
NM_033426	CIPC	0.00	0.43	214	240	462	717
NM_014812	CEP170	0.00	0.43	8327	8099	11240	15626
NM_182491	ZFAND2A	-0.01	0.43	505	430	553	848
NM_177938	P4HTM	0.00	0.43	302	359	809	1214
NM_006734	HIVEP2	0.00	0.43	2739	2790	3876	5495
NM_014999	RAB21	0.00	0.43	1433	1359	1518	2214
NM_001172700	SHROOM1	0.00	0.43	172	153	310	495
NM_001123392	TBC1D3H	0.00	0.43	180	169	214	353
NM_032258	TBC1D3F	0.00	0.43	178	167	210	347
NM_001003940	BMF	0.00	0.43	16	21	139	240
NM_170753	PGBD3	0.00	0.43	393	349	341	540
NM_032561	C22orf23	0.00	0.43	895	818	616	937
NM_002850	PTPRS	0.00	0.43	1513	1624	4130	5835
NM_024312	GNPTAB	0.00	0.43	1067	1117	2082	2996
NM_014117	C16orf72	0.00	0.43	1360	1438	2647	3780
NM_003107	SOX4	0.00	0.43	420	440	767	1150
NM_001134655	ZNF213	0.00	0.43	300	288	335	530
NM_001040445	ASB1	0.00	0.43	2965	2938	3827	5407
NM_014044	UNC50	0.00	0.43	596	517	740	1111
NM_030802	FAM117A	0.00	0.43	42	52	112	198
NM_001163922	VSIG10L	-0.30	0.43	119	68	112	198
NM_018215	PNMAL1	0.00	0.43	111	148	299	477
NM_004454	ETV5	0.00	0.43	1619	1624	2689	3832
NM_016433	GLTP	0.00	0.43	2313	2364	2760	3930
NM_001252127	AP4E1	0.00	0.43	629	585	755	1131
NM_005665	EVI5	0.00	0.42	893	874	894	1327
NM_004369	COL6A3	-0.11	0.42	31491	28566	126573	171367
NM_001015880	PAPSS2	0.00	0.42	7619	7633	6316	8809
NM_001003795	GTF2IRD2B	0.00	0.42	142	127	195	323

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_024784	ZBTB3	0.00	0.42	153	164	177	296
NM_001291462	LOC101060321	0.00	0.42	179	169	214	351
NM_020765	UBR4	0.01	0.42	14337	14831	24696	33768
NM_080489	SDCBP2	-0.08	0.42	103	68	100	179
NM_152778	MFSD8	0.00	0.42	160	165	202	333
NM_173822	FAM126B	-0.14	0.42	271	198	324	512
NM_176891	IFNE	0.00	0.42	9	11	121	211
NM_020729	ODF2L	-0.10	0.42	309	235	345	542
NM_024541	C10orf76	0.00	0.42	416	397	630	950
NM_016049	EMC9	0.00	0.42	178	190	191	316
NM_001014283	DCUN1D2	0.00	0.42	293	293	364	569
NM_025106	SPSB1	0.00	0.42	487	555	497	760
NM_032995	ARHGEF4	0.00	0.42	172	137	349	547
NM_080669	SLC46A1	0.00	0.42	440	493	853	1264
NM_005981	TSPAN31	0.00	0.42	366	399	1059	1553
NM_001755	CBFB	0.00	0.42	1496	1606	1947	2786
NM_018378	FBXL8	0.00	0.42	67	54	83	152
NM_001018116	MURC	0.00	0.42	48	58	83	152
NM_018197	ZFP64	0.00	0.42	400	426	530	806
NM_001256619	R3HCC1L	-0.14	0.42	414	315	306	484
NM_004747	DLG5	0.00	0.42	2751	2780	4972	6930
NM_002668	PLP2	-0.01	0.42	3124	2912	4382	6124
NM_001963	EGF	0.00	0.42	28	30	64	122
NM_015021	ZNF292	0.00	0.42	798	821	859	1270
NM_001135575	SMIM13	0.00	0.42	347	384	374	582
NM_001896	CSNK2A2	0.00	0.42	824	730	678	1015
NM_000854	GSTT2	0.00	0.42	178	174	356	556
NM_001080843	GSTT2B	0.00	0.42	178	174	356	556
NM_022158	FN3K	0.00	0.42	67	95	146	248
NM_019072	SGTB	-0.04	0.41	1257	1111	1493	2152
NM_016530	RAB8B	0.00	0.41	821	780	1470	2120
NM_020971	SPTBN4	0.00	0.41	42	40	89	161
NM_001148	ANK2	0.00	0.41	100	120	1822	2606
NM_004490	GRB14	0.00	0.41	46	31	177	294
NM_001042483	NUPR1	-0.04	0.41	1550	1379	2785	3930
NM_018216	PANK4	0.00	0.41	1151	1070	780	1157
NM_152271	LONRF1	0.00	0.41	184	197	106	187

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_022900	CASD1	0.00	0.41	124	117	135	231
NM_001136265	IFFO2	-0.05	0.41	1768	1576	1618	2322
NM_012421	RLF	0.00	0.41	612	646	686	1024
NM_001040182	CLDND1	-0.03	0.41	1181	1047	942	1383
NM_148894	BOD1L1	-0.01	0.41	1437	1307	1971	2808
NM_015102	NPHP4	0.00	0.41	376	405	603	906
NM_014106	ZNF770	0.00	0.41	807	848	842	1242
NM_014649	SAFB2	0.00	0.41	617	568	470	717
NM_017983	WIPI1	0.00	0.41	638	661	1242	1798
NM_003801	GPAA1	0.00	0.41	1613	1646	2589	3651
NM_001165958	GSDMB	0.00	0.41	67	85	154	259
NM_014315	KLHDC2	0.01	0.41	544	627	728	1081
NM_014506	TOR1B	0.00	0.41	1792	1732	3662	5115
NM_025179	PLXNA2	-0.01	0.41	3653	3428	5203	7209
NM_006454	MXD4	0.00	0.41	1138	1246	2566	3617
NM_001144757	SCG5	0.00	0.41	589	583	992	1449
NM_001286398	RNF217	0.00	0.41	305	326	358	556
NM_014746	RNF144A	0.00	0.41	15	16	264	420
NM_144964	TRMT10 B	0.00	0.41	102	138	127	218
NM_004854	CHST10	0.00	0.41	252	285	223	360
NM_000801	FKBP1A	-0.03	0.41	4437	4137	9144	12506
NM_014322	OPN3	0.00	0.41	339	359	208	338
NM_138426	GLCCI1	0.00	0.40	401	387	281	444
NM_014938	MLXIP	-0.05	0.40	2329	2103	2959	4140
NM_001271872	SRGAP2 C	0.00	0.40	1012	1093	1410	2022
NM_001278535	NEURL2	-0.74	0.40	71	25	44	89
NM_001270384	FAM73A	0.00	0.40	667	730	1254	1806
NM_005645	TAF13	0.00	0.40	530	489	439	669
NM_000296	PKD1	0.00	0.40	2780	2693	3305	4603
NM_053042	ZNF518B	-0.05	0.40	940	815	1044	1514
NM_002839	PTPRD	0.00	0.40	136	163	510	769
NM_017658	KLHL28	0.00	0.40	343	287	252	401
NM_024756	MMRN2	0.00	0.40	97	80	141	238
NM_021090	MTMR3	-0.14	0.40	1277	1055	1705	2421
NM_006463	STAMBP	0.00	0.40	488	500	435	662
NM_022110	FKBPL	0.00	0.40	106	138	79	144
NM_018379	FAM63A	0.00	0.40	150	153	308	481
NM_013995	LAMP2	0.00	0.40	2337	2446	3452	4793

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_006699	MAN1A2	0.00	0.40	922	888	1545	2200
NM_212481	ARID5A	0.00	0.40	255	267	175	288
NM_003129	SQLE	0.00	0.40	603	679	1643	2333
NM_014935	PLEKHA6	0.00	0.40	78	57	150	251
NM_001006612	WBP5	0.00	0.40	1521	1555	1840	2601
NM_138962	MSI2	0.00	0.40	84	75	239	381
NM_016248	AKAP11	0.00	0.40	1624	1699	2976	4142
NM_001129896	SYTL4	0.00	0.40	350	342	378	580
NM_004446	EPRS	0.00	0.40	3716	3604	6108	8357
NM_001242809	ANKRD6	0.00	0.40	234	199	537	804
NM_001291832	FAM132B	-0.07	0.39	91	59	258	408
NM_001001872	C14orf37	0.00	0.39	176	192	593	882
NM_153188	TNPO1	0.00	0.39	3316	3417	5555	7604
NM_016353	ZDHHC2	-0.03	0.39	1262	1122	1312	1874
NM_032423	ZNF528	0.00	0.39	104	137	412	627
NM_015092	SMG1	0.00	0.39	2891	2989	4675	6418
NM_018169	KIAA1551	0.00	0.39	410	359	420	638
NM_024089	KDELC1	0.00	0.39	207	252	391	597
NM_005512	LRRC32	0.00	0.39	4065	4076	12915	17410
NM_001902	CTH	0.00	0.39	172	203	64	120
NM_001285549	ZDBF2	0.00	0.39	243	227	364	558
NM_014230	SRP68	-0.11	0.39	3007	2624	2801	3889
NM_001008211	OPTN	0.01	0.39	5063	5327	8454	11456
NM_031886	KCNA7	0.00	0.39	215	189	198	320
NM_006609	MAP3K2	0.00	0.39	1321	1391	1843	2591
NM_020717	SHROOM4	0.00	0.39	204	223	518	774
NM_015349	GLTSCR1L	0.01	0.39	353	419	693	1017
NM_153240	NPHP3	-0.21	0.39	593	442	832	1209
NM_017851	PARP16	0.00	0.39	154	197	158	261
NM_024561	NAA16	0.00	0.39	168	205	139	233
NM_004460	FAP	0.00	0.39	1810	1767	4594	6279
NM_001204817	ZNF587	-0.05	0.39	523	434	607	896
NM_012135	FAM50B	0.00	0.39	279	242	241	381
NM_080607	VSTM2L	0.00	0.38	36	44	56	107
NM_002114	HIVEP1	0.00	0.38	1142	1217	1447	2046
NM_001202560	WBSCR22	0.01	0.38	821	924	1506	2126

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_000147	FUCA1	0.00	0.38	111	84	387	588
NM_031946	AGAP3	0.00	0.38	1926	2019	2797	3867
NM_001171816	RNF166	0.00	0.38	188	216	208	333
NM_000132	F8	0.00	0.38	30	45	166	272
NM_005938	FOXO4	-0.01	0.38	308	251	343	525
NM_001007523	F8A2	0.00	0.38	389	342	460	689
NM_001007524	F8A3	0.00	0.38	389	342	460	689
NM_001005463	EBF3	0.00	0.38	502	520	780	1131
NM_018434	RNF130	0.00	0.38	324	386	934	1342
NM_003908	EIF2S2	0.00	0.38	1607	1689	2360	3270
NM_005781	TNK2	0.00	0.38	582	624	813	1176
NM_001136234	SUPT20HL1	0.00	0.38	17	22	73	133
NM_031913	ESYT3	0.00	0.38	75	95	150	248
NM_133496	SLC30A7	0.00	0.38	1042	1077	1217	1726
NM_001291694	NR2C2	0.00	0.38	1625	1559	1747	2442
NM_014952	BAHD1	0.00	0.38	386	394	520	771
NM_001304	CPD	-0.08	0.38	1422	1232	2868	3946
NM_001271870	SRGAP2B	0.00	0.38	988	1050	1346	1900
NM_001277945	ZNF83	0.00	0.38	267	304	455	680
NM_001924	GADD45A	-0.32	0.38	1772	1300	1375	1937
NM_006768	BRAP	0.00	0.38	419	483	636	930
NM_001001330	REEP3	0.00	0.38	1559	1474	1828	2547
NM_013313	YPEL1	0.00	0.38	87	97	158	259
NM_024560	ACSS3	0.00	0.38	25	29	158	259
NM_024725	CCDC82	0.00	0.38	354	344	416	625
NM_001040185	ZNF765	0.00	0.38	135	138	187	301
NM_001079537	TRAPPC6B	0.00	0.37	594	596	834	1200
NM_001993	F3	0.00	0.37	268	261	451	673
NM_001006607	LRRC37A2	0.00	0.37	212	199	370	560
NM_003162	STRN	0.00	0.37	821	916	1113	1579
NM_025075	THOC7	0.00	0.37	383	389	480	713
NM_013272	SLCO3A1	-0.25	0.37	672	493	961	1372
NM_175922	PRR18	-0.41	0.37	54	23	37	76
NM_003799	RNMT	0.00	0.37	696	768	1059	1505
NM_020928	ZSWIM6	0.00	0.37	953	994	1079	1532
NM_006876	B3GNT1	0.00	0.37	369	347	848	1218

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_005713	COL4A3 BP	0.00	0.37	602	668	1177	1664
NM_014157	CCDC113	-0.04	0.37	82	53	175	283
NM_198557	RBM43	0.00	0.37	85	110	175	283
NM_001098402	ZBTB21	0.00	0.37	466	499	638	930
NM_022458	LMBR1	0.00	0.37	474	526	774	1116
NM_018426	TMEM63 B	0.00	0.37	1331	1389	2600	3569
NM_024744	CARF	0.00	0.37	87	88	160	261
NM_014600	EHD3	0.00	0.37	582	633	813	1168
NM_024580	EFTUD1	0.00	0.37	910	948	1510	2109
NM_001204477	CDRT4	0.00	0.37	150	149	183	294
NM_145265	CCDC127	0.00	0.37	309	364	530	780
NM_025219	DNAJC5	-0.12	0.37	3547	3082	3833	5196
NM_025191	EDEM3	0.00	0.37	1097	1212	2182	3005
NM_014155	ZBTB44	0.00	0.37	475	526	613	893
NM_015621	CCDC69	0.00	0.37	61	67	137	227
NM_020974	SCUBE2	0.00	0.37	43	38	81	144
NM_005450	NOG	0.00	0.37	149	122	135	224
NM_032494	ZC3H8	0.00	0.37	46	62	62	115
NM_052911	ESCO1	0.00	0.37	281	273	260	403
NM_015038	KIAA075 4	0.00	0.37	1854	1893	3361	4566
NM_001278503	STT3A	0.00	0.37	5046	5237	6800	9094
NM_001282903	TRPS1	0.00	0.37	505	501	896	1277
NM_000709	BCKDHA	0.00	0.36	673	665	782	1122
NM_001278940	GTF2A1	0.00	0.36	1071	1155	1054	1490
NM_025164	SIK3	-0.02	0.36	749	653	1739	2408
NM_032242	PLXNA1	0.00	0.36	5485	5596	9523	12647
NM_001012454	FAM71F2	0.00	0.36	51	40	106	181
NM_015966	ERGIC3	0.00	0.36	3835	3977	6971	9299
NM_001144769	DST	-0.22	0.36	9290	7703	22150	29075
NM_012151	F8A1	0.00	0.36	612	575	753	1081
NM_001256486	GOLGB1	0.00	0.36	2455	2390	4488	6039
NM_001284201	JKAMP	0.00	0.36	892	893	1566	2174
NM_173542	PLBD2	-0.03	0.36	883	773	2909	3957
NM_001271837	RCN2	0.00	0.36	1133	1136	1984	2730
NM_152313	SLC36A4	-0.06	0.36	368	295	424	630
NM_130468	CHST14	0.00	0.36	782	755	709	1020
NM_003635	NDST2	0.00	0.36	701	765	1054	1486
NM_020528	PCBP3	0.00	0.36	61	38	6	26

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_018259	TTC17	0.00	0.36	1086	1031	1508	2092
NM_152914	NATD1	0.00	0.36	357	351	406	604
NM_001134651	EIF4E3	0.00	0.36	126	101	349	525
NM_001017969	KIAA2026	0.00	0.36	587	513	857	1218
NM_198279	CXorf23	0.00	0.36	119	126	268	412
NM_032779	CCDC142	-0.05	0.36	279	219	316	479
NM_001130726	CCDC149	0.00	0.36	491	481	844	1200
NM_001080496	RGP1	0.00	0.36	566	501	501	734
NM_004562	PARK2	-0.19	0.36	21	5	73	131
NM_001136022	NFATC4	0.00	0.36	1204	1237	2889	3915
NM_021242	MID1IP1	0.00	0.36	590	624	813	1157
NM_001409	MEGF6	0.00	0.36	2221	2211	2404	3274
NM_001199260	TOR1AIP2	0.00	0.36	2900	2998	4159	5580
NM_001360	DHCR7	0.00	0.35	1147	1042	2475	3366
NM_153605	CRYBG3	0.00	0.35	1109	1082	1316	1830
NM_001144013	RGPD3	0.00	0.35	191	165	216	338
NM_001288608	ADAMTSL4	0.00	0.35	233	245	576	835
NM_001040653	ZXDC	0.00	0.35	862	920	919	1298
NM_006405	TM9SF1	0.00	0.35	1614	1712	3111	4198
NM_016651	DACT1	0.00	0.35	802	850	1086	1521
NM_001172659	ZFYVE28	0.00	0.35	73	74	193	305
NM_003966	SEMA5A	0.00	0.35	1095	1144	1691	2325
NM_001281495	CTNNBL1	0.00	0.35	701	632	730	1042
NM_001282167	PORCN	0.00	0.35	595	568	1452	2007
NM_138463	TLCD1	0.00	0.35	147	111	131	216
NM_001284209	MED6	0.00	0.35	439	384	403	597
NM_001025100	MBP	0.00	0.35	450	476	476	697
NM_015101	COLGALT2	0.00	0.35	185	202	545	791
NM_005920	MEF2D	0.00	0.35	2638	2623	3086	4159
NM_001135844	SIRPB1	0.00	0.35	155	190	243	375
NM_003112	SP4	-0.31	0.35	243	154	116	194
NM_021942	TRAPPC11	0.00	0.35	519	564	986	1384
NM_025140	CCDC92	0.00	0.35	1157	1194	2119	2885
NM_002379	MATN1	-0.79	0.35	377	177	125	207
NM_001010898	SLC6A17	0.00	0.35	166	178	599	863
NM_001199179	ATP2C1	0.00	0.35	2410	2577	4294	5730

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_032312	YIPF4	-0.13	0.35	412	317	482	704
NM_003620	PPM1D	0.00	0.35	306	303	212	331
NM_199186	BPGM	-0.15	0.35	435	330	688	983
NM_152221	CSNK1E	-0.04	0.35	3499	3209	3105	4176
NM_001172509	SATB2	0.00	0.35	728	738	834	1179
NM_016542	MST4	0.00	0.35	148	122	139	227
NM_001166111	PNPLA6	0.01	0.35	2934	3132	5447	7225
NM_194356	STX2	0.00	0.35	999	1028	1402	1935
NM_133631	ROBO1	0.00	0.35	1216	1309	2275	3083
NM_001204519	P2RX5	0.00	0.35	156	196	780	1105
NM_001101426	ISPD	-0.03	0.34	75	48	79	139
NM_001286606	CRACR2B	-0.15	0.34	37	17	79	139
NM_024980	GPR157	0.00	0.34	104	96	75	133
NM_101395	DYRK1A	0.00	0.34	1558	1572	1689	2310
NM_022061	MRPL17	0.00	0.34	2604	2784	3259	4366
NM_023072	ZSWIM4	0.00	0.34	336	317	424	623
NM_002489	NDUFA4	0.00	0.34	639	613	1029	1436
NM_207123	GAB1	0.00	0.34	211	235	235	362
NM_006029	PNMA1	-0.02	0.34	1372	1238	1868	2543
NM_016018	PHF20L1	0.00	0.34	812	893	1393	1917
NM_015512	DNAH1	0.00	0.34	305	326	618	885
NM_015974	CRYL1	0.00	0.34	268	217	836	1177
NM_001282913	TCAIM	0.00	0.34	162	134	287	434
NM_001258	CDK3	0.00	0.34	54	52	56	104
NM_001194958	KCNJ18	0.00	0.34	35	22	56	104
NM_001290322	DMXL1	0.00	0.34	818	821	1736	2366
NM_006829	ADIRF	-0.07	0.34	883	748	1138	1577
NM_198507	FAM174A	0.00	0.34	186	194	270	410
NM_001178085	ZFX	0.00	0.34	1452	1410	2036	2758
NM_203459	CAMSAP2	0.00	0.34	1534	1510	1999	2708
NM_020422	TMEM159	0.00	0.34	554	607	1192	1647
NM_032870	PNISR	0.00	0.34	1197	1229	1468	2011
NM_181836	TMED7	0.00	0.34	3008	3107	4698	6214
NM_015144	ZCCHC14	0.00	0.34	839	876	1160	1604
NM_022095	ZNF335	0.00	0.34	951	879	1015	1412
NM_004273	CHST3	0.00	0.34	2867	2935	2766	3706
NM_020840	FNIP2	0.00	0.34	1420	1534	2283	3076

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_006455	LEPREL4	0.00	0.34	2600	2651	2211	2981
NM_001190737	NFIB	0.00	0.34	1079	1131	231	355
NM_014714	IFT140	0.00	0.34	227	252	705	998
NM_001172671	ZNF430	0.00	0.34	133	119	89	153
NM_020978	AMY2B	0.00	0.34	10	26	102	172
NM_001278299	WIPI2	0.00	0.34	2119	2216	3926	5205
NM_014971	EFR3B	0.00	0.34	130	145	443	645
NM_001084	PLOD3	0.00	0.34	4858	5093	9525	12403
NM_197941	ADAMTS 6	0.00	0.34	1589	1625	1096	1516
NM_005107	EXOG	0.00	0.34	247	201	368	543
NM_006682	FGL2	0.00	0.33	265	230	177	279
NM_005575	LNPEP	0.00	0.33	956	1024	1805	2447
NM_001286527	ATP2C2	0.00	0.33	92	84	83	144
NM_178314	RILPL1	0.00	0.33	657	728	873	1220
NM_020778	ALPK3	0.00	0.33	155	127	225	346
NM_018351	FGD6	0.00	0.33	419	411	749	1055
NM_001040202	PAQR3	0.00	0.33	432	429	555	795
NM_014872	ZBTB5	0.00	0.33	442	456	308	460
NM_001075098	MOCS1	0.00	0.33	162	136	154	246
NM_001135057	LRRC15	0.00	0.33	479	517	1917	2588
NM_001412	EIF1AX	-0.05	0.33	1150	1003	1400	1911
NM_001135643	DCTN4	0.00	0.33	1427	1558	3629	4802
NM_001004127	ALG11	0.00	0.33	709	661	715	1007
NM_001040108	MLH3	0.00	0.33	433	474	915	1272
NM_000117	EMD	0.00	0.33	922	1002	1260	1726
NM_052928	SMYD4	0.00	0.33	490	479	547	782
NM_003392	WNT5A	0.00	0.33	1101	994	2789	3712
NM_001130677	C17orf96	0.00	0.33	72	50	21	48
NM_003812	ADAM23	0.00	0.33	318	306	1221	1673
NM_001039693	TYW5	0.00	0.33	90	124	127	207
NM_031301	APH1B	0.00	0.33	258	300	747	1048
NM_002611	PDK2	0.00	0.33	415	462	1142	1569
NM_194283	DNAJC21	-0.04	0.33	792	683	971	1344
NM_001289121	ZCCHC7	0.00	0.33	287	345	528	756
NM_004481	GALNT2	0.00	0.33	6321	6564	9071	11758
NM_024086	METTL16	0.00	0.33	489	491	582	828
NM_031419	NFKBIZ	0.00	0.33	508	436	304	453
NM_194455	KRIT1	0.00	0.33	428	478	695	978
NM_001033503	SAR1B	0.00	0.33	1248	1279	1626	2200

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_000215	JAK3	0.00	0.33	157	194	166	262
NM_001040020	FAM3C	-0.02	0.33	1297	1162	1518	2059
NM_015375	DSTYK	0.00	0.33	1005	920	1851	2492
NM_015455	CNOT6	0.00	0.33	491	450	420	610
NM_022720	DGCR8	0.00	0.33	1837	1861	1285	1754
NM_004507	HUS1	0.00	0.33	339	374	406	591
NM_138782	FCHO2	0.00	0.33	460	486	630	891
NM_145246	FRA10AC1	0.00	0.33	177	196	189	294
NM_007246	KLHL2	0.00	0.33	428	427	514	736
NM_018956	C9orf9	0.00	0.33	65	56	241	366
NM_012120	CD2AP	0.00	0.32	548	558	772	1079
NM_007039	PTPN21	0.01	0.32	1183	1306	1984	2662
NM_020245	TULP4	0.00	0.32	1812	1911	2354	3139
NM_001570	IRAK2	0.00	0.32	197	168	329	486
NM_001134671	DERL1	0.00	0.32	1908	2033	2645	3514
NM_005257	GATA6	0.00	0.32	337	342	185	288
NM_001429	EP300	0.00	0.32	3034	3190	3691	4858
NM_001145313	FSD1L	0.00	0.32	79	105	175	274
NM_001106	ACVR2B	0.00	0.32	73	90	79	137
NM_198892	BMP2K	0.00	0.32	430	417	651	917
NM_001145853	WFS1	0.00	0.32	1983	1969	4561	5970
NM_177533	NUDT14	0.00	0.32	43	28	141	226
NM_001171894	MEF2A	0.00	0.32	1198	1245	2498	3320
NM_004563	PCK2	0.00	0.32	807	770	1077	1477
NM_001080825	TMEM120B	0.00	0.32	772	836	1090	1494
NM_001256126	CERS6	0.00	0.32	699	755	1117	1529
NM_016612	SLC25A37	0.00	0.32	624	634	657	924
NM_004897	MINPP1	0.00	0.32	486	510	599	847
NM_025136	OPA3	0.00	0.32	766	842	1069	1466
NM_173569	UBN2	0.00	0.32	461	432	474	680
NM_153261	CNEP1R1	0.00	0.32	200	217	272	407
NM_015310	PSD3	0.00	0.32	499	545	1926	2577
NM_007114	TMF1	0.00	0.32	1431	1375	1693	2275
NM_144975	SLFN5	0.00	0.32	1442	1476	3720	4880
NM_003549	HYAL3	0.00	0.32	157	143	162	255
NM_018360	TXLNG	0.00	0.32	437	464	354	518
NM_016579	CD320	-0.29	0.32	1068	782	990	1360
NM_001859	SLC31A1	0.00	0.32	2394	2244	3088	4068

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_003466	PAX8	0.00	0.32	218	268	478	684
NM_001204897	TM4SF19	0.00	0.32	61	52	416	601
NM_001267550	TTN	0.00	0.32	672	694	1553	2091
NM_138797	ANKRD54	0.00	0.32	443	501	539	765
NM_030807	SLC2A11	0.00	0.32	82	56	148	235
NM_001498	GCLC	0.01	0.32	392	462	720	1004
NM_152357	ZNF440	0.00	0.32	150	172	247	372
NM_001136041	HDAC11	0.00	0.32	273	230	562	795
NM_080622	ABHD16B	0.00	0.32	55	66	96	161
NM_153367	ZCCHC24	0.00	0.32	1798	1882	3429	4497
NM_002600	PDE4B	-0.14	0.31	252	182	364	530
NM_145294	WDR90	-0.03	0.31	267	211	208	318
NM_005401	PTPN14	0.00	0.31	7452	7306	12409	15861
NM_007220	CA5B	0.00	0.31	261	239	293	434
NM_001197104	KMT2A	0.00	0.31	2487	2534	4151	5412
NM_007225	NXPH3	0.00	0.31	121	148	362	527
NM_031905	ARMC10	-0.01	0.31	270	217	362	527
NM_003470	USP7	0.00	0.31	2230	2284	2743	3614
NM_001142853	HES6	-0.21	0.31	64	34	10	33
NM_030965	ST6GALNAC5	0.00	0.31	109	107	35	70
NM_032246	MEX3B	0.00	0.31	313	263	35	70
NM_003796	URI1	0.00	0.31	1158	1165	1493	2007
NM_001145664	RFX8	0.00	0.31	158	183	836	1153
NM_012287	ACAP2	0.01	0.31	1262	1388	2402	3174
NM_001037131	AGAP1	0.00	0.31	1452	1565	1915	2549
NM_001277325	NPIPA5	0.00	0.31	115	123	160	251
NM_182488	USP12	0.00	0.31	624	675	988	1351
NM_001144000	AGAP5	-0.03	0.31	70	44	58	105
NM_032340	UQCC2	0.00	0.31	923	996	1410	1898
NM_003808	TNFSF13	0.00	0.31	69	55	104	172
NM_001943	DSG2	0.00	0.31	970	1077	5157	6678
NM_025079	ZC3H12A	0.00	0.31	243	295	287	425
NM_182551	LCLAT1	0.00	0.31	606	669	865	1190
NM_014899	RHOBTB3	0.00	0.31	3414	3569	6950	8944
NM_001268284	LRRC8E	-0.02	0.31	743	645	982	1342
NM_020846	SLAIN2	0.00	0.31	1602	1721	2005	2662
NM_004459	BPTF	0.00	0.31	2298	2324	2627	3458

Table 6B: Differentially Upregulated Genes in SEN + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001291466	LOC102723859	0.00	0.31	143	106	143	227
NM_001291459	LOC101060376	-0.01	0.31	144	106	143	227
NM_001123391	TBC1D3	-0.01	0.31	144	106	143	227
NM_001291464	LOC101060351	0.00	0.31	143	106	143	227
NM_001291463	LOC102724862	0.00	0.31	143	106	143	227
NM_001291465	LOC101060389	0.00	0.31	143	106	143	227
NM_018143	KLHL11	0.00	0.31	288	313	393	567
NM_001144892	FGF1	0.00	0.31	287	237	524	741
NM_004992	MECP2	0.00	0.31	1723	1623	2096	2776
NM_001001484	PTER	0.00	0.31	136	109	146	231
NM_001039771	CBLN3	0.00	0.31	40	36	141	224
NM_001025930	TTLL3	0.00	0.31	335	375	888	1218
NM_018999	CCSER2	0.00	0.31	1278	1384	2427	3198
NM_152387	KCTD18	0.00	0.31	357	357	557	784
NM_012234	RYBP	0.00	0.31	565	612	688	956
NM_001010935	RAP1A	0.00	0.31	609	654	780	1076
NM_016174	CERCAM	0.00	0.31	6943	7119	12879	16369
NM_005261	GEM	0.00	0.31	416	415	869	1192
NM_014178	STXBP6	0.00	0.31	229	246	67	118
NM_032836	FIZ1	0.00	0.31	124	153	67	118
NM_001042522	SPRED3	0.00	0.31	85	86	364	527
NM_001207025	POU2F2	0.00	0.31	124	121	160	250
NM_173517	VKORC1L1	0.00	0.31	1597	1556	1874	2486
NM_014709	USP34	0.00	0.30	2922	3017	4960	6403
NM_018691	FAM114A2	0.00	0.30	365	381	699	969
NM_020807	ZNF319	0.00	0.30	431	482	499	706
NM_033393	FHDC1	-0.03	0.30	44	24	19	44
NM_016072	GOLT1B	0.00	0.30	1346	1436	1414	1895
NM_001270974	HYDIN	0.00	0.30	13	18	208	316
NM_001018100	MYZAP	0.00	0.30	100	131	208	316
NM_178526	SLC25A42	0.00	0.30	144	153	272	403
NM_145235	FANK1	0.00	0.30	64	52	85	144
NM_138496	CYHR1	0.00	0.30	422	382	790	1087
NM_001079533	CPEB1	-1.04	0.30	107	33	514	725

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_014881	DCLRE1A	0.00	0.30	106	136	143	226
NM_001173452	TFCP2	0.00	0.30	670	587	684	948
NM_006885	ZFHX3	-0.11	0.30	2389	2061	2092	2760
NM_004177	STX3	0.00	0.30	678	760	626	872
NM_000512	GALNS	0.00	0.30	661	666	890	1216
NM_001288668	HCFC1R1	0.00	0.30	549	495	784	1078
NM_018362	LIN7C	0.00	0.30	1294	1273	1572	2094
NM_015077	SARM1	0.00	0.30	387	380	776	1067
NM_004804	CIAO1	0.00	0.30	1425	1460	2483	3255
NM_004620	TRAF6	0.00	0.30	556	543	562	787
NM_021167	GATAD1	-0.26	0.30	694	505	705	974
NM_001144823	DENND4A	0.00	0.30	678	654	1029	1394
NM_032452	JPH4	0.00	0.30	43	35	79	135
NM_001286581	PHRF1	0.00	0.30	1387	1447	1227	1649
NM_001025108	AFF3	0.00	0.30	88	111	250	372
NM_173791	PDZD8	0.00	0.30	1055	1153	1747	2314
NM_020911	PLXNA4	0.00	0.30	36	35	262	388
NM_006224	PITPNA	-0.10	0.30	1858	1604	2724	3554
NM_139280	ORMDL3	0.00	0.30	1525	1594	2433	3185
NM_020399	GOPC	0.00	0.30	994	946	1404	1874
NM_145169	SFT2D1	0.00	0.30	443	443	599	834
NM_001137552	LRRFIP1	-0.39	0.30	1023	697	1206	1619
NM_001199161	USP19	0.00	0.30	1321	1384	1657	2196
NM_199336	FAHD2B	-0.15	0.30	143	95	135	214
NM_207644	LRRC75B	0.00	0.30	57	64	125	200
NM_003718	CDK13	0.00	0.30	1200	1192	1526	2028
NM_001127615	ENOX1	0.00	0.30	19	18	96	159
NM_198449	EMB	0.00	0.30	265	226	826	1128
NM_001001890	RUNX1	0.00	0.30	1982	1889	3872	4996
NM_001012398	AKTIP	0.00	0.30	172	197	329	477
NM_138389	FAM114A1	0.00	0.30	2607	2719	4099	5281
NM_003477	PDHX	0.00	0.30	806	853	892	1213
NM_182767	SLC6A15	0.00	0.30	65	94	146	229
NM_001256667	FAM193A	0.00	0.30	967	1014	1123	1510
NM_032832	LRP11	0.00	0.29	1024	1018	1934	2545
NM_001287349	ZNF852	0.00	0.29	86	74	50	92
NM_003070	SMARCA	0.00	0.29	1601	1688	2288	2993

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
	2						
NM_024790	CSPP1	0.00	0.29	166	164	189	288
NM_001271938	MEGF8	0.00	0.29	635	717	1618	2142
NM_001288645	ZNF286A	0.00	0.29	112	141	195	296
NM_001164315	ANKRD36	0.00	0.29	383	357	510	715
NM_001277090	ZNF550	-0.04	0.29	160	117	160	248
NM_003367	USF2	0.00	0.29	1860	1778	2296	3000
NM_024753	TTC21B	0.00	0.29	450	454	543	758
NM_001039590	USP9X	0.00	0.29	4589	4606	9009	11399
NM_018714	COG1	0.00	0.29	1846	1974	2810	3647
NM_001001795	C8orf82	0.00	0.29	181	169	327	473
NM_198076	COX20	-0.42	0.29	483	305	474	667
NM_000124	ERCC6	0.00	0.29	1586	1640	2044	2678
NM_001282569	ZCCHC17	0.00	0.29	864	905	1206	1612
NM_025040	ZNF614	0.00	0.29	204	223	191	290
NM_001001418	TBC1D3C	-0.04	0.29	146	106	148	231
NM_001278277	E2F6	0.00	0.29	174	217	175	268
NM_003170	SUPT6H	-0.02	0.29	2072	1894	4132	5298
NM_053055	THEM4	0.00	0.29	88	119	220	329
NM_138367	ZNF251	0.00	0.29	252	233	543	756
NM_032270	LRRC8C	0.00	0.29	1041	983	491	688
NM_017933	PID1	0.00	0.29	270	294	264	388
NM_001271675	LOC441155	0.00	0.29	716	796	836	1135
NM_024529	CDC73	0.00	0.29	985	989	1383	1834
NM_001024210	S100A13	0.00	0.29	2237	2366	5430	6913
NM_025054	VCPIP1	0.00	0.29	946	939	1495	1976
NM_152305	POGLUT1	0.00	0.29	320	274	582	806
NM_138571	HINT3	-0.15	0.29	171	117	356	510
NM_002298	LCP1	0.00	0.29	15	22	277	405
NM_014713	LAPTM4A	0.00	0.29	6061	5946	9618	12105
NM_004996	ABCC1	0.01	0.29	3233	3438	4744	6048
NM_002392	MDM2	0.00	0.28	1487	1553	2849	3678
NM_001001481	UBE2W	0.00	0.28	448	489	786	1068
NM_152272	CHMP7	0.00	0.28	976	1007	1578	2076
NM_014931	PPP6R1	0.00	0.28	3188	3176	3619	4638
NM_012192	TIMM10B	0.00	0.28	616	682	1262	1675

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_017864	INTS8	0.00	0.28	384	426	661	906
NM_001111125	IQSEC2	0.00	0.28	475	433	638	876
NM_006854	KDELR2	0.00	0.28	10362	10647	8911	11201
NM_144666	DNHD1	0.00	0.28	237	223	445	625
NM_005054	RGPD5	0.00	0.28	1425	1330	2003	2608
NM_016374	ARID4B	-0.04	0.28	367	297	401	567
NM_015234	GPR116	0.00	0.28	427	462	817	1105
NM_024830	LPCAT1	-0.20	0.28	2873	2349	2354	3046
NM_020812	DOCK6	0.00	0.28	413	469	1192	1582
NM_002485	NBN	0.00	0.28	576	648	950	1274
NM_001145855	SH3BP2	0.00	0.28	717	728	990	1325
NM_004999	MYO6	0.00	0.28	1095	1167	1635	2142
NM_001170637	SRGAP2	0.00	0.28	1757	1869	2770	3566
NM_006031	PCNT	0.00	0.28	2036	2017	2396	3098
NM_024527	ABHD8	0.00	0.28	195	232	256	375
NM_004330	BNIP2	0.00	0.28	931	973	1508	1981
NM_017423	GALNT7	0.01	0.28	379	448	774	1048
NM_001116	ADCY9	0.00	0.28	2359	2217	3519	4497
NM_001130720	AHCYL2	0.00	0.28	346	290	586	806
NM_001042463	TMEM80	0.00	0.28	187	224	495	688
NM_030964	SPRY4	0.00	0.28	1431	1518	3061	3924
NM_134269	SMTN	0.00	0.28	6625	6496	7645	9602
NM_007372	DDX42	0.00	0.28	2000	2130	3537	4516
NM_001288805	ZNF707	0.00	0.28	177	200	237	349
NM_006675	TSPAN9	0.00	0.28	442	441	690	939
NM_001195192	EFCAB13	0.00	0.28	53	79	162	248
NM_173647	RNF149	0.00	0.28	560	639	1142	1514
NM_001256182	ANKRD11	-0.09	0.28	2578	2261	3677	4684
NM_152556	C7orf60	0.00	0.27	284	292	351	499
NM_138714	NFAT5	-0.08	0.27	3955	3550	3901	4957
NM_020244	CHPT1	-0.12	0.27	702	568	1175	1553
NM_019034	RHOF	0.00	0.27	174	217	308	442
NM_001291163	EPHX1	0.00	0.27	865	967	2269	2924
NM_152517	TTC30B	0.00	0.27	62	44	73	124
NM_019087	ARL15	0.00	0.27	205	190	187	281
NM_016282	AK3	0.00	0.27	610	674	1982	2564
NM_013284	POLM	0.00	0.27	451	426	397	558
NM_001122838	NAPEPLD	0.00	0.27	115	92	241	353

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_020199	C5orf15	0.00	0.27	800	866	1593	2076
NM_144982	ZFC3H1	0.00	0.27	1959	1870	1788	2320
NM_001166263	MTIF3	-0.01	0.27	544	467	763	1028
NM_001288654	DCAKD	0.00	0.27	401	448	959	1277
NM_015525	IBTK	0.00	0.27	1549	1479	1996	2579
NM_015384	NIPBL	0.00	0.27	1446	1544	1824	2364
NM_183075	CYP2U1	0.01	0.27	350	417	830	1113
NM_173537	GTF2IRD 2	0.00	0.27	223	249	416	582
NM_001787	CDK11B	-0.04	0.27	267	209	258	375
NM_014616	ATP11B	0.00	0.27	1790	1884	2213	2847
NM_005619	RTN2	0.00	0.27	136	120	341	484
NM_021645	UTP14C	0.00	0.27	1229	1156	1589	2068
NM_012193	FZD4	0.00	0.27	3636	3831	2048	2641
NM_152457	ZNF597	0.00	0.27	59	62	81	135
NM_001283043	RALGAP A1	0.00	0.27	157	200	291	418
NM_001252335	CGNL1	0.00	0.27	11	22	67	115
NM_017750	RETSAT	0.00	0.27	1488	1552	3169	4028
NM_014654	SDC3	0.00	0.27	1726	1775	4989	6270
NM_005749	TOB1	0.00	0.27	866	914	1025	1357
NM_001281294	ZNF281	0.00	0.27	1184	1266	2828	3603
NM_001145045	ZNF286B	0.00	0.26	52	76	94	153
NM_024518	ULBP3	0.00	0.26	66	47	89	146
NM_004711	SYNGR1	0.00	0.26	92	109	185	277
NM_020233	ADPRM	-0.01	0.26	139	102	185	277
NM_033083	EAF1	0.00	0.26	811	809	1004	1329
NM_003917	AP1G2	0.00	0.26	316	268	372	523
NM_001143819	TPCN1	0.00	0.26	799	855	2127	2732
NM_015205	ATP11A	0.00	0.26	1178	1273	1791	2314
NM_002093	GSK3B	-0.01	0.26	1943	1793	1982	2551
NM_001123363	RGPD6	0.00	0.26	963	938	1395	1819
NM_144775	SMCR8	0.00	0.26	1424	1447	2067	2656
NM_024011	CDK11A	-0.02	0.26	210	163	177	266
NM_001289986	TIPIN	0.00	0.26	124	123	92	150
NM_006977	ZBTB25	-0.02	0.26	110	77	154	235
NM_152281	GORAB	-0.16	0.26	208	145	183	274
NM_000127	EXT1	0.00	0.26	9045	8841	10344	12798
NM_001178138	TFDP2	0.00	0.26	413	456	1042	1375
NM_032871	RELT	0.00	0.26	629	549	331	469

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001251	CD68	-0.02	0.26	3830	3590	9144	11331
NM_000836	GRIN2D	0.00	0.26	299	256	351	495
NM_138783	ZNF653	0.00	0.26	123	132	100	161
NM_025077	TOE1	0.00	0.26	338	369	299	427
NM_001347	DGKQ	0.00	0.26	495	489	730	980
NM_198458	ZNF497	-0.10	0.26	202	146	393	549
NM_002737	PRKCA	0.00	0.26	3139	3258	4215	5298
NM_020435	GJC2	0.00	0.26	39	56	21	46
NM_015157	PHLDB1	0.00	0.26	3020	3044	5719	7140
NM_001289402	ZNF135	0.00	0.26	82	115	333	471
NM_022129	PBLD	0.00	0.26	144	160	291	416
NM_001242546	ANAPC16	0.00	0.26	454	493	809	1079
NM_004577	PSPH	0.00	0.26	252	291	412	573
NM_015884	MBTPS2	0.00	0.26	657	602	1077	1416
NM_153042	KDM1B	0.00	0.26	290	335	616	834
NM_020315	PDXP	0.00	0.26	650	735	616	834
NM_014909	VASH1	0.00	0.26	225	183	250	362
NM_018602	DNAJA4	0.00	0.26	333	332	389	543
NM_001042573	ENGASE	0.00	0.26	227	215	414	575
NM_001080	ALDH5A1	0.00	0.26	28	24	189	281
NM_001271803	REEP2	0.00	0.26	92	109	408	567
NM_032453	ZNF527	0.00	0.26	67	58	96	155
NM_014454	SESN1	0.00	0.26	155	187	360	505
NM_003312	TST	0.00	0.26	530	543	672	904
NM_002198	IRF1	0.00	0.26	290	307	547	745
NM_203487	PCDH9	0.00	0.26	219	184	447	617
NM_152783	D2HGDH	0.00	0.26	395	360	347	488
NM_001291813	SLC25A29	0.00	0.26	119	139	258	372
NM_022494	ZDHHC6	0.00	0.26	599	549	986	1299
NM_147161	ACOT11	0.00	0.26	191	185	166	250
NM_024759	NIPAL2	0.00	0.26	184	164	638	860
NM_001278438	FNDC3A	0.00	0.26	1565	1636	2479	3150
NM_015055	SWAP70	0.00	0.26	1838	1890	1907	2444
NM_021228	SCAF1	0.00	0.26	913	1004	1237	1612
NM_145119	PJA1	0.00	0.25	544	520	647	871
NM_003566	EEA1	-0.11	0.25	1335	1129	2159	2754
NM_002221	ITPKB	0.00	0.25	56	82	339	477
NM_001031701	NT5DC3	0.00	0.25	647	719	948	1250

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001286631	RBM26	0.00	0.25	604	609	720	963
NM_005999	TSNAX	0.00	0.25	454	407	898	1187
NM_022456	RAB3IP	-0.47	0.25	152	80	79	131
NM_005860	FSTL3	-0.05	0.25	3553	3252	1549	1998
NM_001277710	CD99	0.00	0.25	6948	7069	13830	16928
NM_001307	CLDN7	0.00	0.25	37	52	141	216
NM_020240	CDC42SE 2	0.00	0.25	633	635	636	856
NM_003324	TULP3	0.00	0.25	988	979	1115	1457
NM_020135	WRNIP1	0.00	0.25	1043	1092	1233	1604
NM_033549	TRIM41	0.00	0.25	498	555	796	1057
NM_016628	WAC	-0.07	0.25	3135	2804	2914	3675
NM_133264	WIPF2	0.00	0.25	1751	1735	1655	2126
NM_004442	EPHB2	0.00	0.25	28	44	360	503
NM_031407	HUWE1	0.00	0.25	11361	11092	18197	22166
NM_014964	EPN2	0.00	0.25	1334	1350	1543	1987
NM_001184781	DGCR2	-0.08	0.25	2247	1979	2161	2749
NM_015124	GRAMD4	0.00	0.25	205	245	522	710
NM_001007189	IGIP	-0.02	0.25	314	255	589	795
NM_001240	CCNT1	0.00	0.25	1083	1192	1075	1405
NM_018952	HOXB6	0.00	0.25	369	338	372	518
NM_001458	FLNC	-0.07	0.25	135215	127692	109037	130883
NM_001128212	WDSUB1	0.00	0.25	67	83	85	139
NM_001143674	MPC2	0.00	0.25	1203	1260	1668	2139
NM_001099220	ZNF862	0.00	0.25	238	279	543	736
NM_003790	TNFRSF2 5	0.00	0.25	61	68	56	98
NM_001013693	LDLRAD 2	-0.17	0.25	2048	1684	2498	3157
NM_005534	IFNGR2	0.00	0.25	1396	1509	2317	2935
NM_001782	CD72	-0.06	0.25	61	36	73	122
NM_000404	GLB1	0.00	0.25	2424	2563	6484	7998
NM_001046	SLC12A2	0.00	0.25	969	920	851	1122
NM_032368	LZIC	0.00	0.25	326	388	586	789
NM_147780	CTSB	0.00	0.25	28365	28109	115877	138711
NM_003216	TEF	0.00	0.25	427	399	973	1274
NM_001114132	NBEAL1	0.00	0.25	1017	938	2011	2556
NM_032806	POMGNT 2	0.00	0.25	356	350	925	1214
NM_001025579	NDEL1	0.00	0.25	2371	2466	2150	2726
NM_024015	HOXB4	0.00	0.25	332	340	595	800

Table 6B: Differentially Upregulated Genes in SEN + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_000437	PAFAH2	0.00	0.25	144	153	406	560
NM_004419	DUSP5	0.00	0.25	1102	1158	1443	1856
NM_001242784	HLCS	0.00	0.25	719	733	1516	1946
NM_194328	RNF38	0.00	0.25	669	694	747	991
NM_001242885	LOC100287036	0.00	0.24	87	89	81	133
NM_016094	COMMD2	0.00	0.24	432	494	578	778
NM_001290256	KHNYN	0.00	0.24	2109	2113	2421	3055
NM_016447	MPP6	0.00	0.24	391	441	470	641
NM_001083893	STRN3	0.00	0.24	881	872	1038	1353
NM_001256695	PRDM11	0.00	0.24	49	31	35	67
NM_001369	DNAH5	0.00	0.24	34	45	119	185
NM_001085384	ZNF154	0.00	0.24	85	87	148	224
NM_152542	PPM1K	0.00	0.24	294	297	366	508
NM_176782	FAM151A	0.00	0.24	50	55	50	89
NM_007124	UTRN	-0.03	0.24	3589	3322	7699	9442
NM_003338	UBE2D1	0.00	0.24	163	208	374	518
NM_024595	AKIRIN1	0.00	0.24	1333	1434	1533	1963
NM_024665	TBL1XR1	0.00	0.24	989	1077	1899	2412
NM_001166692	C11orf91	0.00	0.24	182	140	131	201
NM_001261459	ZNF484	0.00	0.24	137	149	214	311
NM_002841	PTPRG	0.00	0.24	1560	1584	2350	2963
NM_001037633	SIL1	0.00	0.24	1142	1138	2756	3458
NM_024947	PHC3	0.00	0.24	1500	1600	2213	2795
NM_058181	YBEY	0.00	0.24	70	75	158	237
NM_030821	PLA2G12A	0.00	0.24	189	224	597	800
NM_016614	TDP2	0.00	0.24	542	596	1000	1303
NM_001127605	LIPA	0.00	0.24	392	447	923	1207
NM_138430	ADPRHL1	0.00	0.24	22	30	123	190
NM_032430	BRSK1	0.00	0.24	98	122	123	190
NM_205842	NCKAP1	0.00	0.24	5174	5258	9119	11131
NM_203437	AFTPH	0.00	0.24	565	596	713	945
NM_014818	TRIM66	0.00	0.24	147	150	245	351
NM_005649	ZNF354A	0.00	0.24	165	150	193	283
NM_014752	SPCS2	0.00	0.24	291	286	314	440
NM_015430	PAMR1	-0.05	0.24	1386	1224	5906	7260
NM_000081	LYST	0.00	0.24	518	544	1537	1963

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001037501	NBPF8	-0.17	0.24	982	778	996	1296
NM_017614	BHMT2	0.00	0.24	475	487	2048	2588
NM_031477	YPEL3	0.00	0.24	207	225	510	689
NM_024835	GGNBP2	-0.04	0.24	1386	1232	1714	2179
NM_004850	ROCK2	0.00	0.24	2014	2149	2171	2737
NM_012090	MACF1	0.00	0.24	11306	10967	23899	28761
NM_015630	EPC2	0.00	0.24	288	265	410	562
NM_024956	TMEM62	0.00	0.24	244	247	489	662
NM_024641	MANEA	0.00	0.24	357	310	543	730
NM_015275	KIAA1033	0.00	0.24	1294	1406	2263	2847
NM_145167	PIGM	0.00	0.24	215	239	310	434
NM_173475	DCUN1D3	0.00	0.24	638	667	1077	1394
NM_000663	ABAT	0.00	0.24	94	76	83	135
NM_001170760	SRPK3	-0.04	0.24	72	45	83	135
NM_007167	ZMYM6	0.00	0.24	380	347	545	732
NM_017836	SLC41A3	0.00	0.24	862	960	2400	3011
NM_001134831	AHI1	0.00	0.24	775	794	828	1085
NM_004776	B4GALT5	0.00	0.24	1871	1918	1755	2225
NM_013446	MKRN1	0.00	0.24	880	897	1271	1632
NM_001470	GABBR1	0.00	0.23	276	309	466	632
NM_021259	TMEM8A	0.00	0.23	2352	2395	4663	5745
NM_144694	ZNF570	0.00	0.23	108	77	125	192
NM_181809	BMP8A	-1.00	0.23	79	23	40	74
NM_006264	PTPN13	0.00	0.23	706	772	1445	1845
NM_198147	ABHD15	0.00	0.23	287	310	528	710
NM_183050	BCKDHB	0.00	0.23	152	177	256	364
NM_004973	JARID2	0.00	0.23	828	890	1441	1839
NM_152564	VPS13B	0.00	0.23	1062	1098	2356	2954
NM_014577	BRD1	0.00	0.23	816	838	796	1044
NM_001267698	CD63	-0.15	0.23	12326	10792	27628	33094
NM_153029	N4BP1	0.00	0.23	696	754	1094	1412
NM_015027	PDXDC1	0.00	0.23	3261	3457	3629	4492
NM_002744	PRKCZ	0.00	0.23	137	134	181	266
NM_033637	BTRC	0.00	0.23	490	550	844	1103
NM_024642	GALNT12	0.00	0.23	275	236	840	1098
NM_001172713	GOLGA4	-0.42	0.23	4504	3197	3872	4784
NM_014159	SETD2	0.00	0.23	1467	1578	1853	2340
NM_016463	CXXC5	0.00	0.23	720	798	1709	2164

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001286767	USP46	-0.12	0.23	394	304	541	725
NM_002972	SBF1	0.00	0.23	3413	3449	5384	6597
NM_005385	NKTR	0.00	0.23	1017	1029	1219	1564
NM_003292	TPR	0.00	0.23	2607	2702	3465	4288
NM_138465	GLI4	0.00	0.23	112	125	160	238
NM_022041	GAN	0.00	0.23	416	392	447	606
NM_145059	FUK	0.00	0.23	113	106	173	255
NM_015076	CDK19	0.00	0.23	446	500	736	967
NM_173825	RABL3	0.00	0.23	401	405	626	830
NM_025196	GRPEL1	0.00	0.23	1670	1551	1481	1882
NM_001160302	SYNJ1	0.00	0.23	400	406	555	741
NM_032042	FAM172 A	0.00	0.23	316	320	1050	1353
NM_001099922	ALG13	0.00	0.23	422	397	401	547
NM_001288661	CRMP1	0.00	0.23	168	209	401	547
NM_023926	ZSCAN18	0.00	0.23	277	307	861	1120
NM_002267	KPNA3	0.00	0.23	1422	1542	1986	2493
NM_203390	RBM12B	0.00	0.23	373	379	327	453
NM_001204456	RBAK	0.00	0.23	385	373	368	505
NM_003655	CBX4	0.00	0.23	233	237	324	449
NM_012097	ARL5A	0.00	0.23	271	283	310	431
NM_032587	CARD6	0.00	0.23	526	589	807	1052
NM_198580	SLC27A1	0.00	0.23	648	592	807	1052
NM_016002	SCCPDH	0.00	0.23	589	545	846	1100
NM_001290205	DCP1A	-0.07	0.23	1188	1028	855	1111
NM_014720	SLK	-0.03	0.22	1020	901	1497	1896
NM_020533	MCOLN1	0.00	0.22	1087	1125	1782	2242
NM_015191	SIK2	0.00	0.22	930	991	1568	1981
NM_006312	NCOR2	-0.07	0.22	4358	3934	4960	6055
NM_000286	PEX12	0.00	0.22	196	195	187	272
NM_005776	CNIH1	0.00	0.22	1168	1117	2315	2882
NM_173550	CCDC171	0.00	0.22	49	33	89	142
NM_001127178	PIGG	0.00	0.22	776	743	1460	1847
NM_207328	GPAT2	0.00	0.22	380	434	586	776
NM_057177	PARD3B	0.00	0.22	255	233	322	445
NM_001136116	ZNF879	0.00	0.22	32	35	73	120
NM_001080744	DGKG	0.00	0.22	11	17	81	131
NM_001204858	TCEB1	0.00	0.22	475	480	755	985
NM_003647	DGKE	0.00	0.22	171	161	152	226
NM_001005851	ZNF780B	0.00	0.22	94	95	208	299

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_004926	ZFP36L1	0.00	0.22	1831	1911	5016	6111
NM_024076	KCTD15	-0.07	0.22	999	854	676	887
NM_001284	AP3S1	0.00	0.22	558	506	844	1094
NM_181336	LEMD2	0.00	0.22	1761	1731	1917	2397
NM_032802	SPPL2A	0.00	0.22	460	440	761	991
NM_005840	SPRY3	0.00	0.22	60	57	87	139
NM_032514	MAP1LC 3A	0.00	0.22	511	456	659	865
NM_015060	AVL9	0.00	0.22	742	781	898	1159
NM_001135553	MKNK1	-0.01	0.22	493	421	613	808
NM_001017916	CYB561	0.00	0.22	931	951	2579	3192
NM_013262	MYLIP	0.00	0.22	108	96	27	54
NM_001145033	C11orf96	0.00	0.22	257	216	322	444
NM_005160	ADRBK2	0.00	0.22	231	185	285	397
NM_001229	CASP9	0.00	0.22	151	131	200	288
NM_182931	KMT2E	-0.07	0.22	956	814	1237	1571
NM_000876	IGF2R	0.00	0.22	4634	4625	13873	16565
NM_006218	PIK3CA	0.00	0.22	519	597	720	939
NM_007045	FGFR1OP	0.00	0.22	165	192	218	311
NM_002141	HOXA4	0.00	0.22	61	56	102	159
NM_004559	YBX1	0.00	0.22	10140	10047	9439	11327
NM_001128827	DLG4	0.00	0.22	711	797	1007	1290
NM_001102654	NTF3	0.00	0.22	357	335	254	357
NM_001164463	RGPD8	0.00	0.22	463	402	607	799
NM_182603	ANKRD4 2	0.00	0.22	294	286	422	569
NM_001136029	DEPDC5	0.00	0.22	402	391	495	660
NM_018358	ABCF3	0.00	0.22	1726	1753	2502	3092
NM_001995	ACSL1	0.00	0.21	996	1061	2059	2560
NM_033212	CCDC102 A	0.00	0.21	91	111	185	268
NM_012329	MMD	0.00	0.21	121	123	185	268
NM_024165	PHF1	0.00	0.21	1738	1611	2096	2604
NM_181705	LYRM7	0.00	0.21	177	137	420	566
NM_183238	ZNF605	0.00	0.21	174	199	543	719
NM_015264	KIAA093 0	0.00	0.21	1509	1641	3205	3930
NM_017709	FAM46C	0.00	0.21	19	24	64	107
NM_001543	NDST1	0.01	0.21	9336	9720	14978	17828
NM_005786	TSHZ1	0.00	0.21	436	498	848	1094
NM_145206	VTI1A	0.00	0.21	672	693	1175	1492

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_003036	SKI	0.01	0.21	2084	2251	2936	3606
NM_018555	ZNF331	0.00	0.21	308	269	275	383
NM_032930	C11orf70	0.00	0.21	13	24	83	133
NM_017653	DYM	0.00	0.21	767	819	1535	1926
NM_153033	KCTD7	0.00	0.21	379	331	769	996
NM_001185060	AQP1	0.00	0.21	16	16	67	111
NM_173471	SLC25A26	0.00	0.21	155	178	376	510
NM_173681	ATG9B	0.00	0.21	37	50	62	104
NM_022735	ACBD3	-0.16	0.21	720	564	996	1272
NM_001286587	AIG1	0.00	0.21	204	234	778	1006
NM_020440	PTGFRN	-0.08	0.21	1827	1591	4571	5541
NM_001277204	P2RY6	0.00	0.21	42	54	98	153
NM_001042551	SMC2	0.00	0.21	957	887	1123	1425
NM_001287054	ZKSCAN1	0.00	0.21	1519	1497	2789	3421
NM_020141	TMEM167B	0.00	0.21	1103	1083	1549	1937
NM_004398	DDX10	0.00	0.21	448	507	426	571
NM_001145312	ETV3	0.00	0.21	432	467	809	1042
NM_006049	SNAPC5	0.00	0.21	505	545	661	861
NM_175902	OGFOD3	0.00	0.21	604	678	988	1259
NM_022078	GPATCH3	0.00	0.21	217	268	277	384
NM_004874	BAG4	0.00	0.21	642	715	786	1013
NM_001145548	ZDHHC7	0.00	0.21	2633	2694	3388	4126
NM_020644	TMEM9B	0.00	0.21	753	752	1551	1937
NM_015296	DOCK9	0.00	0.21	401	382	715	926
NM_003341	UBE2E1	0.00	0.21	1014	961	2231	2749
NM_024704	KIF16B	0.00	0.21	439	395	601	786
NM_000489	ATRX	-0.35	0.21	842	583	1543	1926
NM_001005746	CACNB4	0.00	0.20	242	235	121	183
NM_032408	BAZ1B	0.00	0.20	2931	3030	3816	4627
NM_152511	DUSP18	0.00	0.20	108	117	291	401
NM_001098272	HMGCS1	0.00	0.20	511	539	1350	1693
NM_017636	TRPM4	0.00	0.20	804	792	1830	2268
NM_032632	PAPOLA	0.00	0.20	2105	2230	3354	4079
NM_001043318	ELMSAN1	0.00	0.20	1199	1303	1223	1540
NM_015520	MAGI1	0.00	0.20	1339	1356	2306	2835
NM_005067	SIAH2	0.00	0.20	824	895	570	747

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001166339	SPDYE2B	0.00	0.20	91	105	106	163
NM_006166	NFYB	-0.01	0.20	195	150	106	163
NM_001031618	SPDYE2	0.00	0.20	91	105	106	163
NM_001243186	PIM1	0.01	0.20	281	341	106	163
NM_005751	AKAP9	-0.04	0.20	1762	1585	2059	2540
NM_001135178	ZNF397	0.00	0.20	85	104	141	209
NM_006577	B3GNT2	0.00	0.20	463	473	638	830
NM_005341	ZBTB48	0.00	0.20	146	146	324	442
NM_001270	CHD1	0.00	0.20	1022	950	1040	1318
NM_025132	WDR19	0.00	0.20	201	246	653	848
NM_022491	SUDS3	0.00	0.20	512	553	884	1129
NM_020156	C1GALT1	0.00	0.20	1196	1162	1510	1882
NM_030819	GFOD2	0.00	0.20	212	247	366	494
NM_138444	KCTD12	0.00	0.20	2071	2025	2695	3292
NM_183416	KIF1B	0.00	0.20	2111	2210	2556	3127
NM_001291964	MLLT4	0.00	0.20	859	871	911	1161
NM_001800	CDKN2D	-0.10	0.20	404	317	354	479
NM_004993	ATXN3	0.00	0.20	290	322	616	802
NM_006738	AKAP13	0.01	0.20	1679	1824	3943	4765
NM_012326	MAPRE3	-0.10	0.20	186	133	657	852
NM_000548	TSC2	0.00	0.20	1727	1836	4342	5233
NM_015089	CUL9	0.00	0.20	716	795	1277	1601
NM_006915	RP2	0.00	0.20	822	765	747	961
NM_015483	KBTBD2	0.00	0.20	983	1041	1133	1427
NM_004249	RAB28	0.00	0.20	162	183	202	287
NM_016609	SLC22A17	0.00	0.20	245	261	374	503
NM_016570	ERGIC2	0.00	0.20	643	611	884	1126
NM_001284338	NEDD4	0.01	0.20	2996	3199	2545	3107
NM_033201	C16orf45	0.00	0.20	669	696	1568	1946
NM_021241	WIZ	0.00	0.20	746	780	1171	1471
NM_001145437	LSS	0.00	0.20	2263	2346	6006	7174
NM_014738	KIAA0195	0.00	0.20	666	715	1389	1732
NM_015409	EP400	-0.10	0.20	2486	2167	2891	3514
NM_004839	HOMER2	0.00	0.20	117	136	279	384
NM_015208	ANKRD12	-0.09	0.20	1047	884	1346	1680
NM_001607	ACAA1	-0.06	0.20	741	627	1568	1945
NM_001185072	CLDN12	0.00	0.20	925	961	842	1074
NM_001099401	SGCE	0.00	0.20	762	693	1171	1469

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001278547	MAPK8	0.00	0.20	843	901	593	771
NM_001161499	ZNF611	0.00	0.20	163	190	333	451
NM_006010	MANF	0.00	0.20	1647	1547	1722	2126
NM_001081563	DMPK	-0.05	0.20	877	754	1666	2059
NM_001146	ANGPT1	0.00	0.20	386	406	1069	1346
NM_001080481	USP45	0.00	0.19	178	196	262	362
NM_152699	SENP5	0.00	0.19	1291	1380	2019	2477
NM_001167	XIAP	0.00	0.19	954	928	1720	2122
NM_001124756	PABPC1L	0.00	0.19	102	112	166	240
NM_016423	ZNF219	0.00	0.19	144	117	166	240
NM_001008707	EML1	0.00	0.19	680	692	1847	2272
NM_144709	PUS10	0.00	0.19	74	52	94	146
NM_001122770	ZBTB37	0.00	0.19	120	120	156	227
NM_002505	NFYA	0.00	0.19	1086	1126	1262	1575
NM_033271	BTBD6	0.00	0.19	916	1020	1491	1848
NM_003377	VEGFB	0.00	0.19	989	1070	1832	2253
NM_001008224	UACA	-0.01	0.19	2500	2317	6185	7357
NM_017791	FLVCR2	0.00	0.19	49	30	60	100
NM_001134233	C1orf204	0.00	0.19	39	51	60	100
NM_006511	RSC1A1	0.00	0.19	212	250	241	335
NM_021626	SCPEP1	0.00	0.19	661	594	1614	1993
NM_013349	NENF	0.00	0.19	630	702	1574	1945
NM_016481	C9orf156	0.00	0.19	131	150	200	283
NM_024831	TGS1	0.00	0.19	433	447	472	621
NM_018109	MTPAP	0.00	0.19	481	521	595	771
NM_080677	DYNLL2	0.00	0.19	968	1063	1202	1501
NM_005476	GNE	0.00	0.19	893	921	1108	1388
NM_001044264	MSMP	0.00	0.19	231	284	299	407
NM_001286522	PARP11	0.00	0.19	81	78	158	229
NM_004586	RPS6KA3	0.00	0.19	1431	1541	1934	2368
NM_020645	NRIP3	0.00	0.19	1169	1198	1986	2429
NM_057169	GIT2	-0.04	0.19	1688	1511	2406	2924
NM_030762	BHLHE41	0.00	0.19	416	434	609	787
NM_001278529	ARHGEF 40	0.00	0.19	2216	2079	4193	5018
NM_000600	IL6	0.00	0.19	434	502	782	996
NM_001040628	NCALD	0.01	0.19	314	377	851	1079
NM_024685	BBS10	0.00	0.19	204	221	329	444
NM_007043	KRR1	0.00	0.19	825	916	1547	1909
NM_033070	CECR5	0.00	0.19	608	688	559	726

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001040177	AKR1E2	0.00	0.19	213	249	206	290
NM_004453	ETFDH	0.00	0.19	337	329	663	852
NM_025195	TRIB1	0.00	0.19	535	595	491	643
NM_001109662	HECTD4	0.00	0.19	1699	1825	3088	3723
NM_005038	PPID	0.00	0.19	464	424	726	928
NM_182838	SLC35E2	0.00	0.19	693	718	1296	1610
NM_001042750	STAG2	0.00	0.19	1272	1274	1799	2205
NM_181715	CRTC2	0.00	0.19	831	849	923	1164
NM_014949	KIAA0907	0.00	0.19	588	668	848	1074
NM_018140	CEP72	0.00	0.19	107	142	75	120
NM_001077690	ALG9	-0.08	0.19	694	576	1069	1338
NM_016263	FZR1	0.00	0.19	1169	1207	1736	2129
NM_001282659	USP47	0.00	0.19	1311	1204	2213	2691
NM_001009881	ZCCHC11	0.00	0.19	432	462	684	876
NM_032772	ZNF503	-0.22	0.19	273	188	867	1096
NM_001198777	CUL2	0.00	0.19	877	971	1418	1752
NM_001113575	CDKL3	0.00	0.19	28	35	64	105
NM_022072	NSUN3	0.00	0.18	81	85	106	161
NM_014982	PCNX	0.00	0.18	2292	2240	5180	6150
NM_002199	IRF2	0.00	0.18	393	430	322	434
NM_006037	HDAC4	-0.07	0.18	502	410	499	651
NM_003054	SLC18A2	0.00	0.18	76	91	179	255
NM_004691	ATP6V0D1	0.00	0.18	2855	2818	4910	5834
NM_001277058	ERCC6-PGBD3	0.00	0.18	1044	962	1065	1331
NM_032027	TM2D1	-0.13	0.18	478	371	844	1067
NM_133447	AGAP11	0.00	0.18	88	65	100	153
NM_020371	AVEN	0.00	0.18	645	689	1056	1320
NM_005809	PRDX2	0.00	0.18	1009	1091	2302	2791
NM_015312	KIAA1109	0.00	0.18	1917	1857	5303	6288
NM_015344	LEPROTL1	0.00	0.18	374	383	595	767
NM_004667	HERC2	-0.11	0.18	4379	3858	6971	8220
NM_015221	DNMBP	0.00	0.18	2235	2202	4407	5244
NM_015001	SPEN	-0.09	0.18	2365	2078	2479	2996
NM_020640	DCUN1D1	0.00	0.18	318	342	551	713
NM_014765	TOMM20	0.00	0.18	2334	2210	3284	3935
NM_030937	CCNL2	-0.03	0.18	1650	1482	2202	2669

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_032846	RAB2B	0.00	0.18	559	552	784	993
NM_017916	PIH1D1	0.00	0.18	626	707	903	1135
NM_001172681	ZNF641	0.00	0.18	210	211	216	301
NM_014041	SPCS1	0.00	0.18	892	820	1593	1952
NM_012455	PSD4	-0.03	0.18	520	437	499	649
NM_016078	TVP23B	-0.12	0.18	486	381	499	649
NM_007249	KLF12	0.00	0.18	734	771	1113	1384
NM_003030	SHOX2	0.00	0.18	302	288	372	494
NM_001291965	WASF3	0.00	0.18	764	679	961	1203
NM_020959	ANO8	0.00	0.18	297	247	233	322
NM_001136037	LIMS2	0.00	0.18	1252	1364	1194	1479
NM_206825	GNL3	0.00	0.18	1761	1767	1435	1763
NM_001694	ATP6V0C	-0.10	0.18	3092	2708	4147	4926
NM_015994	ATP6V1D	-0.05	0.18	1908	1710	2487	2996
NM_000328	RPGR	0.00	0.18	79	67	102	155
NM_014320	HEBP2	0.00	0.18	634	616	1936	2351
NM_020328	ACVR1B	-0.09	0.18	874	731	1059	1318
NM_032164	ZNF394	0.00	0.18	376	383	443	580
NM_001282531	ADNP	0.00	0.18	2120	1993	2325	2806
NM_001042683	SHPRH	0.00	0.18	342	347	366	486
NM_006442	DRAP1	0.00	0.18	5589	5634	7776	9113
NM_001076675	ZNF626	0.00	0.18	72	67	195	274
NM_031296	RAB33B	0.00	0.18	240	243	195	274
NM_004486	GOLGA2	0.00	0.18	5127	5348	5603	6606
NM_024874	KIAA0319L	0.00	0.18	862	954	2350	2834
NM_014646	LPIN2	0.00	0.18	1762	1689	2132	2579
NM_001256865	DNAJC6	0.00	0.18	98	105	293	396
NM_153257	ZNF461	0.00	0.18	86	75	119	177
NM_024116	TAF1D	0.00	0.18	733	717	564	726
NM_014015	DEXI	0.00	0.18	790	836	1206	1490
NM_018477	ACTR10	-0.04	0.18	678	580	1751	2131
NM_000332	ATXN1	0.00	0.18	1049	1027	1734	2111
NM_032373	PCGF5	0.00	0.17	1612	1703	2321	2797
NM_001161841	SULF2	0.00	0.17	58	41	166	237
NM_031431	COG3	0.00	0.17	514	540	815	1026
NM_014643	ZNF516	0.00	0.17	891	861	1508	1845
NM_033063	MAP6	0.00	0.17	99	132	453	591
NM_015562	UBXN7	0.00	0.17	598	580	1113	1379
NM_015322	FEM1B	0.00	0.17	1692	1830	2581	3098

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_198150	ARSK	0.00	0.17	445	461	530	684
NM_003205	TCF12	0.00	0.17	1776	1818	2710	3248
NM_001198862	TMEM206	0.00	0.17	385	431	335	447
NM_015962	FCF1	0.00	0.17	265	298	426	558
NM_033215	PPP1R3F	0.00	0.17	87	86	127	187
NM_001077472	NR1I3	0.00	0.17	70	93	110	165
NM_032888	COL27A1	0.00	0.17	464	471	437	571
NM_172159	KCNAB1	-0.01	0.17	186	143	206	287
NM_000617	SLC11A2	-0.15	0.17	705	556	1077	1335
NM_001198961	ECHDC2	0.00	0.17	110	99	131	192
NM_031492	RBM4B	0.00	0.17	348	377	424	555
NM_001079839	OCIAD1	0.00	0.17	946	1022	1753	2129
NM_033512	TSPYL5	0.00	0.17	463	482	549	706
NM_007110	TEP1	0.00	0.17	1816	1748	2429	2917
NM_018453	EAPP	0.00	0.17	435	378	634	808
NM_030930	UNC93B1	-0.21	0.17	399	288	453	590
NM_017870	TMEM132A	0.00	0.17	257	277	374	494
NM_032575	GLIS2	0.01	0.17	543	625	482	625
NM_138421	SAAL1	0.00	0.17	144	168	104	157
NM_001145343	ZNF566	0.00	0.17	80	79	104	157
NM_015575	GIGYF2	0.00	0.17	2081	2145	2882	3442
NM_020834	HOMEZ	0.00	0.17	187	188	312	418
NM_018439	IMPACT	0.00	0.17	285	319	611	780
NM_001278593	ALDH6A1	0.00	0.17	183	205	412	540
NM_007282	RNF13	0.00	0.17	357	350	493	638
NM_003786	ABCC3	0.00	0.17	282	328	1431	1750
NM_022737	LPPR2	0.00	0.17	1280	1344	2209	2658
NM_001040099	MOSPD3	0.00	0.17	145	158	418	547
NM_078476	BTN2A1	0.00	0.17	281	261	524	675
NM_006726	LRBA	-0.12	0.17	912	747	1747	2118
NM_001242739	ZNF691	0.00	0.17	104	112	158	226
NM_001018055	BRCC3	0.00	0.17	144	152	364	481
NM_016038	SBDS	0.00	0.17	3520	3446	4658	5486
NM_001243773	GNG2	0.00	0.17	25	31	541	695
NM_001077195	ZNF436	0.01	0.17	246	302	566	725
NM_178040	ERC1	0.00	0.17	1744	1662	3438	4079
NM_182958	KAT8	0.00	0.17	463	455	547	702
NM_025015	HSPA12A	-0.03	0.17	1144	1012	2161	2599

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_002336	LRP6	0.00	0.17	1354	1366	2223	2671
NM_018017	CCDC186	0.00	0.17	305	309	356	471
NM_002843	PTPRJ	0.00	0.17	1790	1748	1655	2009
NM_003592	CUL1	0.00	0.17	1515	1494	1739	2107
NM_004914	RAB36	0.00	0.17	30	20	133	194
NM_017842	SLC48A1	0.00	0.17	367	365	1181	1453
NM_013302	EEF2K	0.00	0.17	1168	1169	1791	2166
NM_020897	HCN3	0.00	0.17	70	87	148	213
NM_017450	BAIAP2	0.00	0.17	272	327	844	1055
NM_024599	RHBDF2	0.00	0.17	311	288	331	440
NM_001136157	OTUD5	0.00	0.17	1295	1405	2100	2525
NM_001162501	TNRC6B	-0.01	0.17	1842	1691	3768	4453
NM_015510	DHRS7B	0.00	0.17	344	359	547	701
NM_145725	TRAF3	0.00	0.17	1473	1384	2315	2774
NM_001135218	TAF12	0.00	0.17	419	388	624	793
NM_005631	SMO	0.00	0.17	26	27	83	129
NM_153223	CEP120	0.00	0.17	420	475	703	887
NM_003473	STAM	0.00	0.17	1601	1604	1512	1839
NM_022736	MFSD1	0.00	0.17	877	964	2117	2543
NM_030640	DUSP16	0.00	0.17	445	461	441	573
NM_001128325	SPON2	0.00	0.17	752	706	4993	5856
NM_018438	FBXO6	0.00	0.17	73	70	333	442
NM_001171741	C3orf18	0.00	0.17	254	284	786	985
NM_030581	WDR59	-0.19	0.17	656	500	824	1030
NM_016281	TAOK3	0.00	0.17	1291	1196	2144	2573
NM_031288	INO80B	0.00	0.16	294	271	541	693
NM_001018072	BTBD11	0.00	0.16	43	27	71	113
NM_001278141	NBPF12	0.00	0.16	234	230	385	505
NM_000534	PMS1	-0.08	0.16	339	266	289	388
NM_001100397	RAPGEF4	0.00	0.16	487	548	414	540
NM_153026	PRICKLE 1	0.00	0.16	156	184	474	612
NM_001145447	ZNF200	0.00	0.16	140	149	154	220
NM_015106	RAD54L2	0.00	0.16	999	1098	1029	1270
NM_001001521	UGP2	0.00	0.16	1664	1579	3275	3872
NM_003190	TAPBP	0.00	0.16	3127	3266	5648	6591
NM_018094	GSPT2	0.00	0.16	809	846	1011	1248
NM_001281433	ZNHIT3	0.00	0.16	382	411	433	562
NM_014991	WDFY3	0.00	0.16	2133	2177	4066	4780
NM_015202	KIAA055	0.00	0.16	646	661	1387	1688

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
	6						
NM_003087	SNCG	0.00	0.16	51	37	125	183
NM_020317	RSRP1	0.00	0.16	758	774	961	1189
NM_001113407	LDB1	0.00	0.16	1296	1361	2144	2567
NM_032410	HOOK3	0.00	0.16	2021	2119	2857	3390
NM_021103	TMSB10	-0.20	0.16	41209	35245	46245	52478
NM_001256732	SSBP2	0.00	0.16	212	206	406	529
NM_001142640	TNRC6C	0.00	0.16	332	288	187	261
NM_080652	TMEM41 A	0.00	0.16	392	395	537	686
NM_005811	GDF11	0.00	0.16	655	694	1541	1865
NM_001135642	INPP5K	0.00	0.16	634	715	1004	1238
NM_013233	STK39	0.00	0.16	1047	1084	1115	1368
NM_006912	RIT1	0.00	0.16	784	836	824	1026
NM_014892	SCAF8	0.00	0.16	1290	1304	1718	2070
NM_001042681	RERE	0.00	0.16	1313	1222	1422	1726
NM_001660	ARF4	0.00	0.16	5936	5927	7098	8231
NM_014008	CCDC22	0.00	0.16	493	477	932	1153
NM_014377	DNAJC2	0.00	0.16	347	337	428	555
NM_001257137	ITCH	0.01	0.16	1751	1903	2828	3351
NM_001032280	TFAP2A	0.00	0.16	44	43	27	52
NM_213613	SLC26A1	0.00	0.16	127	103	168	237
NM_015042	ZNF609	0.00	0.16	1587	1646	1788	2150
NM_001277	CHKA	0.00	0.16	419	401	310	412
NM_182715	SYPL1	-0.16	0.16	1654	1362	2568	3050
NM_024090	ELOVL6	0.00	0.16	999	1055	1260	1536
NM_030806	C1orf21	0.00	0.16	857	946	998	1229
NM_001080503	CCDC159	-0.09	0.16	73	44	181	253
NM_006635	ZNF460	0.00	0.16	770	856	1237	1508
NM_194285	SPTY2D1	0.01	0.16	874	978	942	1163
NM_001282755	MTA3	-0.06	0.16	387	312	717	898
NM_014290	TDRD7	0.00	0.16	273	270	453	584
NM_198467	RSBN1L	0.00	0.16	193	217	202	279
NM_005530	IDH3A	0.00	0.16	982	1057	1524	1841
NM_001007527	LMBRD2	0.00	0.16	284	258	489	627
NM_030912	TRIM8	0.00	0.16	2173	2295	3552	4174
NM_023070	ZFP69B	0.00	0.16	69	80	73	115
NM_014834	LRRC37A	0.00	0.16	176	174	241	327
NM_007159	SLMAP	0.00	0.16	921	954	1223	1490
NM_006329	FBLN5	0.00	0.15	5879	6117	8801	10137

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_173811	HARBI1	0.00	0.15	45	59	110	163
NM_001272034	STXBP2	0.00	0.15	650	603	472	606
NM_001288718	STAT5A	0.00	0.15	562	633	803	998
NM_018064	AKIRIN2	0.00	0.15	504	537	653	821
NM_001134369	LRRFIP2	0.00	0.15	1869	1941	2340	2780
NM_032145	FBXO30	0.00	0.15	573	634	1073	1314
NM_013376	SERTAD1	0.00	0.15	530	587	665	835
NM_015622	CCZ1	0.00	0.15	769	789	898	1109
NM_007212	RNF2	0.00	0.15	314	360	408	529
NM_033504	TMEM54	0.00	0.15	252	226	547	695
NM_001190983	COQ7	0.00	0.15	159	147	243	329
NM_080916	DGUOK	0.00	0.15	469	528	672	843
NM_139015	SPPL3	0.00	0.15	477	485	553	702
NM_001173487	NKRF	0.00	0.15	293	317	293	390
NM_152519	KANSL1L	0.00	0.15	255	250	345	453
NM_001286276	KIAA1586	0.00	0.15	194	214	266	357
NM_015141	GPD1L	0.00	0.15	100	136	460	591
NM_001029882	AHDC1	0.00	0.15	515	559	713	891
NM_001271641	MTCH1	0.00	0.15	5598	5417	8622	9920
NM_018121	FAM178A	0.00	0.15	933	879	1289	1564
NM_015358	MORC3	0.00	0.15	887	831	1237	1503
NM_007195	POLI	0.00	0.15	174	191	416	538
NM_138459	NUS1	0.00	0.15	714	786	830	1028
NM_004232	SOCS6	0.00	0.15	795	758	1250	1518
NM_201444	DGKA	0.00	0.15	1303	1400	2202	2617
NM_018120	ARMC1	0.00	0.15	611	644	819	1015
NM_138492	PRELID2	0.00	0.15	114	135	104	155
NM_003342	UBE2G1	0.00	0.15	1199	1182	1258	1527
NM_013379	DPP7	0.00	0.15	1303	1265	3589	4203
NM_001290259	PHF3	0.00	0.15	1200	1153	1680	2015
NM_012094	PRDX5	0.00	0.15	2093	2093	3887	4542
NM_000140	FECH	0.00	0.15	559	584	1079	1318
NM_004239	TRIP11	-0.06	0.15	986	851	1190	1447
NM_024933	ANKRD53	0.00	0.15	61	69	94	142
NM_006026	H1FX	0.00	0.15	2012	2162	930	1144
NM_021930	RINT1	0.00	0.15	555	628	813	1007

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001042601	TTC14	0.00	0.15	466	418	722	900
NM_024989	PGAP1	0.00	0.15	201	200	283	377
NM_004285	H6PD	0.00	0.15	2069	2212	5199	6029
NM_032582	USP32	0.00	0.15	2316	2338	2984	3508
NM_015383	NBPF14	-0.09	0.15	476	382	834	1031
NM_001173539	BANP	0.00	0.15	436	446	247	333
NM_021738	SVIL	0.00	0.15	1117	1070	2521	2978
NM_014247	RAPGEF2	0.00	0.15	978	1062	1753	2096
NM_001500	GMDS	0.00	0.15	255	236	337	442
NM_203351	MAP3K3	0.00	0.15	1932	1896	2283	2704
NM_001135586	C5orf24	0.00	0.15	1800	1701	2500	2952
NM_014547	TMOD3	0.00	0.15	3025	3063	2579	3042
NM_017926	GPATCH 2L	0.01	0.15	824	927	1801	2150
NM_021008	DEAF1	0.00	0.15	1036	1020	1346	1625
NM_053043	RBM33	0.00	0.15	977	991	1264	1530
NM_015104	ATG2A	0.00	0.15	817	819	1046	1277
NM_005955	MTF1	0.00	0.15	383	365	562	710
NM_001025091	ABCF1	0.00	0.15	2545	2399	3180	3726
NM_175063	EMC10	-0.04	0.15	1293	1143	1508	1811
NM_032169	ACAD11	0.00	0.15	213	209	537	680
NM_004738	VAPB	0.00	0.15	1399	1511	1801	2148
NM_022574	GIGYF1	0.00	0.15	887	937	942	1155
NM_001017930	DCAF8L1	0.00	0.15	56	68	92	139
NM_001173990	TMEM21 6	0.00	0.15	98	108	92	139
NM_001013627	NHSL2	0.00	0.15	83	69	92	139
NM_001039671	YIF1B	0.00	0.15	1828	1758	2084	2471
NM_007034	DNAJB4	0.00	0.15	2631	2621	7077	8131
NM_005359	SMAD4	0.00	0.15	1975	2035	2219	2625
NM_015203	RPRD2	0.00	0.15	1511	1536	1868	2222
NM_001024455	RGAG4	0.00	0.14	260	281	435	558
NM_001278173	ZNF33A	0.00	0.14	325	301	358	466
NM_033198	PIGS	0.00	0.14	1770	1760	2776	3259
NM_001080475	PLEKHM 3	0.00	0.14	370	369	809	998
NM_001098484	SLC4A4	0.00	0.14	2533	2684	2252	2660
NM_002897	RBMS1	0.00	0.14	807	861	1258	1519
NM_017420	SIX4	0.00	0.14	229	261	426	547
NM_001204890	ISY1-RAB43	0.00	0.14	1036	1148	1366	1643

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_030791	SGPP1	0.00	0.14	1023	1117	1077	1309
NM_016024	RBMX2	-0.40	0.14	326	200	231	312
NM_005654	NR2F1	0.00	0.14	246	259	520	658
NM_005426	TP53BP2	0.00	0.14	1071	1141	1140	1381
NM_181725	METTL2A	0.00	0.14	622	692	670	834
NM_032268	ZNRF1	0.00	0.14	485	479	441	564
NM_017924	C14orf119	0.00	0.14	1461	1370	2092	2473
NM_001113324	TEN1	0.00	0.14	389	438	784	967
NM_015325	ICE1	0.00	0.14	1076	1127	1755	2087
NM_001185039	ACOX1	0.00	0.14	1430	1392	3086	3603
NM_001291586	TMEM106A	0.00	0.14	481	494	996	1213
NM_182703	ANKDD1A	0.00	0.14	109	131	206	281
NM_176787	PIGN	0.00	0.14	418	383	751	928
NM_207310	CCDC74B	0.00	0.14	27	19	64	102
NM_005486	TOM1L1	0.00	0.14	106	124	64	102
NM_015046	SETX	0.00	0.14	1160	1114	2808	3285
NM_001289999	NFIL3	0.00	0.14	606	528	913	1116
NM_024884	L2HGDH	0.00	0.14	91	80	58	94
NM_001102564	IFT43	0.00	0.14	264	250	649	808
NM_001002857	ANXA2	-0.03	0.14	14766	14085	27335	30694
NM_018341	ERMARD	-0.17	0.14	273	195	327	427
NM_000674	ADORA1	0.00	0.14	52	66	98	146
NM_001167614	LEMD3	0.00	0.14	556	576	790	972
NM_024623	OGFOD2	0.00	0.14	416	376	572	717
NM_020823	TMEM181	0.00	0.14	1863	1882	3196	3719
NM_007198	PROSC	0.00	0.14	422	493	643	800
NM_007349	PAXIP1	0.00	0.14	501	472	349	453
NM_015909	NBAS	0.00	0.14	2372	2506	3862	4469
NM_032549	IMMP2L	0.00	0.14	55	67	141	200
NM_178836	PLD6	0.00	0.14	180	196	133	190
NM_001195296	MIPOL1	0.00	0.14	90	83	133	190
NM_003590	CUL3	0.00	0.14	1024	979	1034	1253
NM_153369	KIAA1919	0.00	0.14	99	105	166	231
NM_032286	MED10	0.00	0.14	972	1041	1314	1575
NM_001277444	NBPF9	-0.02	0.14	905	799	1335	1599
NM_001199135	TANK	0.00	0.14	546	590	757	932

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_032861	SERAC1	0.00	0.14	356	390	532	669
NM_018474	KIZ	0.00	0.14	162	140	410	525
NM_001023563	ZNF805	0.00	0.14	433	464	655	813
NM_001284280	SMEK1	0.00	0.13	659	746	848	1037
NM_194271	RNF34	0.00	0.13	668	674	880	1074
NM_203462	MRFAP1 L1	0.00	0.13	934	953	1061	1283
NM_020345	NKIRAS1	-0.15	0.13	434	331	412	527
NM_001282161	UBE2A	0.00	0.13	1929	1813	3342	3876
NM_001008397	GPX8	0.00	0.13	1677	1806	3392	3932
NM_017436	A4GALT	0.00	0.13	737	782	815	998
NM_199344	SFT2D2	0.00	0.13	319	300	514	647
NM_024663	NPEPL1	0.00	0.13	606	672	1210	1453
NM_019094	NUDT4	-0.12	0.13	1386	1162	1418	1691
NM_015097	CLASP2	0.01	0.13	1326	1458	1926	2270
NM_003214	TEAD3	0.00	0.13	1031	1096	1412	1684
NM_001193552	ZNF850	0.00	0.13	163	158	168	233
NM_016333	SRRM2	0.00	0.13	9495	9624	14510	16336
NM_019001	XRN1	0.00	0.13	929	969	1670	1978
NM_144973	DENND5 B	0.00	0.13	499	508	936	1137
NM_001093	ACACB	0.00	0.13	40	33	119	172
NM_133372	FNIP1	0.01	0.13	1223	1348	2267	2656
NM_002907	RECQL	0.00	0.13	1670	1633	2067	2429
NM_001084393	DDTL	0.00	0.13	285	320	630	782
NM_173545	APLF	0.00	0.13	47	72	131	187
NM_058230	ZNF354B	0.00	0.13	130	100	156	218
NM_015534	ZZZ3	0.00	0.13	946	990	1431	1704
NM_001164000	MECOM	0.00	0.13	51	52	343	444
NM_005482	PIGK	0.00	0.13	716	700	996	1205
NM_024771	NAA40	0.00	0.13	510	516	599	745
NM_020368	UTP3	0.00	0.13	656	696	921	1118
NM_001244766	MOB1B	0.00	0.13	1371	1400	2075	2434
NM_002027	FNTA	-0.05	0.13	542	451	693	854
NM_001120	MFSD10	0.00	0.13	564	641	1229	1471
NM_014061	MAGEH1	0.00	0.13	612	622	320	416
NM_001033568	RHOT1	0.00	0.13	683	600	842	1026
NM_006380	APPBP2	0.00	0.13	837	872	1102	1325
NM_003668	MAPKAP K5	0.00	0.13	761	806	888	1079
NM_004505	USP6	0.00	0.13	51	77	60	96

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_199464	KCNRG	-0.34	0.13	79	40	94	140
NM_006773	DDX18	0.00	0.13	643	711	703	865
NM_001171606	PREPL	0.00	0.13	693	747	2439	2843
NM_015172	PRRC2C	0.00	0.13	6142	6339	7967	9026
NM_004228	CYTH2	0.00	0.13	1182	1190	1639	1937
NM_006696	BRD8	0.00	0.13	624	622	699	860
NM_006946	SPTBN2	0.00	0.13	31	31	121	174
NM_004430	EGR3	0.00	0.13	43	45	125	179
NM_033632	FBXW7	0.00	0.13	419	396	559	697
NM_001127510	APC	0.00	0.13	1907	1873	3198	3695
NM_020466	LYRM2	0.00	0.13	543	490	957	1157
NM_130809	PRRC1	0.00	0.13	2388	2295	2672	3103
NM_016100	NAA20	0.00	0.13	904	896	1389	1651
NM_032731	TXNDC17	0.00	0.13	642	673	1637	1933
NM_022087	GALNT11	0.00	0.13	893	870	2258	2636
NM_001281504	ATG4D	0.00	0.13	446	491	372	477
NM_172002	HSCB	0.00	0.13	93	114	106	155
NM_001281297	EDF1	0.00	0.13	2922	2781	4586	5248
NM_004229	MED14	0.00	0.13	1548	1518	1949	2286
NM_016480	PAIP2	0.00	0.13	838	917	940	1137
NM_001935	DPP4	-0.05	0.13	356	285	1689	1991
NM_024907	FBXO17	-0.01	0.13	629	547	863	1048
NM_153214	FBLN7	0.00	0.13	201	195	268	353
NM_178191	ATPIF1	-0.14	0.13	862	695	1832	2152
NM_001252612	ZNF638	0.00	0.13	1513	1475	2242	2615
NM_015360	SKIV2L2	0.00	0.13	1263	1362	2103	2458
NM_018032	LUC7L	0.00	0.13	279	272	239	318
NM_006282	STK4	0.00	0.13	979	1040	1456	1725
NM_001098512	PRKG1	0.00	0.12	814	873	1096	1314
NM_006743	RBM3	0.00	0.12	3427	3529	4494	5137
NM_001184889	NIPA2	0.00	0.12	1191	1119	1840	2159
NM_173664	ARL10	0.00	0.12	289	310	451	569
NM_004863	SPTLC2	0.00	0.12	2945	3014	3901	4473
NM_001349	DARS	0.00	0.12	1625	1589	2217	2584
NM_175918	CRIPAK	0.00	0.12	73	50	123	176
NM_000263	NAGLU	0.00	0.12	1008	1007	2051	2396
NM_001039465	SRSF5	0.00	0.12	2117	2168	3178	3662
NM_015132	SNX13	0.00	0.12	594	535	996	1198

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_014051	TMEM14A	0.00	0.12	103	130	247	327
NM_001166005	EPB41	0.00	0.12	241	275	455	573
NM_016406	UFC1	0.00	0.12	716	735	1233	1468
NM_020429	SMURF1	0.00	0.12	1834	1891	2084	2431
NM_032711	MAFG	0.00	0.12	1779	1789	2007	2344
NM_024836	ZNF672	0.00	0.12	1110	1022	1063	1274
NM_001287036	KIAA1958	0.00	0.12	96	109	89	133
NM_005163	AKT1	0.00	0.12	5878	5999	7884	8893
NM_176812	CHMP4B	0.00	0.12	1274	1351	1824	2137
NM_005897	IPP	0.00	0.12	192	163	433	547
NM_004429	EFNB1	0.00	0.12	115	151	289	377
NM_001162371	LOC728392	-0.07	0.12	590	486	493	617
NM_020817	KIAA1407	0.00	0.12	11	22	75	115
NM_001286554	USP49	0.00	0.12	128	120	154	214
NM_021994	ZNF277	0.00	0.12	155	124	214	287
NM_001143909	RPEL1	0.00	0.12	237	290	366	468
NM_014014	SNRNP200	0.01	0.12	6901	7213	8972	10089
NM_015154	MESDC2	0.00	0.12	1005	1034	1244	1479
NM_006355	TRIM38	0.00	0.12	659	646	1009	1211
NM_015091	FAM179B	0.00	0.12	194	231	690	845
NM_001005271	CHD3	-0.07	0.12	2412	2149	3502	4015
NM_032256	TMEM117	0.00	0.12	174	135	235	312
NM_004344	CETN2	0.00	0.12	365	364	753	917
NM_001134415	TBCCD1	0.00	0.12	264	247	341	438
NM_001242797	ZNF322	0.00	0.12	216	244	293	381
NM_001281723	BTD	-0.02	0.12	416	347	697	852
NM_016424	LUC7L3	0.00	0.12	1047	1079	1279	1516
NM_001033561	PHF12	0.00	0.12	839	880	1067	1275
NM_004782	SNAP29	0.00	0.12	907	882	1485	1749
NM_025222	WDR82	0.00	0.12	2483	2580	2656	3065
NM_001105079	FBRS	0.00	0.12	740	824	794	963
NM_152653	UBE2E2	0.00	0.12	535	519	1025	1227
NM_152316	ARL14EP	0.00	0.12	156	170	316	408
NM_001040280	CD83	0.00	0.12	19	27	69	107
NM_002830	PTPN4	0.00	0.12	191	197	264	346
NM_016120	RLIM	0.00	0.12	2471	2611	3708	4235

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_032590	KDM2B	0.00	0.12	654	604	620	762
NM_024672	THAP9	0.00	0.12	64	68	44	74
NM_003458	BSN	0.00	0.12	45	30	44	74
NM_005406	ROCK1	0.00	0.12	2280	2326	2662	3068
NM_001441	FAAH	-0.49	0.12	44	16	33	59
NM_019059	TOMM7	0.00	0.11	607	643	1146	1362
NM_017520	MPHOSPH8	0.00	0.11	279	296	443	556
NM_006540	NCOA2	0.00	0.11	511	583	1250	1479
NM_001288588	ZNF280D	0.00	0.11	256	260	420	529
NM_152551	SNRNP48	0.00	0.11	206	254	252	331
NM_130464	NPIPB3	-0.02	0.11	544	463	526	652
NM_003430	ZNF91	0.00	0.11	143	152	374	475
NM_015542	UPF2	0.00	0.11	672	700	988	1181
NM_001099270	ZBTB34	0.00	0.11	241	228	335	429
NM_138363	CEP95	0.00	0.11	164	203	335	429
NM_005433	YES1	0.00	0.11	999	1078	1545	1810
NM_001144950	SSC5D	0.00	0.11	798	871	1757	2048
NM_001112808	FPGT-TNNI3K	0.00	0.11	63	43	112	161
NM_017950	CCDC40	0.00	0.11	15	25	67	104
NM_003362	UNG	0.00	0.11	418	487	591	726
NM_031208	FAHD1	0.00	0.11	254	306	632	773
NM_004267	CHST2	0.00	0.11	285	281	293	379
NM_001008727	ZNF121	0.00	0.11	243	210	266	347
NM_144600	FOPNL	0.00	0.11	364	424	593	728
NM_024570	RNASEH2B	0.00	0.11	190	218	245	322
NM_031925	TMEM120A	0.00	0.11	739	728	1705	1987
NM_153687	IKBIP	0.00	0.11	865	879	867	1041
NM_001258373	SPATA20	0.00	0.11	357	393	1092	1296
NM_003400	XPO1	0.00	0.11	2982	3093	3910	4438
NM_003450	ZNF174	0.00	0.11	207	242	358	455
NM_016533	NINJ2	0.00	0.11	55	49	139	194
NM_031452	FAM103A1	0.00	0.11	97	129	148	205
NM_001136534	TMEM233	0.00	0.11	79	65	48	79
NM_012098	ANGPTL2	0.00	0.11	1241	1362	4927	5560
NM_177441	TMUB2	0.00	0.11	756	699	1348	1584

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_003169	SUPT5H	-0.01	0.11	2766	2574	4255	4815
NM_005319	HIST1H1C	-0.11	0.11	15716	14224	8543	9530
NM_015517	HINFP	0.00	0.11	226	268	385	486
NM_147189	FAM110B	0.00	0.11	458	470	281	364
NM_021033	RAP2A	0.00	0.11	901	935	1256	1479
NM_001042358	PTPN20B	0.00	0.11	35	41	202	270
NM_001242823	C4B_2	0.00	0.11	131	105	127	179
NM_007293	C4A	0.00	0.11	131	105	127	179
NM_001002029	C4B	0.00	0.11	131	105	127	179
NM_001031712	TRMT11	0.00	0.11	164	157	168	229
NM_001001419	SMAD5	0.00	0.11	1677	1729	2317	2665
NM_001286509	SLC35B2	0.00	0.11	2909	2922	6280	7039
NM_032679	ZNF577	0.00	0.11	66	64	123	174
NM_015087	SPG20	0.00	0.11	1720	1677	2290	2634
NM_004661	CDC23	0.00	0.11	671	731	903	1079
NM_021156	TMX4	0.00	0.11	624	567	1514	1767
NM_172089	TNFSF12-TNFSF13	0.00	0.11	268	259	464	577
NM_001199281	CABIN1	0.00	0.11	1786	1919	2664	3048
NM_001114137	DMTN	0.00	0.11	28	38	83	124
NM_002613	PDPK1	0.00	0.11	1497	1525	2739	3131
NM_021216	ZNF71	0.00	0.11	271	322	510	630
NM_182565	UBALD2	0.00	0.11	431	394	570	699
NM_003737	DCHS1	0.00	0.10	116	134	179	242
NM_032287	LDOC1L	-0.23	0.10	2009	1583	2078	2396
NM_032472	PPIL3	0.00	0.10	145	165	241	316
NM_001334	CTSO	0.01	0.10	222	275	499	617
NM_000108	DLD	-0.05	0.10	943	817	1370	1604
NM_012239	SIRT3	0.00	0.10	332	281	474	588
NM_014467	SRPX2	0.00	0.10	694	726	2227	2560
NM_001032372	ZNF226	0.00	0.10	162	187	356	451
NM_015659	RSL1D1	0.00	0.10	2078	2209	2951	3362
NM_001172687	GGA1	0.00	0.10	1312	1362	2063	2377
NM_014255	CNPY2	-0.15	0.10	867	696	1680	1950
NM_152622	MIER3	0.00	0.10	293	353	412	516
NM_001031617	COX19	0.00	0.10	326	345	339	431
NM_001012732	DCTD	0.00	0.10	2432	2439	3498	3965
NM_175872	ZNF792	0.00	0.10	49	51	152	209
NM_001160094	ACOT13	-0.01	0.10	307	250	705	852

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_032024	C10orf11	0.00	0.10	23	29	181	244
NM_006980	MTERF1	0.00	0.10	86	103	125	176
NM_024646	ZYG11B	0.00	0.10	1428	1508	2161	2484
NM_016021	UBE2J1	0.00	0.10	2773	2600	2450	2804
NM_018229	AP5M1	0.00	0.10	569	609	971	1153
NM_020121	UGGT2	0.00	0.10	590	629	917	1092
NM_017940	NBPF1	0.00	0.10	475	507	774	930
NM_173500	TTBK2	0.00	0.10	340	394	422	527
NM_001272004	EPC1	0.00	0.10	339	390	534	656
NM_001282640	SUSD1	0.00	0.10	879	820	1774	2052
NM_001919	ECI1	0.00	0.10	320	332	555	680
NM_013354	CNOT7	0.00	0.10	560	642	734	884
NM_032023	RASSF4	0.00	0.10	114	126	158	216
NM_174869	IDH3G	0.00	0.10	1635	1657	3182	3610
NM_001271977	STK25	-0.01	0.10	3098	2887	5840	6529
NM_018313	PBRM1	0.00	0.10	1869	1852	2600	2967
NM_153045	C9orf91	-0.05	0.10	244	188	362	457
NM_017654	SAMD9	0.00	0.10	433	421	693	837
NM_002015	FOXO1	0.00	0.10	140	106	297	381
NM_002067	GNA11	0.00	0.10	3554	3352	4053	4566
NM_016951	CKLF	0.00	0.10	368	324	703	848
NM_017785	SPDL1	0.00	0.10	639	588	824	985
NM_001127649	PEX26	0.00	0.10	786	851	1697	1963
NM_004775	B4GALT6	0.00	0.10	257	228	605	736
NM_001201338	SAFB	-0.03	0.10	565	479	605	736
NM_006544	EXOC5	0.00	0.10	1086	1133	1878	2164
NM_003679	KMO	0.00	0.10	120	133	89	131
NM_001172679	ZNF764	0.00	0.10	60	79	89	131
NM_005851	CDK2AP2	0.00	0.10	411	476	495	610
NM_001310	CREBL2	0.00	0.10	547	565	1231	1442
NM_001289824	FURIN	0.00	0.10	4833	4901	7499	8329
NM_001099666	PTAR1	0.00	0.10	1272	1214	2258	2584
NM_001129993	KIAA1841	0.00	0.10	145	171	324	412
NM_001289166	ZNF227	0.00	0.10	177	177	277	357
NM_020320	RARS2	0.00	0.10	609	644	1269	1484
NM_002814	PSMD10	0.00	0.10	382	406	638	773
NM_032683	MPV17L2	0.00	0.10	570	560	576	702
NM_000454	SOD1	0.00	0.10	2838	2726	5251	5869

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_006377	UNC13B	0.00	0.10	1028	1123	2876	3264
NM_024909	ATAT1	0.00	0.10	96	123	137	190
NM_001195150	LOC100130705	0.00	0.10	70	89	27	50
NM_017619	RNPC3	0.00	0.10	120	132	191	255
NM_015852	ZNF117	-0.24	0.10	106	62	191	255
NM_001080821	ZNF799	0.00	0.10	56	54	94	137
NM_177476	LYNX1	-0.12	0.10	178	125	616	747
NM_032718	MFSD9	-0.21	0.10	127	79	133	185
NM_213590	TRIM13	0.00	0.10	394	406	668	806
NM_025185	TANC2	0.00	0.10	2352	2463	5332	5952
NM_015960	CUTC	0.00	0.10	249	250	304	388
NM_182498	ZNF428	0.00	0.10	251	267	385	482
NM_002513	NME3	0.00	0.09	231	219	512	628
NM_001078177	SLC29A1	0.00	0.09	609	611	693	834
NM_001002878	THOC5	0.00	0.09	1187	1293	1857	2135
NM_153812	PHF13	0.00	0.09	968	963	975	1152
NM_001177387	ATXN7	0.00	0.09	814	895	1067	1255
NM_016006	ABHD5	0.00	0.09	854	947	1279	1492
NM_015694	ZNF777	0.00	0.09	637	652	665	802
NM_006285	TESK1	0.00	0.09	1056	1139	1360	1582
NM_002016	FLG	0.00	0.09	128	124	312	397
NM_001918	DBT	0.00	0.09	326	329	586	712
NM_005188	CBL	0.00	0.09	1941	1829	2365	2695
NM_000033	ABCD1	0.00	0.09	463	471	713	856
NM_002079	GOT1	0.00	0.09	702	781	1031	1214
NM_014988	LIMCH1	0.00	0.09	966	1050	2728	3094
NM_014880	CD302	-0.28	0.09	175	109	173	233
NM_001013620	ALG10B	0.01	0.09	93	128	79	118
NM_020884	MYH7B	0.00	0.09	98	69	79	118
NM_022166	XYLT1	0.00	0.09	5763	5923	4407	4933
NM_024309	TNIP2	0.00	0.09	742	792	905	1072
NM_199337	TMEM179B	0.00	0.09	645	715	1285	1497
NM_018316	KLHL26	0.00	0.09	197	199	239	311
NM_001012301	ARSI	0.00	0.09	616	629	2015	2305
NM_003502	AXIN1	0.00	0.09	559	503	676	813
NM_001040454	SLC26A6	0.00	0.09	326	372	480	590
NM_006623	PHGDH	-0.01	0.09	2003	1851	1942	2224
NM_003196	TCEA3	-0.27	0.09	267	177	724	867

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001197026	PLEKHA8	0.00	0.09	330	334	281	360
NM_014932	NLGN1	0.00	0.09	207	193	229	299
NM_016396	CTDSPL2	0.00	0.09	441	434	401	499
NM_153713	LIX1L	0.00	0.09	1588	1535	1512	1747
NM_001567	INPPL1	0.00	0.09	3955	4079	7447	8229
NM_005994	TBX2	0.00	0.09	856	922	1150	1344
NM_001007531	NKAPL	0.00	0.09	124	102	127	177
NM_182476	COQ6	0.00	0.09	326	326	715	856
NM_032510	PARD6G	0.00	0.09	8	14	146	200
NM_006721	ADK	0.00	0.09	724	726	1129	1320
NM_003432	ZNF131	0.00	0.09	466	510	493	604
NM_015295	SMCHD1	0.00	0.09	928	1012	1229	1431
NM_005223	DNASE1	0.00	0.09	105	124	214	281
NM_006875	PIM2	0.00	0.09	252	248	214	281
NM_016373	WWOX	-0.01	0.09	59	36	137	189
NM_001170580	HHAT	0.00	0.09	55	47	123	172
NM_152705	POLR1D	0.00	0.09	431	461	778	926
NM_024818	UBA5	0.00	0.09	369	409	512	625
NM_015878	AZIN1	0.00	0.09	2620	2604	3045	3429
NM_002973	ATXN2	-0.13	0.09	2071	1760	1882	2152
NM_015503	SH2B1	-0.24	0.09	1035	783	975	1146
NM_030798	WBSCR16	0.00	0.09	853	886	1106	1292
NM_004278	PIGL	0.00	0.09	108	139	189	251
NM_024544	MUL1	0.00	0.09	1013	1057	1749	2004
NM_012255	XRN2	0.00	0.09	2056	2106	2970	3344
NM_017719	SNRK	0.00	0.09	696	674	861	1018
NM_022915	MRPL44	0.00	0.09	519	523	599	723
NM_001028	RPS25	0.00	0.09	2882	2849	3858	4312
NM_002730	PRKACA	-0.03	0.09	1849	1675	2647	2989
NM_018992	KCTD5	0.00	0.09	1341	1336	1581	1817
NM_014007	ZBTB43	0.00	0.08	585	606	819	970
NM_001287757	DCUN1D4	0.00	0.08	473	435	699	835
NM_001163280	HTATSF1	0.00	0.08	730	719	1071	1251
NM_004225	MFHAS1	0.00	0.08	646	657	774	919
NM_001003801	SMARCD3	0.00	0.08	492	505	934	1098
NM_153267	MAMDC2	0.00	0.08	445	494	466	571

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_022913	GPBP1	0.00	0.08	917	956	919	1081
NM_001005407	CACNA1H	0.00	0.08	60	70	23	44
NM_006357	UBE2E3	0.00	0.08	240	270	453	556
NM_001204055	NDUFC2	0.00	0.08	1151	1130	2265	2566
NM_006468	POLR3C	0.00	0.08	790	820	1329	1536
NM_001278346	PHYKPL	0.00	0.08	444	509	763	906
NM_004337	OSGIN2	-0.32	0.08	827	586	1048	1224
NM_139126	PPIL4	0.00	0.08	286	330	462	566
NM_003631	PARG	0.00	0.08	387	402	605	728
NM_206962	PRMT2	0.00	0.08	1832	1969	3754	4188
NM_001040450	FAM63B	0.01	0.08	252	309	545	660
NM_181783	TMTC3	0.00	0.08	995	972	1978	2249
NM_001025248	DUT	0.00	0.08	298	274	347	434
NM_181742	ORC4	0.00	0.08	264	297	347	434
NM_181808	POLN	0.00	0.08	14	17	67	102
NM_001282515	ZFP37	0.00	0.08	39	44	67	102
NM_001031689	PLAA	0.00	0.08	976	960	1483	1704
NM_152345	ANKRD13B	0.00	0.08	121	88	104	148
NM_001455	FOXO3	0.00	0.08	2006	1908	1990	2261
NM_173632	ZNF776	0.00	0.08	250	281	474	579
NM_000070	CAPN3	0.00	0.08	34	39	83	122
NM_001271	CHD2	0.00	0.08	2018	1946	3288	3675
NM_022350	ERAP2	0.00	0.08	792	817	1470	1688
NM_178833	SLC9B2	0.00	0.08	478	472	980	1146
NM_018367	ACER3	-0.10	0.08	313	239	364	453
NM_023008	KRI1	0.00	0.08	347	288	351	438
NM_138418	FAM195A	0.00	0.08	102	92	133	183
NM_001082537	TCTN1	0.00	0.08	133	160	372	462
NM_021012	KCNJ12	0.00	0.08	59	83	148	201
NM_022165	LIN7B	-0.05	0.08	141	101	225	292
NM_018051	WDR60	0.00	0.08	127	105	231	299
NM_018086	FIGN	0.00	0.08	157	144	37	63
NM_004822	NTN1	-0.96	0.08	67	19	6	22
NM_021627	SENP2	0.00	0.08	705	754	1154	1338
NM_001082968	TOM1L2	0.00	0.08	2030	2097	4438	4917
NM_016538	SIRT7	0.00	0.08	362	377	489	595
NM_014974	DIP2C	0.00	0.08	2396	2336	4465	4946
NM_001057	TACR2	0.00	0.08	40	41	64	98

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_005027	PIK3R2	0.00	0.08	1580	1600	3236	3614
NM_001080495	TNRC18	0.00	0.08	1905	2037	2398	2702
NM_152279	ZNF585B	0.00	0.08	270	319	665	793
NM_001037165	FOXK1	0.00	0.08	2187	2156	3282	3662
NM_207012	AP3M1	0.01	0.08	1133	1253	1882	2137
NM_001204193	SRP19	0.00	0.08	286	325	270	344
NM_022126	LHPP	0.00	0.08	289	324	693	824
NM_001292018	CYTH1	0.00	0.08	397	418	532	643
NM_001856	COL16A1	-0.12	0.08	3354	2903	3032	3388
NM_014296	CAPN7	0.00	0.08	518	549	757	895
NM_006693	CPSF4	0.00	0.08	659	723	836	983
NM_012115	CASP8AP2	0.00	0.08	418	476	422	518
NM_032936	TMEM60	0.00	0.08	231	213	331	414
NM_012302	LPHN2	0.00	0.08	1798	1775	1653	1884
NM_001114394	PAPD4	0.00	0.08	588	642	1038	1207
NM_000068	CACNA1A	0.00	0.08	94	102	318	399
NM_001080425	BEX4	0.00	0.08	156	165	229	296
NM_001142300	CCNYL1	0.00	0.08	401	403	453	553
NM_032291	SGIP1	0.00	0.08	162	199	618	739
NM_012154	AGO2	0.00	0.07	1586	1721	1537	1756
NM_015885	PCF11	0.00	0.07	910	862	799	941
NM_015617	PYGO1	0.00	0.07	255	275	333	416
NM_001173425	DFNB31	0.00	0.07	150	193	341	425
NM_014939	TRAPPC8	0.00	0.07	705	795	1375	1577
NM_007245	ATXN2L	0.00	0.07	2178	2072	1709	1943
NM_199203	TMEM189-UBE2V1	0.00	0.07	3016	3143	5326	5858
NM_001284267	EFCAB11	0.00	0.07	46	58	69	104
NM_015401	HDAC7	0.00	0.07	3460	3495	3286	3656
NM_001282291	ABCB8	0.00	0.07	475	545	836	981
NM_033449	FCHSD1	0.00	0.07	847	940	1585	1806
NM_006135	CAPZA1	0.00	0.07	2616	2781	5089	5599
NM_030624	KLHL15	0.00	0.07	342	351	316	396
NM_001146110	MIER1	0.00	0.07	916	845	1287	1479
NM_004468	FHL3	0.00	0.07	487	561	705	835
NM_001288767	ARMC5	0.00	0.07	690	668	416	510
NM_001257964	BOD1L2	0.00	0.07	66	88	108	152
NM_134442	CREB1	0.00	0.07	741	806	1135	1311

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_173829	SREK1IP1	0.00	0.07	323	315	551	662
NM_024097	C1orf50	-0.31	0.07	118	67	123	170
NM_002657	PLAGL2	0.00	0.07	451	444	391	481
NM_004491	ARHGAP35	0.01	0.07	4907	5163	7435	8103
NM_004215	EBAG9	-0.05	0.07	216	164	223	288
NM_001695	ATP6V1C1	0.00	0.07	1161	1178	2078	2340
NM_173474	NTAN1	-0.16	0.07	590	457	1092	1262
NM_007041	ATE1	0.00	0.07	462	468	755	889
NM_001271592	LOC100129361	0.00	0.07	442	396	659	782
NM_001193511	MAP3K12	0.00	0.07	512	475	932	1085
NM_181708	BCDIN3D	0.00	0.07	27	47	139	189
NM_001143936	C15orf61	0.00	0.07	132	168	119	165
NM_007371	BRD3	0.00	0.07	934	902	1102	1272
NM_000722	CACNA2D1	0.00	0.07	466	460	826	967
NM_001099670	C8orf59	-0.15	0.07	261	189	195	255
NM_001145029	ANKRD30B	0.00	0.07	299	296	195	255
NM_001008388	CISD2	0.00	0.07	439	433	613	730
NM_001194937	POGZ	0.00	0.07	1501	1464	1816	2052
NM_001135243	TCOF1	0.00	0.07	1369	1413	1306	1495
NM_152720	NEK3	0.00	0.07	111	119	156	209
NM_178502	DTX3	0.00	0.07	333	379	730	860
NM_001145641	SRRM5	0.00	0.07	150	158	214	277
NM_000635	RFX2	0.00	0.07	334	286	485	586
NM_020706	SCAF4	0.00	0.07	1118	1218	1098	1266
NM_032970	SEC22C	0.00	0.07	1010	1034	2163	2427
NM_152424	AMER1	0.00	0.07	139	161	272	344
NM_007130	ZNF41	0.00	0.07	160	196	306	383
NM_001039887	PROSER3	0.00	0.07	228	207	327	407
NM_001100874	SLC9B1	0.00	0.07	51	34	79	116
NM_021145	DMTF1	0.00	0.07	620	689	1021	1181
NM_000341	SLC3A1	-0.09	0.07	149	104	335	416
NM_006267	RANBP2	-0.26	0.07	1632	1249	3059	3394
NM_000552	VWF	0.00	0.07	52	54	75	111
NM_006642	SDCCAG8	0.00	0.07	749	690	1553	1763

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_020825	CRAMP1L	-0.04	0.07	836	724	859	1002
NM_006349	ZNHIT1	0.00	0.07	1287	1221	2903	3225
NM_032172	USP42	0.00	0.07	397	358	322	401
NM_001099678	LRRC58	0.00	0.07	1075	1083	1452	1652
NM_033081	DIDO1	0.00	0.07	1338	1389	2073	2327
NM_003769	SRSF9	-0.07	0.07	1723	1509	2157	2418
NM_025194	ITPKC	0.00	0.07	511	495	826	965
NM_001098787	BET1L	0.00	0.07	2029	2169	2335	2610
NM_017686	GDAP2	0.00	0.06	421	454	955	1107
NM_005321	HIST1H1E	0.00	0.06	7602	7405	2945	3268
NM_001098638	RNF169	0.00	0.06	1399	1502	1732	1956
NM_001136036	ZNF692	0.00	0.06	279	322	324	403
NM_145728	SYNM	0.00	0.06	391	367	414	505
NM_020676	ABHD6	0.00	0.06	305	277	422	514
NM_001007561	IRGQ	0.00	0.06	1049	1044	1425	1621
NM_001260	CDK8	0.00	0.06	291	345	447	542
NM_005791	MPHOSPH10	0.00	0.06	326	308	447	542
NM_016271	RNF138	0.00	0.06	160	139	98	139
NM_015045	WAPAL	0.00	0.06	1428	1516	1747	1970
NM_138446	MALSU1	0.00	0.06	395	378	672	793
NM_014946	SPAST	0.00	0.06	336	381	426	518
NM_001285439	RICTOR	-0.03	0.06	878	765	1354	1542
NM_194259	UBE2I	0.00	0.06	2177	2178	3134	3466
NM_024045	DDX50	0.00	0.06	678	635	788	921
NM_020993	BCL7A	0.00	0.06	1682	1655	761	891
NM_014313	TMEM50A	0.00	0.06	3446	3481	4777	5224
NM_005389	PCMT1	0.01	0.06	1977	2137	3136	3466
NM_012430	SEC22A	0.00	0.06	431	416	520	623
NM_024899	CEP76	0.00	0.06	180	195	150	201
NM_001514	GTF2B	0.00	0.06	348	391	497	597
NM_024697	ZNF385D	0.00	0.06	32	39	81	118
NM_001288781	TTC8	0.00	0.06	258	273	722	847
NM_001135993	TTC39C	-0.12	0.06	261	193	441	534
NM_144703	LSM14B	0.00	0.06	1155	1152	1545	1747
NM_020137	GRIPAP1	0.00	0.06	548	610	821	956
NM_032830	CIRH1A	0.00	0.06	1287	1338	1736	1954
NM_014663	KDM4A	-0.07	0.06	553	454	774	904

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001005408	NEURL4	0.01	0.06	498	577	624	738
NM_173611	FAM98B	0.00	0.06	581	547	599	710
NM_000410	HFE	0.00	0.06	189	168	420	510
NM_032352	BRMS1L	0.00	0.06	105	130	193	251
NM_030755	TMX1	0.00	0.06	561	619	884	1024
NM_001282231	ARMCX2	0.00	0.06	672	751	1612	1817
NM_006287	TFPI	-0.01	0.06	2382	2212	2884	3187
NM_144597	C15orf40	0.00	0.06	118	149	206	266
NM_172003	CBWD2	0.00	0.06	255	280	324	401
NM_212550	BLOC1S3	0.00	0.06	488	500	362	444
NM_018368	LMBRD1	0.00	0.06	97	108	370	453
NM_006785	MALT1	0.00	0.06	1114	1102	1352	1534
NM_001620	AHNAK	-0.01	0.06	110432	108601	198713	208233
NM_001253875	UXS1	0.00	0.06	889	978	1811	2031
NM_001270485	CAMKK2	0.00	0.06	1229	1305	2473	2743
NM_005230	ELK3	0.00	0.06	2347	2403	3400	3736
NM_018053	XKR8	0.01	0.06	515	595	593	702
NM_001288563	WDR63	0.00	0.06	19	10	121	166
NM_001745	CAMLG	0.00	0.06	521	559	1069	1225
NM_014859	ARHGAP 44	0.00	0.06	85	69	25	46
NM_000322	PRPH2	0.00	0.06	65	58	25	46
NM_001195156	ZMYM6N B	-0.27	0.06	587	419	975	1122
NM_144607	CYB5D1	0.00	0.06	176	211	472	567
NM_001270401	RXRB	0.00	0.06	1084	1147	1564	1762
NM_018989	RBM27	0.00	0.06	738	774	1079	1235
NM_024509	LRFN3	0.00	0.05	174	152	250	316
NM_007187	WBP4	0.00	0.05	394	347	460	553
NM_001076786	QSER1	-0.06	0.05	821	700	873	1009
NM_013450	BAZ2B	-0.12	0.05	532	421	730	852
NM_153638	PANK2	0.00	0.05	499	576	853	987
NM_002380	MATN2	-0.33	0.05	528	359	643	756
NM_020998	MST1	0.00	0.05	67	57	79	115
NM_004760	STK17A	0.00	0.05	827	912	1749	1959
NM_003927	MBD2	0.00	0.05	1286	1278	1510	1701
NM_001037172	PXYLP1	0.00	0.05	82	93	218	279
NM_001142648	SAR1A	0.00	0.05	3206	3378	5432	5887
NM_003847	PEX11A	0.00	0.05	57	52	123	168
NM_152341	PAQR4	0.00	0.05	615	609	281	351

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_030792	GDPD5	0.00	0.05	333	344	482	577
NM_006100	ST3GAL6	0.00	0.05	124	98	212	272
NM_014572	LATS2	0.00	0.05	2975	3090	2466	2728
NM_001143935	CROT	0.00	0.05	124	162	406	492
NM_003681	PDXK	-0.02	0.05	6372	6019	6653	7177
NM_031935	HMCN1	0.00	0.05	290	269	2570	2839
NM_018079	SRBD1	0.00	0.05	187	228	289	360
NM_001101654	CXXC1	0.00	0.05	1000	1066	886	1022
NM_201269	ZNF644	0.00	0.05	544	587	751	874
NM_001286416	SUMO3	0.00	0.05	2581	2702	4413	4802
NM_001531	MR1	0.00	0.05	600	538	1431	1614
NM_000866	HTR1F	0.00	0.05	135	107	485	580
NM_001190826	FAM217B	0.00	0.05	261	210	175	229
NM_001198759	LY75-CD302	-0.23	0.05	175	113	175	229
NM_001258213	PCID2	0.00	0.05	853	873	1088	1242
NM_138400	NOM1	0.00	0.05	610	688	624	734
NM_001284304	TBC1D22A	0.00	0.05	734	714	1325	1499
NM_032595	PPP1R9B	0.00	0.05	2155	2228	3051	3351
NM_003171	SUPV3L1	0.00	0.05	447	501	745	867
NM_004589	SCO1	0.00	0.05	537	491	705	823
NM_152905	NEDD1	0.00	0.05	281	330	291	362
NM_001145358	SIN3A	0.01	0.05	1155	1274	1682	1884
NM_018288	PHF10	0.00	0.05	263	253	306	379
NM_016352	CPA4	0.00	0.05	36	41	214	274
NM_001261406	MPDZ	0.01	0.05	1860	2012	3700	4041
NM_019095	CRLS1	0.00	0.05	532	580	562	665
NM_001077654	TNFAIP8	0.00	0.05	109	101	67	100
NM_138809	CMBL	0.00	0.05	368	362	975	1118
NM_181706	DNAJC24	0.00	0.05	224	230	370	451
NM_014023	WDR37	0.00	0.05	1037	1010	1439	1621
NM_025134	CHD9	0.00	0.05	1535	1514	2780	3059
NM_001099660	LRRN3	0.00	0.05	240	246	114	157
NM_018047	RBM22	0.00	0.05	654	709	1013	1159
NM_152289	ZNF561	0.00	0.05	216	239	397	481
NM_002395	ME1	0.00	0.05	487	524	1452	1634
NM_014673	EMC2	0.00	0.05	318	307	657	769
NM_014182	ORMDL2	0.00	0.05	496	463	1104	1257
NM_138558	PPP1R8	0.00	0.05	770	812	1000	1144

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_080671	KCNE4	0.00	0.05	1172	1105	834	963
NM_032811	TBRG1	0.00	0.05	976	1060	1287	1455
NM_152617	RNF168	0.00	0.05	960	933	1227	1390
NM_000051	ATM	0.00	0.05	907	856	1633	1828
NM_014516	CNOT3	0.00	0.05	1025	1057	936	1074
NM_001100814	TMEM55B	0.00	0.05	787	743	1123	1277
NM_030818	CCDC130	0.00	0.05	473	542	661	773
NM_018046	AGGF1	0.00	0.05	456	519	651	762
NM_015120	ALMS1	0.00	0.05	728	715	1042	1189
NM_001204504	DGKH	0.00	0.05	378	440	445	534
NM_001170791	RMDN2	0.00	0.05	62	41	110	152
NM_015355	SUZ12	0.00	0.05	694	744	811	937
NM_001256163	BIRC2	0.00	0.05	2499	2566	2697	2965
NM_003080	SMPD2	0.00	0.05	75	69	173	226
NM_152581	MOSPD2	0.00	0.05	921	889	969	1109
NM_003028	SHB	0.00	0.05	967	984	1343	1514
NM_006111	ACAA2	0.00	0.05	520	554	1314	1482
NM_001251845	TRPC1	0.00	0.05	187	199	406	490
NM_003478	CUL5	0.00	0.05	784	801	1156	1311
NM_014727	KMT2B	0.00	0.05	946	894	932	1068
NM_006458	TRIM3	0.00	0.05	550	603	682	795
NM_018233	OGFOD1	0.00	0.05	1183	1193	1581	1769
NM_152449	LYSMD4	0.00	0.05	170	162	200	257
NM_001287391	C9orf131	-0.48	0.05	62	26	60	91
NM_003218	TERF1	0.00	0.05	109	141	187	242
NM_020753	CASKIN2	0.00	0.05	275	318	416	501
NM_001143835	NFRKB	0.00	0.05	947	1017	1260	1423
NM_001001433	STX16	0.00	0.05	1160	1251	2121	2347
NM_020832	ZNF687	0.00	0.05	736	715	1054	1200
NM_001164501	EIF4ENIF1	0.00	0.05	688	730	1081	1229
NM_001257133	COX14	0.00	0.05	306	361	586	689
NM_005559	LAMA1	0.00	0.04	2812	2685	4313	4673
NM_005086	SSPN	0.00	0.04	300	335	811	935
NM_014804	KIAA0753	0.00	0.04	278	260	503	597
NM_001195563	CAMTA1	0.00	0.04	302	332	345	421
NM_020888	KIAA1522	0.00	0.04	567	624	1183	1338
NM_152245	CPT1B	0.00	0.04	29	32	69	102

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_024852	AGO3	0.00	0.04	437	507	626	732
NM_153265	EML3	0.00	0.04	843	876	1493	1671
NM_170692	RASAL2	0.00	0.04	2394	2373	4240	4590
NM_012477	WBP1	0.00	0.04	241	237	547	645
NM_003006	SELPLG	0.00	0.04	105	132	339	414
NM_005146	SART1	0.00	0.04	1640	1745	2225	2453
NM_002387	MCC	0.00	0.04	159	194	435	521
NM_015365	AMMECR1	0.00	0.04	263	290	239	301
NM_018318	CCDC91	-0.29	0.04	255	165	445	532
NM_015323	UFL1	0.00	0.04	919	860	1192	1346
NM_005273	GNB2	0.00	0.04	4944	5151	6204	6654
NM_004541	NDUFA1	-0.23	0.04	667	495	888	1017
NM_001144936	C11orf95	0.01	0.04	270	329	466	555
NM_007044	KATNA1	0.00	0.04	105	124	212	270
NM_080430	SELM	0.00	0.04	1399	1490	3854	4177
NM_139159	DPP9	0.00	0.04	3465	3378	4091	4427
NM_001039885	FKRP	0.00	0.04	490	531	647	754
NM_012207	HNRNPH3	0.00	0.04	2045	2036	2175	2397
NM_000252	MTM1	0.00	0.04	280	268	422	506
NM_004506	HSF2	0.00	0.04	289	236	220	279
NM_015905	TRIM24	0.00	0.04	401	468	451	538
NM_022098	XPNPEP3	0.00	0.04	484	488	705	817
NM_001099415	POM121C	0.00	0.04	1921	1902	1828	2026
NM_080821	FAM210B	0.00	0.04	564	490	1512	1688
NM_019008	MIEF1	0.00	0.04	1574	1640	2439	2676
NM_032840	SPRYD3	0.00	0.04	1329	1309	2539	2782
NM_002033	FUT4	0.00	0.04	488	448	408	490
NM_019044	CCDC93	0.01	0.04	1515	1654	2824	3083
NM_013361	ZNF223	0.00	0.04	59	66	104	144
NM_001040157	CEP44	0.00	0.04	258	209	237	298
NM_003748	ALDH4A1	0.00	0.04	530	500	876	1002
NM_006227	PLTP	0.00	0.04	709	752	2219	2440
NM_001991	EZH1	0.00	0.04	794	818	1728	1917
NM_001203260	NDUFC2-KCTD14	0.00	0.04	824	882	1714	1902
NM_006568	CGRRF1	0.00	0.04	82	85	195	250
NM_033107	GTPBP10	-0.03	0.04	270	214	412	494
NM_020195	SDR39U1	0.00	0.04	700	659	857	981

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_018452	TMEM242	0.00	0.04	298	353	478	567
NM_003993	CLK2	-0.08	0.04	404	322	368	445
NM_018328	MBD5	0.00	0.04	183	197	622	725
NM_001242491	FAM156A	0.00	0.04	637	650	593	693
NM_003482	KMT2D	-0.27	0.04	4235	3338	4357	4695
NM_015627	LDLRAP1	0.00	0.04	905	822	988	1122
NM_001165258	TMEM14C	0.01	0.04	770	868	1620	1800
NM_001001563	TIMM50	0.00	0.04	1348	1292	1685	1869
NM_022170	EIF4H	0.00	0.04	6228	6195	9733	10318
NM_024316	LENG1	0.00	0.04	130	153	177	229
NM_017415	KLHL3	0.00	0.04	28	37	337	410
NM_024731	KLHL36	0.00	0.04	859	867	1350	1510
NM_033505	EPT1	0.00	0.04	695	706	1092	1233
NM_006366	CAP2	0.00	0.04	739	809	1603	1780
NM_004041	ARRB1	0.00	0.04	566	590	1042	1179
NM_005680	TAF1B	0.00	0.04	302	351	668	774
NM_005068	SIM1	0.00	0.04	97	109	306	375
NM_014997	KLHDC10	0.00	0.04	674	711	919	1046
NM_145207	SPATA5	0.00	0.03	515	562	522	614
NM_021934	ATG101	0.00	0.03	1647	1548	1840	2031
NM_005643	TAF11	0.00	0.03	207	253	308	377
NM_198243	ASB7	0.01	0.03	356	423	493	582
NM_172195	EIF2B4	0.00	0.03	694	742	1071	1209
NM_018244	UQCC1	0.00	0.03	553	528	1019	1153
NM_080742	B3GAT2	0.00	0.03	97	102	112	153
NM_001199107	TBC1D24	0.00	0.03	877	948	1242	1392
NM_013398	ZNF224	0.00	0.03	150	178	285	351
NM_001355	DDT	0.00	0.03	278	302	636	738
NM_001099684	FAM156B	0.00	0.03	611	642	595	693
NM_000297	PKD2	0.00	0.03	3107	3270	4010	4316
NM_018648	NOP10	0.00	0.03	2266	2381	3438	3715
NM_145166	ZBTB47	0.00	0.03	1921	1951	3342	3614
NM_024047	NUDT9	0.00	0.03	479	484	957	1085
NM_005896	IDH1	0.00	0.03	493	529	1922	2115
NM_152267	RNF185	0.00	0.03	1375	1483	2444	2667
NM_001198807	MSANTD3	0.00	0.03	2155	2177	2753	2993

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001407	CELSR3	0.00	0.03	156	153	175	226
NM_006528	TFPI2	-0.12	0.03	18837	16887	45731	47463
NM_001143769	ZNF438	-0.08	0.03	189	138	225	283
NM_022761	C11orf1	0.00	0.03	46	67	119	161
NM_004383	CSK	0.00	0.03	1583	1625	1464	1627
NM_133473	ZNF431	0.00	0.03	91	89	92	129
NM_001040662	VCPKMT	0.00	0.03	70	58	92	129
NM_016544	DNAJC27	0.00	0.03	113	82	92	129
NM_006212	PFKFB2	0.00	0.03	266	309	788	902
NM_001278559	ZNF316	0.00	0.03	407	435	601	699
NM_015492	C15orf39	0.00	0.03	936	1016	980	1109
NM_001040715	KIAA0895L	-1.15	0.03	1032	407	547	640
NM_182515	ZNF714	-0.53	0.03	249	135	125	168
NM_001242659	C1orf233	0.01	0.03	75	107	108	148
NM_015138	RTF1	0.00	0.03	1491	1589	2217	2425
NM_001128928	INPP1	0.00	0.03	571	566	734	843
NM_018036	ATG2B	0.00	0.03	918	858	1870	2057
NM_001382	DPAGT1	0.00	0.03	1001	1059	1695	1871
NM_001184743	PGBD1	0.00	0.03	204	223	268	331
NM_001271918	SEC11A	-0.03	0.03	985	866	1104	1240
NM_144601	CMTM3	0.00	0.03	464	410	925	1048
NM_001005920	JMJD8	0.00	0.03	2700	2653	5521	5882
NM_176795	HRAS	0.00	0.03	604	604	996	1124
NM_001286611	REPS1	0.00	0.03	570	628	917	1039
NM_001142405	SLMO1	0.00	0.03	64	89	133	177
NM_001161425	ZNF610	0.00	0.03	29	24	127	170
NM_002439	MSH3	0.00	0.03	285	344	497	584
NM_001184970	PACSIN2	0.00	0.03	2428	2567	3650	3926
NM_004888	ATP6V1G1	0.00	0.03	1435	1401	2506	2725
NM_014633	CTR9	0.00	0.03	1288	1376	1861	2044
NM_001170755	NBPF15	0.00	0.03	656	658	1102	1237
NM_001136264	DAZAP2	-0.04	0.03	3305	3031	3841	4124
NM_020207	ERCC6L2	0.00	0.03	411	443	940	1063
NM_001143942	RBM24	0.00	0.03	327	342	545	636
NM_198291	SRC	0.00	0.03	1196	1165	2362	2571
NM_001267039	LARP7	0.00	0.03	459	439	593	688
NM_020453	ATP10D	0.00	0.03	1061	1142	2263	2466
NM_001190810	AGAP9	0.00	0.03	107	129	154	201

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_014291	GCAT	0.00	0.03	271	315	283	347
NM_020933	ZNF317	0.00	0.03	629	716	1258	1401
NM_022039	FBXW4	0.00	0.02	257	311	580	673
NM_001136574	LANCL1	0.00	0.02	832	897	1855	2033
NM_007342	NUPL2	0.00	0.02	258	271	349	420
NM_012213	MLYCD	0.01	0.02	283	343	439	519
NM_173690	SCAI	0.00	0.02	221	206	304	370
NM_002481	PPP1R12B	0.00	0.02	195	200	399	475
NM_145298	APOBEC3F	0.00	0.02	82	107	198	251
NM_005173	ATP2A3	0.00	0.02	54	61	198	251
NM_014071	NCOA6	0.00	0.02	1485	1567	2048	2235
NM_031917	ANGPTL6	-0.50	0.02	339	195	279	342
NM_032792	ZBTB45	0.00	0.02	585	557	541	630
NM_001170629	CHD8	0.00	0.02	2690	2666	3976	4253
NM_144970	CXorf38	0.00	0.02	568	622	649	747
NM_001100819	MOB4	0.00	0.02	413	458	674	774
NM_001199302	CNOT2	0.00	0.02	976	952	1506	1662
NM_001198595	STON1	0.00	0.02	98	114	403	479
NM_012100	DNPEP	-0.13	0.02	1509	1265	1886	2063
NM_001039374	CCDC183	0.00	0.02	36	37	96	133
NM_017671	FERMT1	0.00	0.02	76	70	264	325
NM_052951	DNTTIP1	-0.13	0.02	519	406	607	701
NM_001145309	LRTOMT	0.00	0.02	285	299	549	638
NM_015490	SEC31B	0.00	0.02	108	100	158	205
NM_001932	MPP3	-0.09	0.02	313	241	225	281
NM_002567	PEBP1	-0.06	0.02	2519	2266	5501	5830
NM_004641	MLLT10	0.00	0.02	713	787	796	904
NM_198273	LYSMD3	0.00	0.02	533	610	410	486
NM_015189	EXOC6B	0.00	0.02	439	477	1400	1547
NM_024029	YIPF2	-0.02	0.02	1419	1278	1720	1885
NM_003632	CNTNAP1	0.00	0.02	2055	2094	2543	2749
NM_024511	HAUS3	0.00	0.02	234	229	166	214
NM_001080415	U2SURP	0.00	0.02	1055	1105	1254	1392
NM_004831	MED26	-0.10	0.02	387	303	412	488
NM_006709	EHMT2	-0.05	0.02	1521	1347	2021	2201
NM_001104587	SLFN11	0.00	0.02	879	970	647	743
NM_002894	RBBP8	0.00	0.02	422	427	470	551

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_003136	SRP54	0.00	0.02	1385	1513	1755	1920
NM_001287585	NUP35	0.00	0.02	129	95	87	122
NM_005837	POP7	0.00	0.02	737	821	761	865
NM_001198801	EIF4G3	0.00	0.02	2683	2675	5914	6246
NM_022483	C5orf28	0.00	0.02	222	213	347	416
NM_024573	C6orf211	0.00	0.02	517	468	593	684
NM_007313	ABL1	0.00	0.02	5902	5847	6875	7236
NM_001164407	TLCD2	-0.26	0.02	380	264	349	418
NM_001949	E2F3	0.00	0.02	598	656	755	858
NM_032140	ENKD1	0.00	0.02	138	146	231	287
NM_001272071	AP1S2	0.00	0.02	311	309	401	475
NM_001127208	TET2	0.00	0.02	444	451	445	523
NM_012118	CCRN4L	0.00	0.02	462	475	312	377
NM_032127	FAM160 A2	0.00	0.02	543	550	724	824
NM_024095	ASB8	0.00	0.02	561	636	928	1042
NM_001221	CAMK2D	0.00	0.02	2453	2623	4245	4510
NM_020191	MRPS22	0.00	0.02	463	445	701	799
NM_005116	SLC23A2	-0.05	0.02	693	589	1691	1848
NM_014284	NCDN	0.00	0.01	1039	982	2194	2375
NM_145036	CEP112	0.00	0.01	83	80	316	381
NM_030929	KAZALD 1	0.00	0.01	195	214	100	137
NM_001478	B4GALN T1	0.00	0.01	136	121	514	597
NM_003151	STAT4	0.00	0.01	43	62	106	144
NM_014813	LRIG2	0.00	0.01	290	265	470	549
NM_022757	CCDC14	0.00	0.01	448	497	772	874
NM_194313	KIF24	0.00	0.01	231	207	291	353
NM_198535	ZNF699	0.00	0.01	99	87	166	213
NM_152558	IQCE	0.00	0.01	466	491	1383	1521
NM_001204062	COMMD 3-BMI1	0.00	0.01	764	837	1422	1562
NM_001131034	RNF212	0.00	0.01	66	77	119	159
NM_005732	RAD50	0.00	0.01	920	857	1834	1994
NM_152420	C9orf41	0.00	0.01	176	205	430	505
NM_005017	PCYT1A	0.00	0.01	317	354	801	904
NM_022353	OSGEPL1	-0.21	0.01	160	103	146	190
NM_030891	LRRC3	0.00	0.01	45	35	60	89
NM_004501	HNRNPU	0.00	0.01	4140	4232	4480	4739
NM_002547	OPHN1	0.00	0.01	1223	1336	1260	1390

Table 6B: Differentially Upregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_005772	RCL1	0.00	0.01	174	207	250	307
NM_001195087	GGACT	-0.04	0.01	151	110	108	146
NM_001281453	MBD3	0.00	0.01	1837	1942	1892	2052

Table 6C: Differentially Downregulated Genes in SR + IL-2

Table 6C: Differentially Downregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_138340	ABHD3	-0.04	0.00	161	118	110	109
NM_001607	ACAA1	-0.06	0.20	741	627	1568	1945
NM_014716	ACAP1	-0.03	0.00	116	81	87	94
NM_022735	ACBD3	-0.16	0.21	720	564	996	1272
NM_018367	ACER3	-0.10	0.08	313	239	364	453
NM_001160094	ACOT13	-0.01	0.10	307	250	705	852
NM_018477	ACTR10	-0.04	0.18	678	580	1751	2131
NM_020445	ACTR3B	-0.31	0.00	326	215	241	224
NM_020328	ACVR1B	-0.09	0.18	874	731	1059	1318
NM_138448	ACYP2	-0.17	0.55	112	70	146	272
NM_030957	ADAMTS 10	-0.50	1.11	139	70	87	250
NM_139025	ADAMTS 13	-0.13	0.50	41	20	46	98
NM_001102470	ADH6	-1.02	0.00	67	18	12	20
NM_006829	ADIRF	-0.07	0.34	883	748	1138	1577
NM_020233	ADPRM	-0.01	0.26	139	102	185	277
NM_000679	ADRA1B	-0.04	0.00	82	53	46	68
NM_001144000	AGAP5	-0.03	0.31	70	44	58	105
NM_005751	AKAP9	-0.04	0.20	1762	1585	2059	2540
NM_005787	ALG3	-0.04	0.00	844	730	1004	974
NM_001077690	ALG9	-0.08	0.19	694	576	1069	1338
NM_001145374	ALKBH2	-0.30	0.00	269	175	185	190
NM_138775	ALKBH8	-0.08	0.00	206	152	281	279
NM_025144	ALPK1	-0.10	0.00	97	62	198	203
NM_001118887	ANGPT2	-0.47	0.58	430	259	89	179
NM_031917	ANGPTL 6	-0.50	0.02	339	195	279	342
NM_001256182	ANKRD1 1	-0.09	0.28	2578	2261	3677	4684
NM_015208	ANKRD1 2	-0.09	0.20	1047	884	1346	1680
NM_001256053	ANKRD2 6	-0.15	0.00	332	246	356	388
NM_025190	ANKRD3 6B	-0.02	0.00	276	221	339	366
NM_181726	ANKRD3 7	-0.06	2.14	339	269	50	312
NM_001195144	ANKRD4 4	-0.20	0.80	387	280	618	1205
NM_001002857	ANXA2	-0.03	0.14	14766	14085	27335	30694

Table 6C: Differentially Downregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001130524	AP1M1	-0.12	0.00	3040	2625	2851	2834
NM_153360	APCDD1L	-0.03	1.00	2412	2212	6576	13626
NM_001130415	APOLD1	-0.22	0.00	245	167	135	157
NM_015193	ARC	-0.93	0.80	68	20	21	65
NM_006015	ARID1A	-0.03	0.00	3424	3172	3396	3473
NM_016374	ARID4B	-0.04	0.28	367	297	401	567
NM_006886	ATP5E	-0.12	0.00	1135	946	1466	1436
NM_001694	ATP6V0C	-0.10	0.18	3092	2708	4147	4926
NM_145230	ATP6V0E2	-0.10	0.00	204	148	320	372
NM_015994	ATP6V1D	-0.05	0.18	1908	1710	2487	2996
NM_178191	ATPIF1	-0.14	0.13	862	695	1832	2152
NM_000489	ATRX	-0.35	0.21	842	583	1543	1926
NM_002973	ATXN2	-0.13	0.09	2071	1760	1882	2152
NM_001098833	ATXN7L3	-0.11	0.00	1917	1644	1824	1786
NM_001698	AUH	-0.76	0.00	129	52	216	238
NM_018842	BAIAP2L1	-0.15	0.46	588	457	595	924
NM_001291428	BAX	-0.59	0.00	2775	1722	2647	2675
NM_013450	BAZ2B	-0.12	0.05	532	421	730	852
NM_001204108	BCL2L11	-0.22	0.77	69	37	35	94
NM_004183	BEST1	-0.03	0.47	165	123	424	680
NM_001001786	BLID	-0.43	0.00	94	46	73	91
NM_181809	BMP8A	-1.00	0.23	79	23	40	74
NM_199186	BPGM	-0.15	0.35	435	330	688	983
NM_001281723	BTD	-0.02	0.12	416	347	697	852
NM_001009894	C12orf29	-0.22	0.01	582	430	478	556
NM_001194995	C12orf65	-0.01	0.00	380	316	264	309
NM_001173978	C14orf178	-0.82	0.00	52	15	17	31
NM_181656	C17orf58	-0.72	0.00	186	83	181	176
NM_001288980	C18orf54	-0.06	0.00	197	147	202	170
NM_018381	C19orf66	-0.05	0.00	648	545	878	932
NM_024097	C1orf50	-0.31	0.07	118	67	123	170
NM_001256609	C1orf85	-0.09	0.00	1489	1278	4226	4092
NM_001286476	C21orf58	-0.29	0.00	195	122	156	140
NM_182520	C22orf15	-0.10	0.00	85	53	106	140
NM_001142964	C22orf46	-0.33	0.00	221	137	241	277
NM_001170330	C4orf3	-0.17	0.78	1159	932	1479	2737
NM_178569	C5orf38	-0.44	0.00	48	19	17	24
NM_001204173	C8orf44-	-0.12	0.00	404	313	372	362

Table 6C: Differentially Downregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
	SGK3						
NM_001013842	C8orf58	-0.10	0.00	356	275	347	346
NM_001099670	C8orf59	-0.15	0.07	261	189	195	255
NM_001287391	C9orf131	-0.48	0.05	62	26	60	91
NM_183241	C9orf142	-0.03	0.00	267	211	312	275
NM_153045	C9orf91	-0.05	0.10	244	188	362	457
NM_001242369	CACFD1	-0.15	0.00	120	77	206	207
NM_001184902	CARD8	-0.06	0.00	231	175	378	364
NM_020649	CBX8	-0.19	0.00	79	45	46	41
NM_001040440	CCDC112	-0.29	0.00	105	59	154	176
NM_014157	CCDC113	-0.04	0.37	82	53	175	283
NM_138771	CCDC126	-0.28	0.00	171	106	204	198
NM_032779	CCDC142	-0.05	0.36	279	219	316	479
NM_001080503	CCDC159	-0.09	0.16	73	44	181	253
NM_001012506	CCDC66	-0.13	0.00	208	148	252	266
NM_018318	CCDC91	-0.29	0.04	255	165	445	532
NM_148672	CCL28	-0.20	1.39	68	37	44	170
NM_030937	CCNL2	-0.03	0.18	1650	1482	2202	2669
NM_014880	CD302	-0.28	0.09	175	109	173	233
NM_016579	CD320	-0.29	0.32	1068	782	990	1360
NM_001267698	CD63	-0.15	0.23	12326	10792	27628	33094
NM_001251	CD68	-0.02	0.26	3830	3590	9144	11331
NM_001782	CD72	-0.06	0.25	61	36	73	122
NM_001785	CDA	-0.23	0.89	220	146	293	640
NM_145057	CDC42EP 5	-0.28	0.00	94	52	52	48
NM_024011	CDK11A	-0.02	0.26	210	163	177	266
NM_001787	CDK11B	-0.04	0.27	267	209	258	375
NM_001800	CDKN2D	-0.10	0.20	404	317	354	479
NM_001127893	CEACAM 19	-0.11	0.00	124	83	127	146
NM_001285878	CEBPB	-0.05	0.55	2040	1825	2240	3503
NM_001408	CELSR2	-0.18	0.51	88	52	27	65
NM_001194998	CEP152	-0.10	0.00	482	385	245	231
NM_025114	CEP290	-0.14	0.00	368	278	688	743
NM_004365	CETN3	-0.26	0.00	177	112	125	126
NM_006324	CFDP1	-0.01	0.00	982	874	1042	1046
NM_001005271	CHD3	-0.07	0.12	2412	2149	3502	4015
NM_017780	CHD7	-0.26	0.00	296	200	223	187
NM_020244	CHPT1	-0.12	0.27	702	568	1175	1553

Table 6C: Differentially Downregulated Genes in SR + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001171087	CLCN2	-0.43	0.00	242	141	233	264
NM_001146079	CLDN14	-0.07	1.45	868	734	164	551
NM_001040182	CLDND1	-0.03	0.41	1181	1047	942	1383
NM_003993	CLK2	-0.08	0.04	404	322	368	445
NM_015041	CLUAP1	-0.15	0.00	305	224	514	527
NM_014255	CNPY2	-0.15	0.10	867	696	1680	1950
NM_000614	CNTF	-0.75	0.00	78	28	35	46
NM_017738	CNTLN	-0.02	0.00	228	178	277	335
NM_001843	CNTN1	-0.13	0.00	61	34	4	0
NM_001856	COL16A1	-0.12	0.08	3354	2903	3032	3388
NM_000093	COL5A1	-0.07	1.02	14317	13263	13133	27299
NM_004369	COL6A3	-0.11	0.42	31491	28566	126573	171367
NM_025147	COQ10B	-0.11	0.52	1232	1037	1073	1684
NM_017421	COQ3	-0.26	0.00	162	101	146	122
NM_005694	COX17	-0.83	0.00	265	115	447	434
NM_198076	COX20	-0.42	0.29	483	305	474	667
NM_004374	COX6C	-0.15	0.00	615	482	749	726
NM_001304	CPD	-0.08	0.38	1422	1232	2868	3946
NM_001079533	CPEB1	-1.04	0.30	107	33	514	725
NM_001286606	CRACR2B	-0.15	0.34	37	17	79	139
NM_020825	CRAMP1L	-0.04	0.07	836	724	859	1002
NM_014171	CRIPT	-0.04	0.00	400	328	518	595
NM_015989	CSAD	-0.12	0.00	161	111	343	347
NM_005211	CSF1R	-0.27	0.98	80	43	189	455
NM_152221	CSNK1E	-0.04	0.35	3499	3209	3105	4176
NM_000100	CSTB	-0.15	0.50	3010	2546	7004	10268
NM_172241	CTAGE1	-1.33	0.00	160	43	112	107
NM_004388	CTBS	-0.09	0.44	389	307	591	908
NM_001336	CTSZ	-0.02	0.70	6070	5747	10047	16785
NM_005869	CWC27	-0.61	0.00	79	32	83	104
NM_152434	CWF19L2	-0.22	0.00	282	195	306	338
NM_001037333	CYFIP2	-0.11	0.00	109	71	79	79
NM_000782	CYP24A1	-0.03	0.00	56	33	25	13
NM_001136264	DAZAP2	-0.04	0.03	3305	3031	3841	4124
NM_001290205	DCP1A	-0.07	0.23	1188	1028	855	1111
NM_001184781	DGCR2	-0.08	0.25	2247	1979	2161	2749
NM_001012957	DISC1	-0.37	0.00	44	18	62	79
NM_000108	DLD	-0.05	0.10	943	817	1370	1604

Table 6C: Differentially Downregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_020730	DLG3	-0.11	0.00	169	119	410	433
NM_013391	DMGDH	-0.43	0.00	67	30	121	120
NM_001081563	DMPK	-0.05	0.20	877	754	1666	2059
NM_012328	DNAJB9	-0.09	1.02	487	390	327	774
NM_194283	DNAJC21	-0.04	0.33	792	683	971	1344
NM_025219	DNAJC5	-0.12	0.37	3547	3082	3833	5196
NM_012100	DNPEP	-0.13	0.02	1509	1265	1886	2063
NM_052951	DNTTIP1	-0.13	0.02	519	406	607	701
NM_001280543	DPF3	-0.25	0.00	49	23	29	28
NM_001935	DPP4	-0.05	0.13	356	285	1689	1991
NM_001242901	DPP9-AS1	-0.17	0.00	425	319	451	390
NM_024094	DSCC1	-0.20	0.00	118	73	108	81
NM_001144769	DST	-0.22	0.36	9290	7703	22150	29075
NM_001256303	DTNB	-0.27	0.00	145	88	98	129
NM_001130987	DYSF	-0.20	0.99	695	530	2392	5033
NM_004215	EBAG9	-0.05	0.07	216	164	223	288
NM_001290360	EBF1	-0.12	0.00	896	734	821	887
NM_001199687	EDA2R	-0.09	0.00	264	199	663	688
NM_003566	EEA1	-0.11	0.25	1335	1129	2159	2754
NM_005864	EFS	-0.13	0.00	1084	892	1102	1135
NM_006709	EHMT2	-0.05	0.02	1521	1347	2021	2201
NM_001412	EIF1AX	-0.05	0.33	1150	1003	1400	1911
NM_003750	EIF3A	-0.60	0.00	2520	1547	4265	4044
NM_015904	EIF5B	-0.37	0.00	601	399	869	937
NM_175063	EMC10	-0.04	0.15	1293	1143	1508	1811
NM_006331	EMG1	-0.02	0.00	1080	964	1004	996
NM_020354	ENTPD7	-0.07	0.51	1171	1008	1362	2107
NM_015409	EP400	-0.10	0.20	2486	2167	2891	3514
NM_022140	EPB41L4A	-0.02	0.00	53	31	23	33
NM_018341	ERMARD	-0.17	0.14	273	195	327	427
NM_207582	ERVFRD-1	-1.15	0.00	67	16	21	24
NM_007036	ESM1	-0.34	1.94	2562	1887	1863	7612
NM_001003927	EVI2A	-0.14	0.00	47	24	112	85
NM_001441	FAAH	-0.49	0.12	44	16	33	59
NM_199336	FAHD2B	-0.15	0.30	143	95	135	214
NM_173822	FAM126B	-0.14	0.42	271	198	324	512
NM_001291832	FAM132B	-0.07	0.39	91	59	258	408
NM_032130	FAM186B	-0.84	0.00	62	19	35	20

Table 6C: Differentially Downregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001039762	FAM196A	-0.16	0.00	49	25	202	222
NM_001082967	FAM19A5	-0.37	1.19	407	262	106	314
NM_001040020	FAM3C	-0.02	0.33	1297	1162	1518	2059
NM_014722	FAM65B	-0.25	0.00	76	41	146	144
NM_174911	FAM84B	-0.21	0.00	46	22	27	28
NM_174905	FAM98C	-0.24	0.00	146	91	189	201
NM_001018113	FANCB	-0.30	0.00	221	140	52	57
NM_012166	FBXO10	-0.13	0.00	675	539	788	769
NM_033393	FHDC1	-0.03	0.30	44	24	19	44
NM_000801	FKBP1A	-0.03	0.41	4437	4137	9144	12506
NM_001458	FLNC	-0.07	0.25	135215	127692	109037	130883
NM_014053	FLVCR1	-0.22	0.00	191	126	110	142
NM_002027	FNTA	-0.05	0.13	542	451	693	854
NM_005938	FOXO4	-0.01	0.38	308	251	343	525
NM_005860	FSTL3	-0.05	0.25	3553	3252	1549	1998
NM_017647	FTSJ3	-0.10	0.00	1235	1042	1250	1248
NM_000152	GAA	-0.40	0.77	591	384	1387	2556
NM_001924	GADD45 A	-0.32	0.38	1772	1300	1375	1937
NM_138801	GALM	-0.29	0.00	212	134	597	627
NM_001145661	GATA2	-0.10	0.00	441	348	327	384
NM_021167	GATAD1	-0.26	0.30	694	505	705	974
NM_001190259	GCSAM	-0.36	0.00	77	38	67	76
NM_001001557	GDF6	-0.16	0.00	438	330	62	44
NM_001165038	GFRA2	-0.36	0.00	124	68	46	55
NM_001195087	GGACT	-0.04	0.01	151	110	108	146
NM_024835	GGNBP2	-0.04	0.24	1386	1232	1714	2179
NM_057169	GIT2	-0.04	0.19	1688	1511	2406	2924
NM_001261444	GNAL	-0.21	0.00	174	114	351	386
NM_001017998	GNG10	-0.04	0.00	323	258	655	695
NM_001172713	GOLGA4	-0.42	0.23	4504	3197	3872	4784
NM_014498	GOLIM4	-0.08	0.50	1160	994	1595	2431
NM_152281	GORAB	-0.16	0.26	208	145	183	274
NM_001099652	GPR137C	-0.10	0.00	50	27	67	85
NM_020752	GPR158	-0.83	0.00	46	11	4	11
NM_005282	GPR4	-0.56	0.00	151	74	146	166
NM_001142966	GREB1L	-0.08	0.00	51	28	62	65
NM_007325	GRIA3	-0.24	0.99	429	306	1040	2257
NM_001166247	GRIK2	-0.06	0.00	78	49	193	166
NM_001195541	GS1-	-0.37	1.22	66	31	35	126

Table 6C: Differentially Downregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
	259H13.2						
NM_004492	GTF2A2	-0.10	0.00	535	429	676	747
NM_207118	GTF2H5	-0.13	0.00	547	429	799	841
NM_004286	GTPBP1	-0.03	0.00	1725	1560	1963	1896
NM_033107	GTPBP10	-0.03	0.04	270	214	412	494
NM_012227	GTPBP6	-0.32	0.00	2625	1963	2554	2525
NM_014170	GTPBP8	-0.33	0.00	194	118	229	240
NM_006118	HAX1	-0.04	0.00	878	762	1504	1408
NM_005335	HCLS1	-0.29	0.00	47	21	31	26
NM_006037	HDAC4	-0.07	0.18	502	410	499	651
NM_001177479	HDX	-0.03	0.00	112	78	116	98
NM_004667	HERC2	-0.11	0.18	4379	3858	6971	8220
NM_001142853	HES6	-0.21	0.31	64	34	10	33
NM_138571	HINT3	-0.15	0.29	171	117	356	510
NM_005319	HIST1H1C	-0.11	0.11	15716	14224	8543	9530
NM_005320	HIST1H1D	-0.01	0.00	2306	2134	162	133
NM_003532	HIST1H3E	-0.65	0.75	794	440	52	128
NM_003535	HIST1H3J	-0.10	0.00	914	762	225	179
NM_001136180	HSBP1L1	-0.05	0.00	126	88	223	257
NM_025015	HSPA12A	-0.03	0.17	1144	1012	2161	2599
NM_021979	HSPA2	-0.06	0.00	615	514	372	388
NM_001291860	HSPG2	-0.13	0.46	26212	23496	31269	43654
NM_000203	IDUA	-0.38	0.50	329	206	559	898
NM_003897	IER3	-0.14	0.79	6943	6033	3138	5700
NM_001136265	IFFO2	-0.05	0.41	1768	1576	1618	2322
NM_000629	IFNAR1	-0.07	0.44	1096	942	1778	2593
NM_020153	IFT46	-0.05	0.00	378	305	674	743
NM_024660	IGFLR1	-0.12	0.00	45	23	21	24
NM_001007189	IGIP	-0.02	0.25	314	255	589	795
NM_001172128	IL16	-0.35	0.00	129	72	150	120
NM_001167986	INCA1	-0.20	0.00	99	59	100	124
NM_001101426	ISPD	-0.03	0.34	75	48	79	139
NM_002207	ITGA9	-0.51	0.00	50	19	15	7
NM_003724	JRK	-0.09	0.00	845	706	940	887
NM_002245	KCNK1	-0.34	1.06	158	92	60	177
NM_004823	KCNK6	-0.10	0.00	700	575	528	558
NM_199464	KCNRG	-0.34	0.13	79	40	94	140
NM_024076	KCTD15	-0.07	0.22	999	854	676	887

Table 6C: Differentially Downregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_014663	KDM4A	-0.07	0.06	553	454	774	904
NM_015015	KDM4B	-0.12	0.76	1017	839	1138	2096
NM_001040715	KIAA0895L	-1.15	0.03	1032	407	547	640
NM_007054	KIF3A	-0.04	0.00	133	95	264	299
NM_004984	KIF5A	-0.43	0.60	36	11	46	105
NM_004795	KL	-1.21	0.00	60	12	31	24
NM_172193	KLHDC1	-0.43	0.00	67	30	60	85
NM_003482	KMT2D	-0.27	0.04	4235	3338	4357	4695
NM_182931	KMT2E	-0.07	0.22	956	814	1237	1571
NM_001012991	KNOP1	-0.21	0.00	429	312	393	423
NM_002275	KRT15	-0.21	0.96	83	47	181	431
NM_005560	LAMA5	-0.23	0.65	347	243	129	259
NM_014017	LAMTOR2	-0.14	0.00	988	805	1468	1440
NM_006762	LAPTM5	-0.23	0.00	75	41	37	48
NM_001013693	LDLRAD2	-0.17	0.25	2048	1684	2498	3157
NM_032287	LDOC1L	-0.23	0.10	2009	1583	2078	2396
NM_052925	LENG8	-0.01	0.00	1367	1235	2785	2898
NM_022165	LIN7B	-0.05	0.08	141	101	225	292
NM_001292023	LOC100129940	-0.56	0.00	278	149	632	684
NM_001278795	LOC100996758	-0.24	0.00	106	62	12	6
NM_001291459	LOC101060376	-0.01	0.31	144	106	143	227
NM_001162371	LOC728392	-0.07	0.12	590	486	493	617
NM_024830	LPCAT1	-0.20	0.28	2873	2349	2354	3046
NM_001008701	LPHN1	-0.34	0.00	282	178	227	227
NM_001167671	LPP	-0.10	0.00	3484	3072	6619	6874
NM_014839	LPPR4	-0.21	0.00	191	127	223	194
NM_006726	LRBA	-0.12	0.17	912	747	1747	2118
NM_002332	LRP1	-0.08	0.54	60577	56575	116461	171215
NM_022143	LRRC4	-0.05	0.00	105	71	150	183
NM_001142928	LRRC61	-0.56	0.00	23	4	81	96
NM_144702	LRRC71	-0.38	0.00	303	188	119	157
NM_001268284	LRRC8E	-0.02	0.31	743	645	982	1342
NM_001137552	LRRFIP1	-0.39	0.30	1023	697	1206	1619
NM_001013615	LURAP1	-0.22	0.00	60	31	129	124
NM_001198759	LY75-	-0.23	0.05	175	113	175	229

Table 6C: Differentially Downregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
	CD302						
NM_002350	LYN	-0.03	0.48	223	172	312	514
NM_177476	LYNX1	-0.12	0.10	178	125	616	747
NM_014628	MAD2L1 BP	-0.19	0.00	569	429	705	774
NM_001113482	MANEAL	-0.40	0.48	40	15	62	124
NM_005923	MAP3K5	-0.24	0.00	425	303	324	314
NM_012326	MAPRE3	-0.10	0.20	186	133	657	852
NM_002379	MATN1	-0.79	0.35	377	177	125	207
NM_002380	MATN2	-0.33	0.05	528	359	643	756
NM_004831	MED26	-0.10	0.02	387	303	412	488
NM_017592	MED29	-0.02	0.00	1045	930	1770	1760
NM_001123364	METTL24	-0.29	0.00	75	39	85	105
NM_032718	MFSD9	-0.21	0.10	127	79	133	185
NM_014938	MLXIP	-0.05	0.40	2329	2103	2959	4140
NM_001932	MPP3	-0.09	0.02	313	241	225	281
NM_018000	MREG	-0.53	0.99	109	51	106	274
NM_014078	MRPL13	-0.01	0.00	537	459	734	675
NM_023937	MRPL34	-0.02	0.00	481	407	626	680
NM_016640	MRPS30	-0.03	0.00	575	488	674	682
NM_001282755	MTA3	-0.06	0.16	387	312	717	898
NM_021090	MTMR3	-0.14	0.40	1277	1055	1705	2421
NM_015458	MTMR9	-0.08	0.00	879	740	1071	1161
NM_005962	MXI1	-0.08	1.17	598	491	778	1932
NM_138768	MYEOV	-0.34	0.00	177	105	8	15
NM_001256267	MYPN	-0.03	0.52	603	514	630	1018
NM_001085365	MZT2A	-0.06	0.00	655	549	967	1070
NM_018177	N4BP2	-0.49	0.00	131	66	129	139
NM_001039703	NBPF10	-0.04	0.49	669	570	1042	1603
NM_015383	NBPF14	-0.09	0.15	476	382	834	1031
NM_001278267	NBPF20	-0.23	0.49	834	631	1190	1817
NM_001037501	NBPF8	-0.17	0.24	982	778	996	1296
NM_001277444	NBPF9	-0.02	0.14	905	799	1335	1599
NM_207363	NCKAP5	-0.10	0.00	192	138	116	144
NM_006312	NCOR2	-0.07	0.22	4358	3934	4960	6055
NM_004541	NDUFA1	-0.23	0.04	667	495	888	1017
NM_018838	NDUFA12	-0.07	0.00	715	599	990	980
NM_019056	NDUFB11	-0.07	0.00	576	476	647	658
NM_001278645	NDUFB9	-0.19	0.00	961	753	1928	1810

Table 6C: Differentially Downregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001278535	NEURL2	-0.74	0.40	71	25	44	89
NM_138714	NFAT5	-0.08	0.27	3955	3550	3901	4957
NM_006166	NFYB	-0.01	0.20	195	150	106	163
NM_002506	NGF	-0.21	0.00	2337	1879	1135	1214
NM_020345	NKIRAS1	-0.15	0.13	434	331	412	527
NM_198175	NME1	-0.03	0.00	2547	2333	3716	3896
NM_018055	NODAL	-0.99	0.00	51	11	17	9
NM_016167	NOL7	-0.10	0.00	1028	864	1285	1364
NM_153240	NPHP3	-0.21	0.39	593	442	832	1209
NM_130464	NPIPB3	-0.02	0.11	544	463	526	652
NM_001278794	NPY4R	-0.20	0.00	109	66	12	7
NM_173474	NTAN1	-0.16	0.07	590	457	1092	1262
NM_004822	NTN1	-0.96	0.08	67	19	6	22
NM_024815	NUDT18	-0.10	0.00	302	230	289	303
NM_032344	NUDT22	-0.14	0.00	476	367	626	566
NM_019094	NUDT4	-0.12	0.13	1386	1162	1418	1691
NM_001042483	NUPR1	-0.04	0.41	1550	1379	2785	3930
NM_007224	NXPH4	-0.30	0.75	147	87	73	170
NM_024578	OCEL1	-0.02	0.00	168	126	252	266
NM_020729	ODF2L	-0.10	0.42	309	235	345	542
NM_017570	OPLAH	-0.05	0.00	192	144	166	198
NM_153451	ORAOV1	-0.33	0.00	486	328	522	527
NM_022353	OSGEPL1	-0.21	0.01	160	103	146	190
NM_004337	OSGIN2	-0.32	0.08	827	586	1048	1224
NM_015430	PAMR1	-0.05	0.24	1386	1224	5906	7260
NM_001004318	PAPL	-1.30	0.00	74	16	10	2
NM_004562	PARK2	-0.19	0.36	21	5	73	131
NM_001127366	PAX3	-0.06	0.00	88	57	8	7
NM_006196	PCBP1	-0.09	0.00	5487	4937	6511	6797
NM_002600	PDE4B	-0.14	0.31	252	182	364	530
NM_001114107	PDLIM3	-0.05	0.00	219	167	329	375
NM_015032	PDS5B	-0.09	0.00	868	724	1031	930
NM_003681	PDXK	-0.02	0.05	6372	6019	6653	7177
NM_001195263	PDZD7	-0.42	0.45	223	129	231	383
NM_002567	PEBP1	-0.06	0.02	2519	2266	5501	5830
NM_032177	PHAX	-0.15	0.00	963	775	1531	1540
NM_006224	PITPNA	-0.10	0.30	1858	1604	2724	3554
NM_000299	PKP1	-0.33	1.61	196	119	8	68
NM_173542	PLBD2	-0.03	0.36	883	773	2909	3957
NM_001130081	PLD1	-0.81	0.00	112	42	73	98

Table 6C: Differentially Downregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_152666	PLD5	-0.36	0.98	49	21	54	153
NM_201380	PLEC	-0.10	0.60	12686	11469	21412	33088
NM_015549	PLEKHG3	-0.05	0.00	237	182	133	126
NM_002668	PLP2	-0.01	0.42	3124	2912	4382	6124
NM_025179	PLXNA2	-0.01	0.41	3653	3428	5203	7209
NM_017514	PLXNA3	-0.03	0.73	2184	1984	4999	8625
NM_002674	PMCH	-0.40	0.00	59	26	44	46
NM_000534	PMS1	-0.08	0.16	339	266	289	388
NM_006029	PNMA1	-0.02	0.34	1372	1238	1868	2543
NM_002687	PNN	-0.06	0.00	451	367	420	449
NM_203290	POLR1C	-0.11	0.00	602	483	613	686
NM_001281471	PPIP5K2	-0.19	0.00	908	709	1156	1205
NM_001291310	PPP2R2D	-0.21	0.00	1014	787	898	991
NM_001204103	PPT2	-0.02	0.00	469	396	356	392
NM_001127708	PRG4	-0.04	0.00	68	42	58	78
NM_002730	PRKACA	-0.03	0.09	1849	1675	2647	2989
NM_175922	PRR18	-0.41	0.37	54	23	37	76
NM_020200	PRTFDC1	-0.11	0.00	124	83	293	250
NM_012455	PSD4	-0.03	0.18	520	437	499	649
NM_021190	PTBP2	-0.13	0.00	164	113	216	196
NM_004778	PTGDR2	-0.24	0.00	265	179	166	129
NM_020440	PTGFRN	-0.08	0.21	1827	1591	4571	5541
NM_000320	QDPR	-0.04	0.00	744	640	1630	1497
NM_001076786	QSER1	-0.06	0.05	821	700	873	1009
NM_001256619	R3HCC1L	-0.14	0.42	414	315	306	484
NM_022456	RAB3IP	-0.47	0.25	152	80	79	131
NM_006325	RAN	-0.03	0.00	4674	4373	6364	6340
NM_006267	RANBP2	-0.26	0.07	1632	1249	3059	3394
NM_182663	RASSF5	-0.21	0.00	104	62	64	79
NM_016024	RBMX2	-0.40	0.14	326	200	231	312
NM_033544	RCCD1	-0.05	0.00	284	223	324	336
NM_001285439	RICTOR	-0.03	0.06	878	765	1354	1542
NM_001000	RPL39	-0.05	0.00	1113	974	1485	1425
NM_001128850	RRAD	-0.66	2.39	47	15	54	396
NM_016578	RSF1	-0.08	0.00	666	553	1086	1187
NM_001271838	RSRC1	-0.15	0.00	314	232	385	438
NM_001134888	RTL1	-0.37	0.00	256	157	266	264
NM_001015051	RUNX2	-0.02	0.00	166	124	505	508
NM_001031680	RUNX3	-0.20	0.67	188	125	69	153

Table 6C: Differentially Downregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001039517	RUSC1-AS1	-0.44	0.00	362	218	534	514
NM_022753	S100PBP	-0.07	0.00	566	465	566	604
NM_001201338	SAFB	-0.03	0.10	565	479	605	736
NM_178448	SAPCD2	-0.06	0.00	171	125	100	76
NM_001134707	SARDH	-0.72	0.44	199	90	19	48
NM_005505	SCARB1	-0.13	0.00	264	193	458	425
NM_001037582	SCD5	-0.04	0.49	284	224	378	617
NM_080489	SDCBP2	-0.08	0.42	103	68	100	179
NM_001271918	SEC11A	-0.03	0.03	985	866	1104	1240
NM_001033578	SGK3	-0.10	0.00	389	304	370	357
NM_019072	SGTB	-0.04	0.41	1257	1111	1493	2152
NM_015503	SH2B1	-0.24	0.09	1035	783	975	1146
NM_025164	SIK3	-0.02	0.36	749	653	1739	2408
NM_000617	SLC11A2	-0.15	0.17	705	556	1077	1335
NM_001206951	SLC16A3	-0.06	0.75	9943	9200	11315	19558
NM_020309	SLC17A7	-0.08	1.06	44	23	50	152
NM_005116	SLC23A2	-0.05	0.02	693	589	1691	1848
NM_052901	SLC25A25	-0.02	0.00	880	772	693	608
NM_001151	SLC25A4	-0.22	0.67	2057	1631	1237	2137
NM_006516	SLC2A1	-0.01	2.05	6356	6044	1329	5907
NM_152313	SLC36A4	-0.06	0.36	368	295	424	630
NM_144564	SLC39A3	-0.16	0.00	499	381	643	667
NM_000341	SLC3A1	-0.09	0.07	149	104	335	416
NM_005629	SLC6A8	-0.01	0.77	1157	1039	1462	2682
NM_014331	SLC7A11	-0.07	1.04	854	722	1227	2728
NM_004594	SLC9A5	-0.33	0.00	350	229	507	540
NM_013272	SLCO3A1	-0.25	0.37	672	493	961	1372
NM_014720	SLK	-0.03	0.22	1020	901	1497	1896
NM_001042493	SMIM8	-0.18	0.00	60	32	50	67
NM_001270691	SMOX	-0.10	0.73	664	540	549	1028
NM_003955	SOCS3	-0.06	0.00	1425	1245	458	431
NM_023016	SOWAHC	-0.04	0.79	445	368	428	852
NM_003112	SP4	-0.31	0.35	243	154	116	194
NM_023071	SPATS2	-0.04	0.56	1173	1035	1352	2157
NM_015001	SPEN	-0.09	0.18	2365	2078	2479	2996
NM_014230	SRP68	-0.11	0.39	3007	2624	2801	3889
NM_001170760	SRPK3	-0.04	0.24	72	45	83	135
NM_003769	SRSF9	-0.07	0.07	1723	1509	2157	2418

Table 6C: Differentially Downregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_198935	SS18L1	-0.12	0.58	456	355	289	512
NM_006396	SSSCA1	-0.21	0.00	683	515	832	832
NM_014188	SSU72	-0.05	0.00	2165	1946	3267	3318
NM_006011	ST8SIA2	-0.05	0.00	80	51	0	2
NM_020759	STARD9	-0.08	0.00	317	246	447	484
NM_001271977	STK25	-0.01	0.10	3098	2887	5840	6529
NM_003764	STX11	-0.16	0.00	76	44	23	18
NM_145251	STYX	-0.03	0.01	488	409	726	821
NM_003169	SUPT5H	-0.01	0.11	2766	2574	4255	4815
NM_003170	SUPT6H	-0.02	0.29	2072	1894	4132	5298
NM_017673	SWT1	-0.15	0.00	88	53	131	116
NM_182715	SYPL1	-0.16	0.16	1654	1362	2568	3050
NM_001162951	SYTL2	-0.25	0.00	41	18	131	124
NM_003487	TAF15	-0.19	0.00	619	471	828	830
NM_138572	TAF8	-0.01	0.00	448	378	566	579
NM_001123391	TBC1D3	-0.01	0.31	144	106	143	227
NM_001001418	TBC1D3C	-0.04	0.29	146	106	148	231
NM_013254	TBK1	-0.13	0.00	801	647	975	1007
NM_005149	TBX19	-0.63	0.64	74	29	56	126
NM_003196	TCEA3	-0.27	0.09	267	177	724	867
NM_001013632	TCTEX1D4	-0.21	0.00	61	32	75	72
NM_003211	TDG	-0.03	0.00	310	250	227	214
NM_015395	TECPR1	-0.04	0.00	729	626	1289	1390
NM_006528	TFPI2	-0.12	0.03	18837	16887	45731	47463
NM_013342	TFPT	-0.15	0.00	309	227	453	497
NM_006327	TIMM23	-0.32	0.00	1600	1171	1628	1542
NM_001164407	TLCD2	-0.26	0.02	380	264	349	418
NM_032027	TM2D1	-0.13	0.18	478	371	844	1067
NM_001144903	TM6SF1	-0.44	0.58	96	47	60	129
NM_024847	TMC7	-0.74	0.00	58	19	48	50
NM_017510	TMED9	-0.17	0.61	10691	9190	11866	18591
NM_178518	TMEM102	-0.24	0.69	211	139	85	185
NM_015421	TMEM186	-0.17	0.00	220	153	210	200
NM_014187	TMEM208	-0.10	0.00	828	684	1252	1229
NM_001080501	TMEM223	-0.23	0.00	427	305	453	503
NM_182614	TMEM255B	-0.01	0.00	34	17	141	172

Table 6C: Differentially Downregulated Genes in SR + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_018126	TMEM33	-0.20	0.00	1870	1501	1936	2009
NM_001039770	TMPPE	-0.30	0.00	310	205	266	268
NM_021103	TMSB10	-0.20	0.16	41209	35245	46245	52478
NM_001162501	TNRC6B	-0.01	0.17	1842	1691	3768	4453
NM_003291	TPP2	-0.05	0.00	904	777	1501	1582
NM_016058	TPRKB	-0.33	0.00	222	137	198	163
NM_033502	TRERF1	-0.13	0.00	619	492	697	762
NM_032765	TRIM52	-0.03	0.00	216	167	200	176
NM_004239	TRIP11	-0.06	0.15	986	851	1190	1447
NM_019083	TRMT13	-0.27	0.00	180	113	198	194
NM_030934	TRMT1L	-0.08	0.00	300	232	310	362
NM_001258205	TRPV3	-0.24	0.58	99	57	54	118
NM_001195131	TSTD3	-0.11	0.00	67	39	129	111
NM_001135993	TTC39C	-0.12	0.06	261	193	441	534
NM_016078	TVP23B	-0.12	0.18	486	381	499	649
NM_001008224	UACA	-0.01	0.19	2500	2317	6185	7357
NM_030930	UNC93B1	-0.21	0.17	399	288	453	590
NM_001085372	UQCC3	-0.30	0.00	212	133	272	238
NM_001089591	UQCRHL	-0.08	0.00	1684	1466	2111	2203
NM_000375	UROS	-0.27	0.00	579	412	1158	1200
NM_032747	USMG5	-0.04	0.00	335	270	634	588
NM_001286767	USP46	-0.12	0.23	394	304	541	725
NM_005800	USPL1	-0.06	0.00	465	381	422	458
NM_016037	UTP11L	-0.06	0.00	976	837	998	1035
NM_007124	UTRN	-0.03	0.24	3589	3322	7699	9442
NM_198152	UTS2B	-1.13	0.00	50	8	15	13
NM_003372	VBP1	-0.25	0.00	695	512	907	878
NM_001017980	VMA21	-0.14	0.00	1093	895	1163	1216
NM_001163922	VSIG10L	-0.30	0.43	119	68	112	198
NM_016628	WAC	-0.07	0.25	3135	2804	2914	3675
NM_001276376	WDR38	-0.37	0.00	626	418	915	863
NM_030581	WDR59	-0.19	0.17	656	500	824	1030
NM_145294	WDR90	-0.03	0.31	267	211	208	318
NM_194293	XIRP1	-0.11	0.00	501	397	358	401
NM_024029	YIPF2	-0.02	0.02	1419	1278	1720	1885
NM_032312	YIPF4	-0.13	0.35	412	317	482	704
NM_001276320	YOD1	-0.16	0.00	523	401	485	525
NM_145008	YPEL4	-0.95	0.00	89	28	29	48
NM_180990	ZACN	-0.17	0.00	585	448	1142	1168
NM_001164343	ZBTB20	-0.10	0.00	715	587	1612	1538

Table 6C: Differentially Downregulated Genes in SR + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_006977	ZBTB25	-0.02	0.26	110	77	154	235
NM_015070	ZC3H13	-0.25	0.00	928	696	1474	1494
NM_016353	ZDHHC2	-0.03	0.39	1262	1122	1312	1874
NM_182491	ZFAND2A	-0.01	0.43	505	430	553	848
NM_006885	ZFHX3	-0.11	0.30	2389	2061	2092	2760
NM_020917	ZFP14	-0.55	0.00	65	26	83	87
NM_031449	ZMIZ2	-0.21	0.60	1482	1171	1581	2575
NM_001195156	ZMYM6NB	-0.27	0.06	587	419	975	1122
NM_138462	ZMYND19	-0.17	0.00	1017	810	670	693
NM_015394	ZNF10	-0.74	0.00	71	25	92	126
NM_015852	ZNF117	-0.24	0.10	106	62	191	255
NM_003441	ZNF141	-0.48	0.00	104	50	81	100
NM_006991	ZNF197	-0.06	0.00	178	131	239	233
NM_182976	ZNF326	-0.27	0.00	222	144	320	316
NM_006955	ZNF33B	-0.09	0.00	115	77	141	159
NM_001256648	ZNF43	-0.35	0.00	138	78	94	85
NM_001143769	ZNF438	-0.08	0.03	189	138	225	283
NM_198458	ZNF497	-0.10	0.26	202	146	393	549
NM_032772	ZNF503	-0.22	0.19	273	188	867	1096
NM_053042	ZNF518B	-0.05	0.40	940	815	1044	1514
NM_001277090	ZNF550	-0.04	0.29	160	117	160	248
NM_001204817	ZNF587	-0.05	0.39	523	434	607	896
NM_001286054	ZNF595	-0.06	0.00	159	115	164	198
NM_178549	ZNF678	-0.62	0.00	97	41	83	113
NM_021916	ZNF70	-0.16	0.00	308	225	285	344
NM_182515	ZNF714	-0.53	0.03	249	135	125	168
NM_007131	ZNF75D	-0.26	0.00	233	153	308	292
NM_001004309	ZNF774	-0.07	0.00	60	35	67	68
NM_001004301	ZNF813	-0.10	0.00	115	76	148	128
NM_001201552	ZNF821	-0.23	0.00	133	82	154	172
NM_031218	ZNF93	-0.02	0.00	109	76	79	87
NM_001206998	ZNRF3	-0.32	0.00	163	97	243	268
NM_001112734	ZSCAN30	-0.25	0.00	182	116	354	342

Table 6D: Differentially Downregulated Genes in SEN + IL-2

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_153698	AAED1	0.01	-0.20	185	234	487	360
NM_020745	AARS2	0.06	-0.07	476	575	736	616
NM_001261434	AARSD1	0.16	-0.03	274	369	518	436
NM_001271696	ABCB7	0.12	-0.02	153	212	406	338
NM_019625	ABCB9	0.00	-0.32	161	167	279	179
NM_020297	ABCC9	0.23	-0.22	721	949	2161	1723
NM_001040876	ABCE1	0.32	-0.05	852	1178	1312	1152
NM_001025780	ABHD17B	0.00	-0.15	333	340	659	518
NM_013375	ABT1	0.00	-0.02	750	674	682	591
NM_000017	ACADS	0.00	-0.22	162	205	487	355
NM_016557	ACKR4	0.00	-1.33	35	38	235	68
NM_020186	ACN9	0.00	-0.12	140	108	177	124
NM_001037161	ACOT1	0.00	-0.02	153	162	289	233
NM_001037171	ACOT9	0.08	-0.09	949	1114	1897	1645
NM_001111034	ACP5	0.00	-0.44	0	9	146	78
NM_001100	ACTA1	0.31	-0.15	91	153	108	68
NM_001141945	ACTA2	0.28	-0.30	3308	4240	4529	3486
NM_005159	ACTC1	0.52	-0.29	1327	2069	807	582
NM_001199954	ACTG1	0.15	-0.20	124973	139507	229718	199115
NM_005736	ACTR1A	0.38	-0.10	2851	3921	8462	7590
NM_000666	ACY1	0.25	-0.06	258	371	1171	1017
NM_203488	ACYP1	0.16	-0.15	55	91	133	87
NM_001282447	ADAM33	0.00	-0.50	201	193	520	311
NM_014244	ADAMTS2	0.09	-0.06	10108	11082	9512	8822
NM_014243	ADAMTS3	0.23	-0.10	40	74	31	13
NM_004036	ADCY3	0.00	-0.07	1641	1537	1999	1771
NM_000671	ADH5	0.52	-0.23	1369	2133	3629	2924
NM_000026	ADSL	0.07	-0.14	873	1019	1545	1288
NM_022767	AEN	0.13	-0.17	1828	2156	2358	1946
NM_006796	AFG3L2	0.60	-0.12	965	1606	2423	2081
NM_018238	AGK	0.28	-0.03	238	351	551	466
NM_012199	AGO1	0.00	-0.05	1025	1124	2009	1795
NM_000687	AHCY	0.03	-0.15	1941	2136	3261	2765
NM_020731	AHRR	0.12	-0.27	687	842	1572	1192
NM_018836	AJAP1	0.00	-0.90	754	729	873	408
NM_000476	AK1	0.00	-0.11	922	1003	2805	2442
NM_174858	AK5	0.35	-0.61	837	1181	4461	2767
NM_005100	AKAP12	0.08	-0.03	2308	2601	5209	4882

Table 6D: Differentially Downregulated Genes in SEN + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001198656	AKAP2	0.24	-0.16	8623	10504	23286	20445
NM_001353	AKR1C1	0.43	-0.40	11991	16663	17729	13053
NM_001354	AKR1C2	0.27	-0.18	6380	7987	7310	6198
NM_000031	ALAD	0.17	-0.02	404	530	1622	1473
NM_153329	ALDH16A1	0.00	-0.02	213	182	297	240
NM_000693	ALDH1A3	0.16	-0.69	502	645	4477	2617
NM_000692	ALDH1B1	0.44	-0.42	1656	2418	2957	2067
NM_000694	ALDH3B1	0.21	-0.18	365	494	1870	1523
NM_001007027	ALG8	0.26	-0.02	313	444	886	780
NM_052947	ALPK2	0.16	-0.16	3052	3605	4188	3558
NM_000478	ALPL	0.00	-0.28	53	64	37	15
NM_005782	ALYREF	0.15	-0.12	1078	1312	1524	1285
NM_001267782	AMBRA1	0.32	-0.08	686	959	1574	1370
NM_001634	AMD1	0.27	-0.15	1591	2068	2543	2144
NM_016201	AMOTL2	0.26	-0.51	7839	9743	6636	4447
NM_022662	ANAPC1	0.15	-0.04	985	1211	1460	1298
NM_001256708	ANAPC10	0.00	-0.23	130	129	277	190
NM_001242374	ANAPC13	0.55	-0.08	611	1010	1291	1107
NM_013366	ANAPC2	0.11	-0.06	740	899	1674	1481
NM_016238	ANAPC7	0.31	-0.23	812	1118	1999	1577
NM_000037	ANK1	0.00	-0.10	49	53	137	94
NM_030816	ANKRD13C	0.28	-0.11	565	779	1029	854
NM_173505	ANKRD29	0.00	-0.54	0	4	416	237
NM_001164440	ANKRD33B	0.00	-0.07	318	358	591	490
NM_001039888	ANKRD34A	0.00	-0.31	97	110	366	244
NM_016466	ANKRD39	0.00	-0.10	230	271	474	377
NM_020337	ANKRD50	0.13	-0.05	1241	1488	2344	2116
NM_173595	ANKRD52	0.05	-0.03	5569	6021	6208	5828
NM_018685	ANLN	0.15	-1.06	3260	3819	3309	1477
NM_001286615	ANO4	0.09	-0.55	112	159	179	91
NM_006401	ANP32B	0.18	-0.05	759	961	1002	869
NM_007193	ANXA10	0.33	-0.10	3	17	158	111
NM_145869	ANXA11	0.02	-0.02	4548	4854	8306	7896
NM_001159	AOX1	0.00	-0.11	1056	1029	2053	1765
NM_004069	AP2S1	0.46	-0.17	1784	2636	5133	4338
NM_004722	AP4M1	0.32	-0.02	195	302	732	638
NM_001640	APEH	0.00	-0.10	1762	1878	3897	3438
NM_001244249	APEX1	0.00	-0.25	2375	2378	4756	3815
NM_014481	APEX2	0.26	-0.07	498	682	705	591
NM_144772	APOA1BP	0.00	-0.03	593	621	1398	1250

Table 6D: Differentially Downregulated Genes in SEN + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_004900	APOBEC3B	0.00	-0.54	249	236	297	163
NM_014508	APOBEC3C	0.44	-0.29	317	509	1408	1050
NM_152426	APOBEC3D	0.00	-0.25	66	76	108	63
NM_001136540	APOL1	0.33	-0.35	246	374	713	488
NM_030882	APOL2	0.01	-0.03	998	1114	1728	1560
NM_001195249	APTX	0.00	-0.04	371	416	759	652
NM_018011	ARGLU1	0.36	-0.06	648	938	1169	1017
NM_004308	ARHGAP1	0.18	-0.06	4080	4872	9533	8859
NM_014783	ARHGAP11A	0.00	-0.53	1030	1081	1142	710
NM_001199417	ARHGAP23	0.00	-0.07	3425	3226	3086	2758
NM_020754	ARHGAP31	0.33	-0.29	2208	2953	4527	3510
NM_004309	ARHGDIA	0.21	-0.09	7926	9529	12881	11758
NM_005224	ARID3A	0.00	-0.34	238	287	327	211
NM_005737	ARL4C	0.00	-0.13	588	542	1547	1298
NM_015161	ARL6IP1	0.23	-0.14	1327	1696	2084	1760
NM_001290020	ARMC4	0.00	-0.55	13	26	225	118
NM_001199196	ARMC6	0.60	-0.33	506	873	1404	1018
NM_001271466	ARMC9	0.09	-0.45	627	757	3232	2220
NM_016608	ARMCX1	0.18	-0.02	570	735	1160	1037
NM_014862	ARNT2	0.00	-0.56	594	583	482	274
NM_005718	ARPC4	0.17	-0.24	2515	3019	6199	5029
NM_030978	ARPC5L	0.17	-0.04	871	1087	1753	1569
NM_182616	ARPIN	0.29	-0.09	529	737	1248	1067
NM_001247996	ASAP1	0.21	-0.05	3120	3808	6549	6061
NM_017873	ASB6	0.12	-0.07	1758	2067	3271	2928
NM_018154	ASF1B	0.00	-0.28	642	675	362	246
NM_001095	ASIC1	0.65	-0.20	35	87	227	155
NM_004317	ASNA1	0.15	-0.17	1310	1586	3030	2521
NM_018136	ASPM	0.00	-0.98	1399	1311	1318	597
NM_018164	ASUN	0.17	-0.04	432	562	925	802
NM_014109	ATAD2	0.00	-0.15	2002	1911	1146	935
NM_024857	ATAD5	0.02	-0.20	230	287	125	78
NM_025092	ATHL1	0.00	-0.16	112	103	283	205
NM_001940	ATN1	0.00	-0.07	3451	3524	3402	3068
NM_001257335	ATP5A1	0.33	-0.34	3012	4000	7262	5506
NM_001686	ATP5B	0.21	-0.06	10702	12780	23492	21985
NM_001001973	ATP5C1	0.00	-0.19	1506	1636	2851	2335
NM_001688	ATP5F1	0.00	-0.01	865	851	1953	1793
NM_005175	ATP5G1	0.00	-0.80	303	337	796	396

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001190329	ATP5G3	0.56	-0.32	1599	2539	4750	3614
NM_006356	ATP5H	0.32	-0.14	422	611	1458	1205
NM_007100	ATP5I	0.30	-0.13	656	910	1635	1372
NM_018035	ATP5SL	0.41	-0.09	561	846	1364	1172
NM_001198909	ATP6V1F	0.04	-0.28	1068	1207	2660	2041
NM_005603	ATP8B1	0.14	-0.11	3192	3725	4369	3841
NM_198433	AURKA	0.00	-0.27	563	596	670	482
NM_001127229	AURKAIP1	0.00	-0.31	1228	1333	2367	1774
NM_001284526	AURKB	0.00	-0.66	776	825	501	266
NM_021913	AXL	0.26	-0.30	24844	30431	25272	20136
NM_003783	B3GALT2	0.00	-0.10	67	74	31	13
NM_001199873	B4GALT3	0.00	-0.25	1091	1169	1266	963
NM_004282	BAG2	0.03	-0.30	802	916	1375	1013
NM_025045	BAIAP2L2	0.00	-0.13	54	65	337	253
NM_001188	BAK1	0.30	-0.15	395	566	747	591
NM_003860	BANF1	0.17	-0.27	1226	1505	2250	1737
NM_006317	BASP1	0.46	-0.03	3439	4992	5336	4993
NM_001127240	BBC3	0.00	-0.24	32	48	96	55
NM_003567	BCAR3	0.15	-0.06	3909	4555	6958	6407
NM_005872	BCAS2	0.00	-0.05	238	290	495	408
NM_000055	BCHE	0.00	-0.13	41	64	378	288
NM_004765	BCL7C	0.29	-0.04	232	345	668	567
NM_004328	BCS1L	0.00	-0.14	362	407	693	551
NM_020139	BDH2	1.24	-0.13	19	80	200	142
NM_170733	BDNF	0.00	-0.30	3030	2961	3072	2346
NM_001003800	BICD2	0.33	-0.22	2183	2932	5180	4253
NM_001012271	BIRC5	0.00	-1.15	1350	1475	1637	664
NM_001253823	BLVRA	0.16	-0.11	454	586	1341	1129
NM_000713	BLVRB	0.00	-0.47	1026	1069	1628	1074
NM_017637	BNC2	0.00	-0.02	898	895	1445	1303
NM_016074	BOLA1	0.00	-0.30	118	115	175	107
NM_001031827	BOLA2	0.00	-0.06	909	927	1472	1290
NM_001039182	BOLA2B	0.00	-0.06	909	927	1472	1290
NM_001286746	BORA	0.06	-0.24	94	134	146	91
NM_006085	BPNT1	0.85	-0.05	291	617	728	621
NM_152743	BRAT1	0.47	-0.16	387	622	1329	1081
NM_000059	BRCA2	0.00	-0.72	438	377	316	153
NM_001173984	BRD7	0.00	-0.11	279	312	470	370
NM_032043	BRIP1	0.04	-0.24	483	575	275	187
NM_001197247	BTN3A2	0.00	-0.19	373	397	765	591

Table 6D: Differentially Downregulated Genes in SEN + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_004336	BUB1	0.07	-1.05	926	1081	911	383
NM_001211	BUB1B	0.03	-0.98	602	698	514	216
NM_004725	BUB3	0.25	-0.13	3362	4208	4245	3676
NM_032725	BUD13	0.00	-0.08	410	418	426	340
NM_001159767	BZW2	0.67	-0.11	583	1049	1348	1137
NM_001163812	C10orf2	-0.01	-0.07	442	373	393	314
NM_170746	C11orf31	0.00	-0.40	790	782	2248	1577
NM_024099	C11orf48	0.00	-0.15	508	564	809	643
NM_001135635	C11orf68	0.05	-0.06	1741	1941	2379	2124
NM_152318	C12orf45	0.31	-0.38	79	136	256	155
NM_001145199	C12orf75	0.00	-0.22	1155	1156	2034	1621
NM_001102366	C14orf159	0.22	-0.09	325	447	1275	1089
NM_001127393	C14orf2	0.00	-0.02	573	599	1056	939
NM_025108	C16orf59	0.00	-0.30	127	127	83	44
NM_001171251	C17orf53	0.00	-0.73	276	253	302	144
NM_017941	C17orf80	0.01	-0.06	241	297	418	338
NM_001086521	C17orf89	0.00	-0.27	265	262	697	503
NM_001290149	C19orf48	0.21	-0.16	687	895	510	390
NM_014047	C19orf53	0.00	-0.03	1591	1701	3367	3105
NM_205767	C19orf70	0.38	-0.34	248	390	923	647
NM_018186	C1orf112	0.00	-0.09	163	198	202	148
NM_152485	C1orf74	0.00	-0.01	71	79	139	102
NM_001212	C1QBP	0.02	-0.16	1402	1552	1888	1558
NM_015645	C1QTNF5	0.00	-0.35	469	461	1221	867
NM_001733	C1R	0.00	-0.50	739	693	613	373
NM_016546	C1RL	0.00	-0.17	174	138	618	477
NM_001258430	C20orf27	0.00	-0.25	634	646	1543	1187
NM_001143960	C2orf74	0.00	-0.08	111	145	310	240
NM_024616	C3orf52	0.00	-0.08	224	242	312	242
NM_017867	C4orf27	0.00	-0.29	159	196	297	196
NM_001735	C5	0.00	-0.03	44	33	112	78
NM_198566	C5orf34	0.00	-0.22	95	117	79	44
NM_138464	C5orf55	0.00	-0.43	68	58	94	46
NM_178508	C6orf1	0.20	-0.35	529	693	1647	1185
NM_001029863	C6orf120	0.00	-0.05	594	612	1094	950
NM_177965	C8orf37	0.04	-0.45	26	47	92	44
NM_001190972	C8orf88	0.00	-0.29	147	173	127	74
NM_016390	C9orf114	0.07	-0.01	1047	1211	1720	1571
NM_001048265	C9orf116	0.00	-0.18	12	19	106	65
NM_017998	C9orf40	0.17	-0.55	195	272	314	172

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_032307	C9orf64	0.32	-0.06	335	494	603	501
NM_182505	C9orf85	0.00	-0.01	100	98	158	118
NM_001100619	CABLES1	0.00	-0.13	1496	1589	1759	1484
NM_182527	CABP7	0.00	-0.07	79	89	220	165
NM_000723	CACNB1	0.00	-0.10	179	154	368	285
NM_001080543	CACTIN	0.19	-0.11	397	528	595	479
NM_004341	CAD	0.07	-0.07	2925	3251	3519	3159
NM_183394	CADPS	0.00	-0.26	168	211	1955	1508
NM_033138	CALD1	0.29	-0.03	11161	14028	19721	18841
NM_005184	CALM3	0.11	-0.15	6502	7321	12973	11353
NM_020439	CAMK1G	0.00	-0.63	11	15	148	68
NM_024766	CAMKMT	0.00	-0.13	28	33	121	79
NM_014550	CARD10	0.01	-0.39	206	257	162	91
NM_024537	CARS2	0.13	-0.25	1424	1696	3508	2782
NM_144508	CASC5	0.15	-0.86	529	674	670	314
NM_001080125	CASP8	0.47	-0.04	86	162	272	214
NM_014292	CBX6	0.18	-0.06	1274	1571	2851	2566
NM_001002880	CBY1	0.00	-0.04	320	368	564	475
NM_021174	CCAR2	0.11	-0.13	2194	2538	3438	2972
NM_133459	CCBE1	0.25	-0.34	2421	3064	4280	3203
NM_001287390	CCBL1	0.00	-0.16	229	267	586	453
NM_025004	CCDC15	0.03	-0.42	114	155	146	79
NM_138493	CCDC167	0.00	-0.04	136	151	401	327
NM_152499	CCDC24	0.00	-0.19	36	36	225	155
NM_024296	CCDC28B	0.23	-0.33	79	129	160	94
NM_175884	CCDC71L	0.06	-0.15	508	607	1117	909
NM_001080433	CCDC85A	0.50	-0.58	335	558	603	346
NM_006848	CCDC85B	0.42	-0.18	669	1004	965	762
NM_024098	CCDC86	0.08	-0.21	1184	1371	1310	1031
NM_001135597	CCDC88A	0.03	-0.06	1271	1424	2379	2122
NM_018074	CCDC94	0.29	-0.02	239	354	435	364
NM_001105564	CCHCR1	0.38	-0.08	500	743	988	837
NM_002982	CCL2	0.15	-0.23	98	147	160	102
NM_001237	CCNA2	0.28	-0.80	898	1208	778	388
NM_031966	CCNB1	0.24	-0.93	1156	1499	1849	880
NM_004701	CCNB2	0.20	-0.57	355	481	489	277
NM_001287427	CCND3	0.00	-0.41	1606	1704	2564	1797
NM_001134375	CCNJ	0.00	-0.09	175	138	237	177
NM_005125	CCS	0.00	-0.08	383	349	863	725
NM_006431	CCT2	0.15	-0.02	2352	2781	3571	3327

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_006430	CCT4	0.21	-0.03	3016	3695	5648	5292
NM_012073	CCT5	0.36	-0.26	4545	6112	6971	5599
NM_001762	CCT6A	0.32	-0.05	1760	2369	3232	2937
NM_001166285	CCT7	0.19	-0.08	3521	4249	7420	6747
NM_133493	CD109	0.03	-0.05	1845	2033	8131	7582
NM_020404	CD248	0.02	-0.68	5111	5422	9229	5532
NM_006110	CD2BP2	0.10	-0.08	1254	1468	2123	1871
NM_033331	CDC14B	0.00	-0.17	420	462	936	741
NM_001255	CDC20	0.11	-1.31	886	1061	786	270
NM_021873	CDC25B	0.00	-0.40	1510	1513	1597	1109
NM_001287582	CDC25C	0.00	-0.56	54	69	139	67
NM_001039802	CDC42	0.22	-0.02	2680	3308	5632	5301
NM_152243	CDC42EP1	0.36	-0.17	1763	2434	2699	2238
NM_006449	CDC42EP3	0.32	-0.14	1544	2083	3261	2780
NM_001178010	CDC45	0.00	-0.10	427	497	191	137
NM_152562	CDCA2	0.36	-0.21	336	508	626	471
NM_031299	CDCA3	0.19	-0.91	344	463	445	194
NM_080668	CDCA5	0.10	-0.72	803	965	753	397
NM_031942	CDCA7	0.00	-0.29	144	182	25	6
NM_001127370	CDCA7L	0.23	-0.10	697	921	370	287
NM_001256875	CDCA8	0.00	-0.89	849	826	645	296
NM_022478	CDH24	0.00	-0.07	228	237	391	312
NM_001786	CDK1	0.08	-0.42	349	437	314	189
NM_001798	CDK2	0.30	-0.34	1220	1639	1040	734
NM_000075	CDK4	0.28	-0.29	1626	2130	3438	2643
NM_001278167	CDK5RAP1	0.46	-0.03	264	434	751	651
NM_001220778	CDKN1A	0.13	-0.03	13883	15626	32012	30770
NM_080656	CDKN2AIPNL	0.03	-0.03	189	242	343	279
NM_001262	CDKN2C	0.22	-0.33	430	579	339	220
NM_005192	CDKN3	0.03	-0.99	275	339	331	131
NM_207327	CDPF1	0.00	-0.72	98	123	279	133
NM_030928	CDT1	0.00	-0.47	740	794	297	172
NM_005195	CEBPD	0.42	-0.23	62	119	125	76
NM_018689	CEMIP	0.17	-0.38	9699	11231	3955	2869
NM_001809	CENPA	0.00	-0.46	91	121	96	46
NM_001813	CENPE	0.00	-0.68	558	593	665	357
NM_016343	CENPF	0.00	-0.97	1916	1987	2882	1362
NM_022909	CENPH	0.00	-0.78	104	140	189	81
NM_006733	CENPI	0.00	-0.45	231	261	293	172

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_024053	CENPM	0.55	-0.91	230	407	329	139
NM_001100624	CENPN	0.17	-0.24	1035	1282	1179	900
NM_001199803	CENPO	0.00	-0.22	1199	1251	1458	1139
NM_025082	CENPT	0.53	-0.03	741	1193	1984	1806
NM_001012507	CENPW	0.38	-0.96	141	235	237	92
NM_152446	CEP128	0.00	-0.55	225	198	256	137
NM_018718	CEP41	0.38	-0.04	141	235	618	525
NM_018131	CEP55	0.00	-1.08	953	966	734	296
NM_001098802	CEP78	0.30	-0.02	203	308	514	436
NM_032816	CEP89	0.19	-0.08	334	450	990	841
NM_005507	CFL1	0.17	-0.09	15387	17812	29260	26863
NM_001243645	CFL2	0.32	-0.13	1962	2633	4663	4042
NM_005483	CHAF1A	0.09	-0.13	1046	1225	707	566
NM_005441	CHAF1B	0.19	-0.34	332	447	272	172
NM_017812	CHCHD3	0.07	-0.03	540	649	1171	1035
NM_001114122	CHEK1	0.00	-0.26	637	623	462	325
NM_024591	CHMP6	0.00	-0.31	553	556	925	662
NM_001206602	CHN1	0.00	-0.23	416	409	586	431
NM_032630	CINP	0.17	-0.08	411	539	1017	865
NM_001136498	CISD3	0.12	-0.22	716	875	1647	1299
NM_013324	CISH	0.93	-0.42	31	95	56	24
NM_001206999	CIT	0.26	-0.99	1141	1497	1739	791
NM_006079	CITED2	0.00	-0.41	4428	4394	7932	5734
NM_001098525	CKAP2	0.02	-0.03	967	1090	1115	985
NM_152515	CKAP2L	0.05	-0.42	621	729	493	311
NM_001827	CKS2	0.00	-0.37	561	593	586	390
NM_005602	CLDN11	0.07	-1.05	4182	4626	2909	1299
NM_002975	CLEC11A	0.25	-0.02	1071	1403	1601	1449
NM_175060	CLEC14A	0.02	-1.46	125	167	370	104
NM_001287594	CLIC1	0.31	-0.40	6592	8471	17949	13255
NM_015526	CLIP3	0.09	-0.21	487	596	2493	2015
NM_000086	CLN3	0.15	-0.09	666	836	1454	1250
NM_017882	CLN6	0.00	-0.15	716	670	923	743
NM_001258394	CLPB	0.19	-0.13	743	953	1414	1181
NM_022111	CLSPN	0.14	-0.26	892	1088	507	362
NM_182523	CMC1	0.43	-0.27	40	84	141	85
NM_020188	CMC2	0.00	-0.30	794	860	796	571
NM_018235	CNDP2	0.01	-0.17	1479	1621	2903	2418
NM_173515	CNKSR3	0.07	-0.07	435	530	320	250
NM_001299	CNN1	0.00	-0.40	1730	1748	1308	895

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_004368	CNN2	0.11	-0.61	2892	3309	5484	3425
NM_017546	CNOT11	0.00	-0.07	632	629	747	627
NM_007018	CNTRL	0.04	-0.33	273	340	443	296
NM_016565	COA4	0.25	-0.07	630	845	1198	1033
NM_023077	COA7	0.45	-0.13	292	474	611	484
NM_015386	COG4	0.31	-0.02	924	1270	2489	2292
NM_030582	COL18A1	0.00	-0.01	189	231	811	713
NM_130386	COLEC12	0.00	-1.76	38	28	164	31
NM_152516	COMMD1	0.19	-0.18	270	371	803	627
NM_006837	COPS5	0.00	-0.08	874	864	1321	1140
NM_006833	COPS6	0.03	-0.16	1970	2160	4889	4159
NM_016035	COQ4	0.04	-0.29	203	260	1023	750
NM_052820	CORO2A	0.04	-0.12	201	257	383	294
NM_016468	COX16	0.00	-0.10	341	350	707	580
NM_001863	COX6B1	0.40	-0.12	1002	1459	3288	2848
NM_001867	COX7C	0.05	-0.03	662	776	1123	996
NM_004074	COX8A	0.58	-0.40	1081	1764	2993	2116
NM_001177382	CPEB2	0.00	-0.02	1026	967	1029	915
NM_152727	CPNE2	0.11	-0.07	599	734	851	719
NM_014427	CPNE7	0.00	-0.06	664	703	2317	2079
NM_153634	CPNE8	0.00	-0.23	282	275	593	438
NM_001122633	CPS1	0.28	-0.13	102	166	320	240
NM_001256456	CPSF3L	0.57	-0.09	995	1625	2406	2107
NM_001876	CPT1A	0.04	-0.06	2237	2467	4074	3697
NM_198148	CPXM2	0.07	-1.27	73	109	237	72
NM_001144958	CRACR2A	0.23	-0.01	174	256	514	438
NM_014675	CROCC	0.03	-0.02	136	181	387	320
NM_004077	CS	0.13	-0.15	1943	2282	3980	3408
NM_001316	CSE1L	0.14	-0.14	2065	2432	3818	3283
NM_022048	CSNK1G1	0.15	-0.03	755	936	1425	1277
NM_001325	CSTF2	0.21	-0.06	333	455	709	599
NM_015343	CTDNEP1	0.36	-0.22	854	1217	1593	1250
NM_001142544	CTF1	0.00	-0.43	70	72	191	107
NM_175859	CTPS2	0.33	-0.04	240	365	620	525
NM_001814	CTSC	0.19	-0.35	921	1163	607	412
NM_001912	CTSL	0.00	-0.07	3362	3189	9600	8854
NM_005231	CTTN	0.23	-0.04	8090	9832	20056	19079
NM_024040	CUEDC2	0.26	-0.37	596	811	2075	1486
NM_001079872	CUL4B	0.23	-0.06	1410	1799	3558	3222
NM_015921	CUTA	0.00	-0.16	1895	1814	3097	2606

Table 6D: Differentially Downregulated Genes in SEN + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_018294	CWF19L1	0.00	-0.33	280	332	428	285
NM_001914	CYB5A	0.63	-0.16	109	221	576	445
NM_030579	CYB5B	0.47	-0.06	890	1366	2360	2113
NM_016230	CYB5R4	0.00	-0.14	185	184	349	262
NM_001916	CYC1	0.00	-0.11	3330	3349	5347	4743
NM_018947	CYCS	0.00	-0.11	1221	1262	1601	1360
NM_019885	CYP26B1	0.00	-0.79	115	138	501	242
NM_001554	CYR61	0.00	-0.05	31391	30861	12856	12074
NM_032412	CYSTM1	0.29	-0.15	473	665	3088	2612
NM_004227	CYTH3	0.00	-0.12	2292	2424	3592	3120
NM_032552	DAB2IP	0.00	-0.03	546	588	1633	1475
NM_001009996	DALRD3	0.00	-0.03	848	845	1755	1588
NM_001348	DAPK3	0.29	-0.04	1889	2474	3371	3100
NM_018122	DARS2	0.00	-0.14	401	392	801	645
NM_018959	DAZAP1	0.10	-0.26	1886	2179	1612	1231
NM_006716	DBF4	0.00	-0.15	169	177	166	113
NM_017741	DCAF16	0.26	-0.04	492	678	747	643
NM_022836	DCLRE1B	0.00	-0.07	552	531	468	381
NM_001261412	DCTN2	0.43	-0.06	2286	3274	6249	5754
NM_006571	DCTN6	0.00	-0.03	453	454	909	795
NM_024096	DCTPP1	0.57	-0.17	422	723	809	636
NM_005804	DDX39A	0.23	-0.58	1537	1946	2019	1238
NM_004640	DDX39B	0.07	-0.06	1352	1552	2489	2229
NM_019070	DDX49	0.00	-0.25	692	772	1485	1140
NM_152678	DENND6A	0.09	-0.17	227	297	347	255
NM_001114120	DEPDC1	0.00	-0.77	200	233	279	128
NM_022783	DEPTOR	0.09	-0.24	42	70	96	55
NM_001927	DES	0.43	-0.07	362	569	135	94
NM_005675	DGCR6	0.00	-0.17	118	124	299	216
NM_001361	DHODH	0.00	-0.14	252	219	250	181
NM_024308	DHRS11	0.74	-0.17	35	92	154	102
NM_021004	DHRS4	0.00	-0.25	192	229	337	233
NM_001193636	DHRS4L2	0.17	-0.42	103	156	308	185
NM_003587	DHX16	0.40	-0.03	1402	2005	2196	2006
NM_004941	DHX8	0.13	-0.16	1247	1494	2219	1852
NM_001042517	DIAPH3	0.03	-0.63	1363	1521	1050	603
NM_014473	DIMT1	0.08	-0.02	680	809	1034	917
NM_004675	DIRAS3	0.00	-0.23	7	11	175	113
NM_012242	DKK1	0.01	-0.12	16497	17002	18658	16700
NM_001146015	DLGAP5	0.00	-0.98	520	543	603	257

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_178120	DLX1	0.00	-0.32	58	65	119	67
NM_018198	DNAJC11	0.09	-0.06	1429	1652	2298	2055
NM_018163	DNAJC17	0.15	-0.01	146	208	266	213
NM_032317	DNAJC30	0.00	-0.07	122	159	480	390
NM_001278464	DNM1L	0.13	-0.02	1825	2155	3107	2880
NM_001130823	DNMT1	0.04	-0.19	3614	3923	2566	2102
NM_001282062	DOC2A	0.51	-0.08	100	189	225	168
NM_005128	DOPEY2	0.03	-0.13	917	1037	2926	2512
NM_003863	DPM2	0.42	-0.18	544	826	1377	1103
NM_153741	DPM3	0.54	-0.20	176	319	745	569
NM_032574	DPY30	0.00	-0.06	780	792	1113	963
NM_004147	DRG1	0.21	-0.12	963	1227	1689	1427
NM_001388	DRG2	0.10	-0.18	761	914	1564	1261
NM_001939	DRP2	0.00	-0.13	76	90	1015	834
NM_032160	DSEL	0.02	-0.19	2349	2550	4151	3460
NM_080664	DTD2	0.19	-0.06	155	225	387	311
NM_016448	DTL	0.28	-0.37	839	1135	518	342
NM_012145	DTYMK	0.19	-0.05	705	901	1177	1028
NM_017803	DUS2	0.00	-0.44	384	452	701	449
NM_020175	DUS3L	0.17	-0.08	342	455	408	325
NM_007026	DUSP14	0.12	-0.24	3052	3523	6002	4867
NM_006519	DYNLT1	0.23	-0.13	1405	1787	2627	2240
NM_001950	E2F4	0.36	-0.04	1548	2145	2394	2179
NM_001258316	ECT2	0.35	-0.01	599	862	940	835
NM_003797	EED	0.00	-0.21	165	169	193	128
NM_001959	EEF1B2	0.46	-0.03	684	1058	2015	1835
NM_032378	EEF1D	0.19	-0.14	1974	2423	3321	2834
NM_001404	EEF1G	0.44	-0.04	6878	9651	16581	15728
NM_021937	EEFSEC	0.00	-0.16	506	508	944	752
NM_001258354	EFTUD2	0.26	-0.02	2650	3368	5207	4906
NM_005228	EGFR	0.06	-0.09	4980	5431	5971	5368
NM_080732	EGLN2	0.04	-0.10	1313	1473	2365	2059
NM_001166415	EHHADH	0.00	-0.03	73	61	252	198
NM_024757	EHMT1	0.00	-0.18	1654	1733	2616	2155
NM_153232	EID2	0.00	-0.06	249	260	333	264
NM_006893	EIF2D	0.33	-0.17	682	966	1481	1201
NM_001568	EIF3E	0.00	-0.19	657	725	1458	1170
NM_003754	EIF3F	0.22	-0.28	748	977	1239	924
NM_003755	EIF3G	0.26	-0.05	2266	2896	4078	3747
NM_003757	EIF3I	0.18	-0.09	3964	4708	7709	6965

Table 6D: Differentially Downregulated Genes in SEN + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_013234	EIF3K	0.52	-0.10	661	1064	2071	1793
NM_016091	EIF3L	0.38	-0.03	1911	2668	4835	4508
NM_001416	EIF4A1	0.43	-0.29	5254	7364	12022	9547
NM_001970	EIF5A	0.28	-0.18	3606	4616	7495	6346
NM_001099692	EIF5AL1	0.08	-0.01	4612	5115	8013	7662
NM_002212	EIF6	0.13	-0.01	3082	3571	5636	5338
NM_001128636	ELFN1	0.00	-0.50	178	186	651	397
NM_052906	ELFN2	0.00	-0.46	4	9	87	41
NM_001278939	ELN	0.50	-0.41	2316	3480	641	416
NM_001256399	ELOVL1	0.00	-0.11	4142	4262	7144	6360
NM_032048	EMILIN2	0.00	-0.77	940	947	1813	969
NM_019063	EML4	0.00	-0.06	1138	1220	1244	1083
NM_001424	EMP2	0.12	-0.08	1343	1591	1533	1329
NM_001426	EN1	0.49	-0.09	285	475	930	778
NM_000118	ENG	0.13	-0.05	13055	14733	15252	14379
NM_017512	ENOSF1	0.00	-0.07	1286	1269	1004	861
NM_182314	ENOX2	0.00	-0.01	208	195	428	359
NM_006209	ENPP2	0.05	-0.31	491	587	1547	1137
NM_004444	EPHB4	0.15	-0.15	402	521	468	359
NM_004447	EPS8	0.22	-0.12	2317	2882	5800	5102
NM_005702	ERAL1	0.24	-0.03	824	1084	1524	1372
NM_000400	ERCC2	0.21	-0.18	2075	2576	4122	3460
NM_017669	ERCC6L	0.00	-0.53	335	284	179	92
NM_001017420	ESCO2	0.00	-0.16	151	190	102	63
NM_001984	ESD	0.00	-0.01	1959	2043	3779	3545
NM_012291	ESPL1	0.00	-0.59	690	640	424	233
NM_001282451	ESRRA	0.00	-0.16	603	662	832	660
NM_005238	ETS1	0.19	-0.06	4177	5002	4465	4065
NM_001135032	EVA1A	0.32	-0.09	2051	2744	3371	2991
NM_018166	EVA1B	0.04	-0.32	593	696	1160	839
NM_013986	EWSR1	0.40	-0.34	1983	2806	3094	2296
NM_017820	EXD3	0.11	-0.10	60	95	220	161
NM_130398	EXO1	0.29	-0.43	322	467	171	94
NM_014285	EXOSC2	0.28	-0.23	524	726	1002	762
NM_020158	EXOSC5	0.00	-0.16	215	176	354	262
NM_058219	EXOSC6	0.47	-0.16	332	540	626	488
NM_015004	EXOSC7	0.22	-0.07	373	510	780	656
NM_001440	EXTL3	0.40	-0.11	1829	2599	5143	4530
NM_000137	FAH	0.36	-0.30	302	460	2019	1519
NM_016044	FAHD2A	0.02	-0.25	249	307	620	451

Table 6D: Differentially Downregulated Genes in SEN + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001002034	FAM109B	0.01	-0.09	677	770	1061	898
NM_052966	FAM129A	0.23	-0.19	1922	2428	5659	4730
NM_001166698	FAM13C	0.00	-0.57	10	11	79	33
NM_001001710	FAM166A	0.00	-0.19	622	617	684	523
NM_207368	FAM195B	0.50	-0.10	991	1540	3354	2952
NM_016613	FAM198B	0.00	-0.16	228	251	1736	1425
NM_001291328	FAM228B	0.67	-0.20	100	211	618	466
NM_153711	FAM26E	0.46	-0.16	270	443	942	752
NM_052943	FAM46B	0.73	-0.36	175	360	127	70
NM_030797	FAM49A	0.00	-0.46	11	23	195	107
NM_001013622	FAM53A	0.97	-0.17	17	62	42	20
NM_019013	FAM64A	0.16	-1.32	173	244	245	72
NM_001193523	FAM65A	0.43	-0.02	2191	3147	4211	3944
NM_032809	FAM73B	0.53	-0.10	321	544	836	693
NM_030919	FAM83D	0.12	-0.70	450	566	545	283
NM_000136	FANCC	0.00	-0.11	227	271	264	196
NM_001018115	FANCD2	0.16	-0.38	317	421	327	205
NM_001271783	FAR2	0.00	-0.07	191	223	349	275
NM_005687	FARSB	0.23	-0.21	627	832	1518	1201
NM_001136193	FASTKD2	0.26	-0.12	649	879	1266	1054
NM_001008781	FAT3	0.00	-0.16	267	306	1148	924
NM_001291285	FAT4	0.10	-0.50	1098	1297	1512	974
NM_001436	FBL	0.34	-0.01	1064	1480	1221	1098
NM_017556	FBLIM1	0.40	-0.02	968	1412	3271	3044
NM_006486	FBLN1	0.00	-0.85	376	396	524	242
NM_001999	FBN2	0.00	-1.22	2156	2154	2350	922
NM_017703	FBXL12	0.38	-0.01	232	367	686	597
NM_024963	FBXL18	0.00	-0.02	1035	989	1770	1606
NM_018998	FBXW5	0.30	-0.15	2712	3547	5736	4928
NM_001031734	FDX1L	0.14	-0.13	258	345	838	677
NM_001258013	FDXR	0.10	-0.47	119	168	430	259
NM_004111	FEN1	0.19	-0.46	1865	2292	1339	880
NM_002005	FES	0.00	-0.58	370	399	636	364
NM_002006	FGF2	-0.01	-0.05	5573	5301	8776	8185
NM_004464	FGF5	0.34	-0.12	4322	5738	3329	2895
NM_002009	FGF7	0.00	-0.11	756	766	1131	946
NM_001287492	FIGNL1	0.00	-0.03	325	353	225	174
NM_001042459	FILIP1L	0.00	-0.25	573	558	1695	1307
NM_015258	FKBP15	0.25	-0.05	1391	1797	3111	2835
NM_001079802	FKTN	0.00	-0.09	419	485	1312	1120

Table 6D: Differentially Downregulated Genes in SEN + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_025207	FLAD1	0.10	-0.08	426	532	1034	878
NM_005803	FLOT1	0.39	-0.15	1488	2112	4993	4283
NM_002019	FLT1	0.00	-0.26	92	113	148	91
NM_001142500	FLYWCH2	0.00	-0.35	200	245	497	331
NM_005438	FOSL1	0.33	-0.16	4479	5899	3947	3338
NM_001451	FOXF1	0.00	-0.24	91	81	177	113
NM_202002	FOXM1	0.26	-0.86	2104	2690	2175	1098
NM_001102371	FOXRED2	0.00	-0.37	767	775	1813	1292
NM_001018078	FPGS	0.23	-0.23	1094	1406	2521	2006
NM_174938	FRMD3	0.15	-0.29	654	819	851	614
NM_001267046	FRMD6	0.24	-0.05	10248	12522	23265	21989
NM_023037	FRY	0.10	-0.22	263	342	674	503
NM_003088	FSCN1	0.12	-0.22	5767	6530	6033	4967
NM_003902	FUBP1	0.06	-0.16	2579	2854	3157	2651
NM_001170634	FUS	0.08	-0.03	4400	4886	5644	5299
NM_001466	FZD2	0.00	-0.05	1403	1392	1381	1216
NM_005754	G3BP1	0.55	-0.06	1586	2498	2968	2675
NM_007278	GABARAP	0.23	-0.03	1187	1521	3402	3155
NM_000403	GALE	0.11	-0.23	637	779	938	713
NM_000154	GALK1	0.00	-0.14	484	531	1031	839
NM_054110	GALNT15	0.36	-0.65	79	140	749	414
NM_014568	GALNT5	0.00	-0.13	1964	2030	7636	6706
NM_007210	GALNT6	0.00	-0.27	368	396	711	516
NM_000155	GALT	0.04	-0.12	248	311	830	677
NM_000156	GAMT	0.07	-0.22	105	148	630	468
NM_014364	GAPDHS	0.24	-0.27	37	70	131	78
NM_006478	GAS2L1	0.09	-0.01	612	738	1154	1035
NM_174942	GAS2L3	0.38	-0.70	136	228	191	87
NM_004564	GATB	0.26	-0.29	303	433	853	619
NM_001282629	GBGT1	0.66	-0.03	60	136	141	102
NM_002053	GBP1	0.00	-0.15	339	365	526	408
NM_004120	GBP2	0.00	-0.29	65	70	243	157
NM_000159	GCDH	0.00	-0.06	204	238	458	373
NM_000557	GDF5	0.00	-1.00	8	13	177	63
NM_001494	GDI2	0.22	-0.02	4008	4895	6391	6041
NM_001252156	GEMIN5	0.11	-0.09	910	1090	1439	1233
NM_018988	GFOD1	0.00	-0.06	104	133	152	109
NM_001099781	GGT5	0.15	-0.90	21	43	81	26
NM_021067	GINS1	0.00	-0.11	311	330	148	102
NM_016095	GINS2	0.00	-0.21	380	411	260	179

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_032336	GINS4	0.00	-0.07	388	398	378	301
NM_001080383	GJC1	0.11	-0.08	1437	1688	1720	1497
NM_000168	GLI3	0.00	-0.07	759	722	1100	943
NM_006708	GLO1	0.37	-0.09	892	1280	2770	2440
NM_015710	GLTSCR2	0.79	-0.03	368	736	990	871
NM_002065	GLUL	0.31	-0.41	2045	2708	3789	2686
NM_001146686	GMNC	0.00	-0.76	3	11	173	74
NM_015895	GMNN	0.00	-0.49	411	471	254	142
NM_006098	GNB2L1	0.14	-0.01	16273	18409	33137	32212
NM_002075	GNB3	0.00	-0.34	93	96	131	74
NM_004126	GNG11	0.02	-0.03	1274	1410	4480	4166
NM_005471	GNPDA1	0.33	-0.23	963	1332	2510	2000
NM_002080	GOT2	0.00	-0.03	2328	2494	3658	3399
NM_005708	GPC6	0.13	-0.30	505	636	1206	885
NM_032777	GPR124	0.05	-0.16	1568	1763	2529	2115
NM_198827	GPR133	0.00	-0.18	129	157	98	59
NM_001276501	GPSM3	0.23	-0.02	80	130	243	192
NM_201397	GPX1	0.03	-0.18	1172	1315	3188	2656
NM_015696	GPX7	0.47	-0.07	677	1050	1373	1192
NM_013372	GREM1	0.14	-0.22	183659	203725	239474	204292
NM_012203	GRHPR	0.25	-0.13	1219	1581	3575	3078
NM_005308	GRK5	0.25	-0.07	394	546	499	407
NM_001004106	GRK6	0.00	-0.24	788	872	1264	970
NM_031485	GRWD1	0.00	-0.05	1241	1294	1398	1235
NM_001166237	GSDMD	0.00	-0.97	343	350	412	170
NM_000178	GSS	0.00	-0.12	1070	1144	3612	3135
NM_001512	GSTA4	0.00	-0.34	92	90	368	240
NM_001031720	GSTCD	0.00	-0.02	252	253	399	331
NM_001143679	GSTK1	0.81	-0.19	767	1488	3488	2889
NM_004832	GSTO1	0.06	-0.03	1983	2217	5045	4699
NM_001516	GTF2H3	0.00	-0.08	482	431	690	573
NM_001122823	GTF3C5	0.31	-0.09	1065	1449	2051	1786
NM_021927	GUF1	0.00	-0.03	289	337	522	440
NM_177925	H2AFJ	0.18	-0.45	1315	1622	2263	1532
NM_138635	H2AFV	0.34	-0.05	873	1228	1414	1244
NM_002105	H2AFX	0.42	-0.26	946	1397	980	728
NM_002106	H2AFZ	0.28	-0.53	1961	2558	2263	1445
NM_005324	H3F3B	0.00	-0.14	2975	3001	3427	2928
NM_021973	HAND2	0.00	-0.16	172	190	79	46
NM_012208	HARS2	0.11	-0.01	309	398	824	726

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_005328	HAS2	0.30	-0.13	4581	5898	11051	9784
NM_138443	HAUS1	0.43	-0.03	133	231	227	176
NM_001166269	HAUS4	0.19	-0.03	177	254	468	390
NM_001011699	HAUS8	0.00	-0.05	317	321	187	139
NM_178423	HDAC9	0.51	-0.08	165	295	620	510
NM_024602	HECTD3	0.02	-0.04	1182	1315	2425	2198
NM_020760	HECW2	0.05	-0.09	672	784	1331	1137
NM_001289067	HELLS	0.07	-0.07	335	416	195	144
NM_022079	HERC4	0.13	-0.04	3367	3880	6079	5663
NM_001165967	HES7	2.24	-0.39	35	249	225	133
NM_138820	HIGD2A	0.06	-0.02	556	662	1333	1198
NM_032593	HINT2	0.00	-0.05	204	176	347	279
NM_005322	HIST1H1B	0.07	-0.68	7478	8154	3354	1956
NM_003513	HIST1H2AB	0.08	-0.13	513	622	297	220
NM_003512	HIST1H2AC	0.36	-0.06	2031	2792	3369	3055
NM_021065	HIST1H2AD	0.00	-0.20	1097	1046	620	468
NM_021052	HIST1H2AE	0.00	-0.42	3005	3127	1171	786
NM_021064	HIST1H2AG	0.52	-0.25	1398	2168	665	486
NM_080596	HIST1H2AH	0.12	-0.06	1096	1309	476	390
NM_003509	HIST1H2AI	0.00	-0.72	1571	1475	828	438
NM_021066	HIST1H2AJ	0.00	-0.45	1154	1177	501	309
NM_003511	HIST1H2AL	0.00	-0.56	2557	2601	1098	664
NM_003514	HIST1H2AM	0.00	-0.32	1488	1521	634	440
NM_021062	HIST1H2BB	0.25	-0.52	874	1156	545	323
NM_003526	HIST1H2BC	0.10	-0.09	4518	5091	4074	3634
NM_003518	HIST1H2BG	0.40	-0.09	1290	1848	703	580
NM_003525	HIST1H2BI	0.36	-0.47	1494	2076	784	494
NM_003521	HIST1H2BM	0.16	-0.22	1063	1306	410	294
NM_003520	HIST1H2BN	0.22	-0.37	1498	1886	1468	1031
NM_003527	HIST1H2BO	0.00	-0.33	1336	1320	711	495
NM_003537	HIST1H3B	0.11	-0.54	6097	6875	2897	1859
NM_003531	HIST1H3C	0.08	-0.52	4759	5271	2009	1286
NM_003530	HIST1H3D	0.00	-0.33	2430	2402	1441	1044
NM_003536	HIST1H3H	0.16	-0.51	1688	2035	915	566
NM_003533	HIST1H3I	0.00	-0.02	768	823	295	237
NM_003544	HIST1H4B	0.00	-0.08	2461	2621	1462	1268
NM_003542	HIST1H4C	0.29	-0.15	1357	1801	1050	848
NM_003495	HIST1H4I	0.00	-0.09	383	341	146	102
NM_175065	HIST2H2AB	0.22	-0.27	458	617	406	281
NM_003517	HIST2H2AC	0.00	-0.21	1375	1382	1545	1222

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_003528	HIST2H2BE	0.00	-0.20	2823	2960	2065	1667
NM_001005464	HIST2H3A	0.80	-0.61	3293	6017	2466	1501
NM_021059	HIST2H3C	0.80	-0.61	3293	6017	2466	1501
NM_001123375	HIST2H3D	0.28	-0.54	659	902	266	144
NM_003548	HIST2H4A	0.00	-0.34	8406	8202	2920	2155
NM_001034077	HIST2H4B	0.00	-0.34	8406	8202	2920	2155
NM_018410	HJURP	0.22	-0.76	757	987	562	281
NM_000190	HMBS	0.21	-0.17	545	719	1092	876
NM_006339	HMG20B	0.00	-0.16	1459	1420	2812	2364
NM_145901	HMGA1	0.31	-0.31	11513	14723	23733	18724
NM_002128	HMGB1	0.00	-0.19	1500	1384	1949	1579
NM_001130688	HMGB2	0.00	-0.39	1214	1218	657	433
NM_006353	HMGN4	0.00	-0.11	1098	1096	1828	1558
NM_001142556	HMMR	0.00	-0.49	253	288	312	179
NM_001127204	HMOX2	0.00	-0.33	1467	1465	2356	1745
NM_001002032	HN1	0.00	-0.24	1313	1374	1776	1386
NM_031157	HNRNPA1	0.18	-0.20	1272	1569	2144	1726
NM_001011724	HNRNPA1L2	0.00	-0.10	794	873	1102	926
NM_031243	HNRNPA2B1	0.17	-0.08	6298	7396	7674	6968
NM_031370	HNRNPD	0.03	-0.08	933	1056	695	575
NM_001098206	HNRNPF	0.38	-0.06	4775	6489	5786	5309
NM_002140	HNRNPK	0.06	-0.03	2537	2822	4536	4220
NM_001533	HNRNPL	0.26	-0.10	1383	1794	2633	2303
NM_005968	HNRNPM	0.03	-0.23	1954	2151	3130	2505
NM_001102398	HNRNPR	0.00	-0.21	2847	2697	2552	2065
NM_014212	HOXC11	0.43	-0.29	37	79	347	233
NM_022658	HOXC8	0.27	-0.07	545	751	1227	1057
NM_000195	HPS1	0.06	-0.10	1026	1182	3644	3209
NM_022460	HS1BP3	0.28	-0.22	452	632	1986	1580
NM_001037811	HSD17B10	0.06	-0.40	517	617	1054	712
NM_016246	HSD17B14	0.00	-0.10	31	35	329	253
NM_001271969	HSP90AB1	0.47	-0.08	10026	14303	20597	19000
NM_001541	HSPB2	0.36	-0.28	427	635	753	543
NM_001130106	HSPBP1	0.06	-0.32	391	479	838	593
NM_002156	HSPD1	0.15	-0.13	2386	2826	3288	2824
NM_033158	HYAL2	0.15	-0.46	910	1119	2830	1919
NM_001243526	HYI	0.13	-0.25	1583	1880	1148	871
NM_001134793	HYLS1	0.61	-0.15	167	318	310	229
NM_016545	IER5	0.20	-0.03	1035	1306	1343	1196

Table 6D: Differentially Downregulated Genes in SEN + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_032036	IFI27L2	0.10	-0.01	420	525	1169	1048
NM_005533	IFI35	0.17	-0.42	231	317	774	506
NM_002038	IFI6	0.00	-0.14	195	177	168	115
NM_003641	IFITM1	0.18	-0.47	294	399	277	159
NM_006435	IFITM2	0.58	-0.53	1733	2790	2548	1640
NM_021034	IFITM3	0.36	-0.52	4256	5736	5401	3591
NM_014055	IFT81	0.00	-0.25	66	82	262	176
NM_003640	IKBKAP	0.02	-0.11	957	1075	2258	1941
NM_014002	IKBKE	0.22	-0.09	287	401	584	475
NM_001243539	IL15RA	0.00	-0.73	164	177	96	37
NM_000877	IL1R1	0.00	-0.81	1086	1147	2976	1582
NM_002185	IL7R	0.04	-0.02	831	954	634	545
NM_001267809	ILF2	0.43	-0.13	1344	1961	1878	1580
NM_012218	ILF3	0.00	-0.04	5977	5913	6830	6368
NM_001014795	ILK	0.11	-0.03	5437	6108	8647	8164
NM_006844	ILVBL	0.19	-0.04	902	1144	1811	1630
NM_033416	IMP4	0.28	-0.07	1156	1539	1788	1573
NM_000884	IMPDH2	0.18	-0.23	3398	4069	5087	4142
NM_019892	INPP5E	0.17	-0.16	332	442	730	575
NM_020395	INTS12	0.13	-0.03	378	485	842	734
NM_016338	IPO11	0.00	-0.03	446	512	722	621
NM_178229	IQGAP3	0.13	-0.96	1625	1927	1994	933
NM_007199	IRAK3	0.43	-0.13	181	304	613	488
NM_005101	ISG15	0.00	-0.56	166	189	474	270
NM_024710	ISOC2	0.66	-0.03	527	944	1331	1190
NM_018463	ITFG2	0.18	-0.01	252	347	551	473
NM_181501	ITGA1	0.00	-0.20	231	253	1165	913
NM_000885	ITGA4	0.00	-0.33	964	1052	2258	1667
NM_033453	ITPA	0.17	-0.30	340	453	994	721
NM_020433	JPH2	0.00	-0.34	508	585	871	610
NM_001130089	KARS	0.16	-0.12	1917	2303	3065	2656
NM_001017999	KAZN	0.00	-0.25	563	571	578	418
NM_012281	KCND2	0.00	-0.38	265	256	711	475
NM_001017424	KCNK2	0.07	-0.34	2934	3257	3970	2965
NM_173562	KCTD20	0.08	-0.12	5345	5895	9446	8412
NM_153705	KDELC2	0.46	-0.17	892	1360	1329	1074
NM_001251874	KHDC1	0.00	-0.14	116	138	216	153
NM_003685	KHSRP	0.08	-0.19	1516	1738	1874	1519
NM_014736	KIAA0101	0.00	-0.53	311	261	264	144
NM_014846	KIAA0196	0.00	-0.04	1089	1147	3045	2793

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001100425	KIAA0895	0.19	-0.42	118	177	135	72
NM_020890	KIAA1524	0.15	-0.61	297	394	403	218
NM_001029864	KIAA1755	0.00	-0.11	37	51	216	157
NM_004523	KIF11	0.00	-0.35	794	762	485	322
NM_014875	KIF14	0.00	-0.33	329	331	381	251
NM_020242	KIF15	0.43	-0.60	131	228	179	87
NM_001122819	KIF17	0.00	-0.49	264	249	233	129
NM_031217	KIF18A	0.00	-0.34	340	281	433	287
NM_001264573	KIF18B	0.14	-1.16	719	891	520	192
NM_005733	KIF20A	0.10	-1.28	1309	1528	1258	458
NM_001256269	KIF22	0.15	-0.48	963	1183	986	630
NM_138555	KIF23	0.05	-0.54	1094	1251	1013	619
NM_006845	KIF2C	0.22	-0.59	734	959	913	536
NM_012310	KIF4A	0.00	-0.52	277	322	266	146
NM_001099293	KIF4B	0.00	-0.60	343	362	354	190
NM_002263	KIFC1	0.10	-0.36	1217	1429	643	434
NM_001130100	KIFC3	0.12	-0.16	2078	2414	3321	2800
NM_000222	KIT	0.30	-1.55	34	68	77	13
NM_000899	KITLG	0.24	-0.45	1768	2247	3831	2645
NM_031918	KLF16	0.00	-0.20	652	611	630	475
NM_003709	KLF7	0.00	-0.04	1855	1978	5022	4665
NM_173546	KLHDC8B	0.23	-0.18	529	711	1464	1176
NM_014458	KLHL20	0.00	-0.07	308	298	559	460
NM_032775	KLHL22	0.00	-0.13	722	751	1477	1237
NM_001142761	KNSTRN	0.00	-0.21	931	911	853	654
NM_014708	KNTC1	0.02	-0.38	633	729	786	530
NM_002266	KPNA2	0.31	-0.53	1865	2491	2932	1891
NM_002277	KRT31	0.81	-0.45	46	120	403	244
NM_021013	KRT34	0.47	-0.05	1517	2268	7254	6743
NM_031957	KRTAP1-5	0.14	-0.26	328	430	2514	1956
NM_001165252	KRTAP2-3	0.00	-0.22	371	327	1529	1196
NM_016027	LACTB2	0.00	-0.22	154	145	354	251
NM_198129	LAMA3	0.00	-0.75	46	51	890	462
NM_001105207	LAMA4	0.13	-0.90	1519	1805	7836	4002
NM_002291	LAMB1	0.02	-0.20	5680	6023	17211	14556
NM_017907	LAMTOR1	0.33	-0.23	1354	1855	3768	3030
NM_015907	LAP3	0.08	-0.25	422	518	1215	921
NM_015340	LARS2	0.00	-0.08	562	643	1215	1039
NM_031206	LAS1L	0.33	-0.01	441	638	1034	924
NM_001258390	LAYN	0.18	-0.66	629	807	2171	1268

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001170765	LCOR	0.21	-0.04	536	706	776	669
NM_153686	LCORL	0.21	-0.11	175	255	152	105
NM_001130834	LDB2	0.00	-0.33	213	180	426	283
NM_001174097	LDHB	0.20	-0.18	2524	3087	5261	4423
NM_005567	LGALS3BP	0.34	-0.18	4250	5634	5890	4970
NM_001136472	LITAF	0.00	-0.03	1020	1130	1395	1250
NM_170707	LMNA	0.24	-0.22	22240	26812	49065	41411
NM_005573	LMNB1	0.02	-0.55	816	927	283	153
NM_032737	LMNB2	0.00	-0.45	3588	3782	3070	2103
NM_012134	LMOD1	0.40	-0.40	198	322	1522	1052
NM_001290056	LOC101927572	0.00	-0.10	58	61	183	131
NM_001199053	LOC81691	0.79	-0.07	63	154	160	115
NM_024036	LRFN4	0.00	-0.30	754	825	776	553
NM_153377	LRIG3	0.22	-0.23	120	183	225	150
NM_024512	LRRC2	0.19	-0.47	288	393	208	115
NM_001278211	LRRC20	0.78	-0.09	198	414	354	277
NM_018509	LRRC59	0.13	-0.02	11496	12994	10752	10279
NM_001127244	LRRC8A	0.12	-0.02	3710	4256	6709	6370
NM_024652	LRRK1	0.00	-0.37	600	646	1279	895
NM_021177	LSM2	0.26	-0.53	225	330	435	250
NM_012321	LSM4	0.00	-0.34	784	878	2179	1590
NM_016199	LSM7	0.89	-0.17	224	500	678	525
NM_002342	LTBR	0.12	-0.01	2724	3155	5584	5288
NM_001160354	LY6K	0.00	-0.76	755	802	539	268
NM_007260	LYPLA2	0.00	-0.21	345	344	799	608
NM_001164841	LYRM4	0.00	-0.04	234	277	589	499
NM_021020	LZTS1	0.00	-0.25	326	335	304	207
NM_002358	MAD2L1	0.35	-0.43	166	267	208	118
NM_016249	MAGEC2	0.00	-1.31	2	6	87	20
NM_001272061	MAGED4	0.34	-0.08	635	904	730	606
NM_001242362	MAGED4B	0.34	-0.08	635	904	730	606
NM_002370	MAGOH	0.00	-0.08	131	110	181	131
NM_182574	MAMSTR	0.00	-0.61	82	112	129	59
NM_005921	MAP3K1	0.00	-0.06	410	411	333	264
NM_003954	MAP3K14	0.55	-0.08	275	480	607	499
NM_002969	MAPK12	0.00	-0.11	469	457	1133	945
NM_001006617	MAPKAP1	0.17	-0.17	2344	2822	6879	5863
NM_004759	MAPKAPK2	0.07	-0.04	3669	4067	4309	3976
NM_001243925	MAPKAPK3	0.31	-0.02	455	648	1705	1555

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001128608	MAPKBP1	0.00	-0.08	973	1075	2292	2017
NM_014268	MAPRE2	0.36	-0.02	526	772	1520	1375
NM_001042539	MAZ	0.37	-0.24	3022	4128	3492	2784
NM_178496	MB21D2	0.03	-0.66	506	596	632	342
NM_203406	MBLAC2	0.40	-0.10	156	261	206	150
NM_002386	MC1R	0.00	-0.02	112	140	351	288
NM_022132	MCCC2	0.20	-0.02	347	469	857	754
NM_001112732	MCF2L	0.00	-0.43	279	284	231	133
NM_018518	MCM10	0.51	-0.75	474	772	193	85
NM_004526	MCM2	0.11	-0.20	1864	2170	1389	1098
NM_002388	MCM3	0.30	-0.33	2355	3087	1622	1177
NM_005914	MCM4	0.53	-0.22	2312	3545	2685	2157
NM_006739	MCM5	0.08	-0.16	2710	3050	1868	1538
NM_001278595	MCM7	0.02	-0.31	3999	4282	2398	1795
NM_001281520	MCM8	0.36	-0.01	279	427	362	299
NM_014060	MCTS1	0.00	-0.11	240	254	595	479
NM_005918	MDH2	0.22	-0.16	3961	4841	8106	6983
NM_001270550	MDK	0.00	-0.37	181	182	599	399
NM_014611	MDN1	0.00	-0.05	1482	1458	3067	2778
NM_001001683	MED11	0.00	-0.28	181	227	403	277
NM_015335	MED13L	0.05	-0.03	3484	3802	5991	5623
NM_005481	MED16	0.26	-0.19	994	1311	2308	1885
NM_181491	MED22	0.00	-0.18	498	547	1341	1079
NM_080651	MED30	0.00	-0.04	111	88	110	76
NM_004270	MED7	0.00	-0.24	123	105	277	189
NM_018019	MED9	0.00	-0.03	213	264	283	226
NM_001145784	MEF2BNB	0.00	-0.26	176	209	458	322
NM_001193350	MEF2C	0.00	-0.24	261	251	643	473
NM_002398	MEIS1	0.07	-0.17	252	322	944	749
NM_014791	MELK	0.10	-0.20	647	783	593	445
NM_130802	MEN1	0.00	-0.03	952	966	1059	932
NM_022566	MESDC1	0.00	-0.09	368	366	364	285
NM_002402	MEST	0.81	-0.27	182	393	195	124
NM_024042	METRN	0.13	-0.01	271	358	900	797
NM_005371	METTL1	0.00	-0.19	309	267	422	311
NM_001043229	METTL12	0.00	-0.17	34	56	100	61
NM_015935	METTL13	0.06	-0.02	916	1064	1524	1383
NM_022734	METTL17	0.00	-0.17	469	513	653	506
NM_033418	METTL18	0.00	-0.44	59	44	83	39
NM_019852	METTL3	0.25	-0.10	1047	1369	1655	1420

Table 6D: Differentially Downregulated Genes in SEN + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_022840	METTL4	0.00	-0.29	151	169	335	224
NM_001174118	MEX3D	0.06	-0.18	529	634	855	667
NM_031433	MFRP	0.00	-0.35	469	461	1221	867
NM_004668	MGAM	0.00	-0.18	55	72	54	28
NM_002412	MGMT	0.00	-0.02	208	197	349	285
NM_032339	MIEN1	0.17	-0.09	733	923	1522	1312
NM_002417	MKI67	0.00	-0.99	5342	5358	3858	1821
NM_170607	MLX	0.24	-0.12	1716	2180	3198	2763
NM_002421	MMP1	0.50	-0.04	11316	16457	6268	5830
NM_002426	MMP12	0.05	-0.23	14	31	98	57
NM_016155	MMP17	0.00	-0.29	139	179	591	418
NM_002422	MMP3	0.15	-0.04	4384	5116	17523	16658
NM_001286072	MOV10	0.07	-0.09	809	947	2161	1889
NM_004870	MPDU1	0.00	-0.01	1266	1280	1757	1606
NM_002434	MPG	0.54	-0.04	617	1013	1460	1301
NM_005590	MRE11A	0.37	-0.24	162	264	389	274
NM_001272054	MRFAP1	0.02	-0.12	5828	6145	9279	8268
NM_001098515	MRGPRF	0.46	-0.20	249	412	638	482
NM_016050	MRPL11	0.00	-0.33	375	421	534	364
NM_002949	MRPL12	0.19	-0.30	858	1089	1410	1042
NM_032111	MRPL14	0.00	-0.05	1490	1541	2254	2024
NM_017840	MRPL16	0.05	-0.43	420	507	1044	693
NM_017971	MRPL20	0.45	-0.03	451	710	1204	1067
NM_181514	MRPL21	0.03	-0.11	587	684	932	773
NM_021134	MRPL23	0.54	-0.15	490	815	1129	919
NM_145729	MRPL24	0.00	-0.04	383	444	971	848
NM_016504	MRPL27	0.00	-0.04	1023	1056	1383	1225
NM_145212	MRPL30	0.00	-0.06	395	429	732	617
NM_004891	MRPL33	0.05	-0.27	475	570	747	542
NM_032479	MRPL36	0.12	-0.04	647	793	1140	1002
NM_032478	MRPL38	0.01	-0.12	713	808	1248	1041
NM_146388	MRPL4	0.00	-0.04	1023	1123	1341	1189
NM_003776	MRPL40	0.31	-0.31	214	326	786	556
NM_032477	MRPL41	0.13	-0.17	463	585	1381	1118
NM_019051	MRPL50	0.00	-0.40	175	209	412	259
NM_016497	MRPL51	0.14	-0.05	974	1189	1770	1579
NM_181304	MRPL52	0.15	-0.14	650	816	1616	1342
NM_053050	MRPL53	0.00	-0.09	150	163	351	274
NM_181462	MRPL55	0.53	-0.14	245	427	848	682
NM_024026	MRPL57	0.44	-0.31	302	485	890	636

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_031420	MRPL9	0.00	-0.07	794	839	1231	1065
NM_022839	MRPS11	0.29	-0.28	512	715	1239	924
NM_033363	MRPS12	0.38	-0.15	483	719	932	749
NM_031280	MRPS15	0.08	-0.04	976	1140	2225	2015
NM_018135	MRPS18A	0.34	-0.14	387	572	838	673
NM_014046	MRPS18B	0.00	-0.02	844	871	1491	1346
NM_001286748	MRPS27	0.00	-0.20	1119	1112	1944	1567
NM_023936	MRPS34	0.08	-0.22	964	1131	1934	1534
NM_138777	MRRF	0.00	-0.29	213	203	505	351
NM_016183	MRTO4	0.03	-0.20	718	824	1185	932
NM_130385	MRVI1	0.05	-0.99	657	768	3103	1455
NM_001256532	MSTO1	0.65	-0.15	255	480	903	723
NM_005946	MT1A	0.00	-0.18	13	28	121	76
NM_001099625	MTFR1L	0.35	-0.03	833	1177	2535	2320
NM_005956	MTHFD1	0.16	-0.29	1020	1258	1957	1475
NM_001190487	MTRNR2L6	2.14	-0.03	56	344	1701	1536
NM_025128	MUS81	0.64	-0.04	571	1003	1215	1074
NM_002461	MVD	0.46	-0.16	276	453	824	654
NM_002466	MYBL2	0.48	-1.15	958	1471	327	115
NM_001163424	MYEOV2	0.00	-0.10	454	458	749	614
NM_021019	MYL6	0.44	-0.08	10866	15214	22801	21125
NM_001199629	MYL6B	0.00	-0.18	306	282	730	567
NM_006097	MYL9	0.83	-0.21	10584	19391	38407	32665
NM_001163735	MYO19	0.18	-0.25	1563	1921	1988	1543
NM_004998	MYO1E	0.18	-0.13	2962	3547	8920	7887
NM_012335	MYO1F	0.00	-0.13	26	32	83	50
NM_013451	MYOF	0.11	-0.13	16695	18456	32033	28645
NM_032356	NAA38	0.00	-0.15	635	634	1402	1148
NM_199290	NACA2	0.04	-0.20	1980	2190	3529	2900
NM_144653	NACC2	0.05	-0.06	1557	1744	2776	2493
NM_001018159	NAE1	0.00	-0.19	589	632	1225	974
NM_018946	NANS	0.20	-0.33	2987	3623	3030	2264
NM_005969	NAP1L4	0.20	-0.08	1768	2187	3635	3248
NM_003827	NAPA	0.49	-0.07	1716	2597	4852	4392
NM_001286829	NAPRT	0.00	-0.10	147	149	208	152
NM_001256281	NARR	0.34	-0.05	290	437	757	647
NM_024678	NARS2	0.27	-0.35	250	365	403	264
NM_002482	NASP	0.35	-0.29	578	835	564	396
NM_024662	NAT10	0.24	-0.03	1273	1642	1716	1545
NM_020378	NAT14	0.00	-0.44	94	118	462	287

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001244963	NAV2	0.00	-0.02	6546	6417	7732	7325
NM_014865	NCAPD2	0.33	-0.50	1673	2269	2612	1717
NM_015261	NCAPD3	0.05	-0.17	1334	1506	1429	1161
NM_022346	NCAPG	0.13	-0.86	696	855	846	405
NM_001281932	NCAPG2	0.04	-0.72	1148	1294	1323	721
NM_001281710	NCAPH	0.00	-0.56	679	692	599	347
NM_002486	NCBP1	0.10	-0.23	681	826	1680	1312
NM_014286	NCS1	0.08	-0.09	4139	4613	10953	9972
NM_018087	NDC1	0.00	-0.08	582	643	724	603
NM_006101	NDC80	0.00	-0.82	412	393	320	144
NM_001242835	NDRG4	1.38	-0.11	24	105	162	113
NM_004544	NDUFA10	0.05	-0.02	1363	1542	2968	2749
NM_004542	NDUFA3	0.00	-0.32	261	282	645	447
NM_005001	NDUFA7	0.00	-0.12	401	356	855	697
NM_005003	NDUFAB1	0.03	-0.25	564	658	1017	765
NM_002493	NDUFB6	0.00	-0.02	541	597	1235	1105
NM_004146	NDUFB7	0.23	-0.11	824	1075	2019	1732
NM_002496	NDUFS8	0.20	-0.33	1361	1705	3783	2848
NM_001166102	NDUFV1	0.00	-0.11	1802	1705	3433	3002
NM_021074	NDUFV2	0.00	-0.10	255	281	433	342
NM_001144966	NEDD4L	0.41	-0.14	517	782	455	349
NM_006156	NEDD8	0.18	-0.17	977	1224	2460	2039
NM_006403	NEDD9	0.15	-0.01	2617	3093	2123	1956
NM_006158	NEFL	0.00	-0.82	106	99	247	107
NM_018248	NEIL3	0.00	-0.56	151	169	102	46
NM_002497	NEK2	0.00	-1.11	170	185	195	65
NM_001166171	NEK6	0.23	-0.38	1956	2469	6370	4682
NM_001142651	NEURL1B	0.02	-0.96	115	155	116	39
NM_181832	NF2	0.01	-0.15	6567	6905	7713	6671
NM_001134673	NFIA	0.00	-0.47	806	762	753	475
NM_206915	NGFRAP1	0.06	-0.04	1257	1438	4527	4177
NM_017838	NHP2	0.00	-0.24	480	495	1131	861
NM_032316	NICN1	0.00	-0.09	100	85	289	220
NM_016101	NIP7	0.00	-0.02	716	729	936	828
NM_003634	NIPSNAP1	0.09	-0.11	517	631	1435	1214
NM_001014445	NLE1	0.58	-0.17	275	489	611	471
NM_021077	NMB	0.23	-0.14	79	129	3752	3216
NM_002512	NME2	0.38	-0.21	2409	3329	5715	4713
NM_001286438	NME4	0.16	-0.21	1706	2056	4852	3985
NM_012343	NNT	0.00	-0.12	1640	1771	4207	3664

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_015658	NOC2L	0.47	-0.16	1143	1730	2408	2006
NM_015462	NOL11	0.53	-0.20	205	363	416	305
NM_022917	NOL6	0.19	-0.40	1820	2227	2803	1985
NM_001145408	NONO	0.44	-0.12	2593	3736	5299	4662
NM_016391	NOP16	0.04	-0.29	713	826	1179	869
NM_015934	NOP58	0.00	-0.05	967	953	944	817
NM_001270960	NOSIP	0.00	-0.06	347	300	586	488
NM_002514	NOV	0.43	-0.19	457	710	216	148
NM_001291926	NOX4	0.57	-0.12	22	58	166	115
NM_000272	NPHP1	0.00	-0.21	13	6	127	79
NM_002520	NPM1	0.00	-0.24	1772	1914	2387	1878
NM_006993	NPM3	0.26	-0.47	270	388	730	458
NM_000906	NPR1	0.00	-0.48	47	68	62	26
NM_001243247	NPRL3	0.00	-0.28	778	835	1106	821
NM_002522	NPTX1	0.00	-0.70	210	203	512	264
NM_000903	NQO1	0.63	-0.08	5148	8328	15747	14464
NM_021005	NR2F2	0.13	-0.14	2093	2448	3047	2590
NM_000901	NR3C2	0.50	-0.15	612	974	1996	1664
NM_001142481	NREP	0.00	-0.11	579	628	2186	1885
NM_198465	NRK	0.27	-0.46	98	159	385	231
NM_001270707	NRM	0.00	-0.55	264	309	470	268
NM_001286798	NTMT1	0.18	-0.05	1671	2042	2113	1893
NM_001113226	NTNG1	0.00	-0.21	174	191	510	377
NM_030952	NUAK2	0.14	-0.90	477	607	443	194
NM_025152	NUBPL	0.43	-0.25	42	87	239	159
NM_001193452	NUDT16L1	0.00	-0.28	306	273	643	458
NM_145697	NUF2	0.19	-0.84	215	302	254	109
NM_018230	NUP133	0.65	-0.07	508	904	1275	1105
NM_004298	NUP155	0.16	-0.18	879	1091	1433	1152
NM_015354	NUP188	0.29	-0.27	3261	4208	5817	4597
NM_005085	NUP214	0.00	-0.09	1834	1883	3180	2813
NM_024844	NUP85	0.63	-0.12	635	1103	1144	950
NM_014669	NUP93	0.37	-0.06	1342	1885	2206	1965
NM_001243142	NUSAP1	0.00	-0.76	794	883	661	335
NM_022463	NXN	0.03	-0.02	1270	1418	1400	1266
NM_178507	OAF	0.10	-0.13	2203	2531	4962	4310
NM_006187	OAS3	0.01	-0.27	144	188	162	100
NM_000274	OAT	0.02	-0.20	2509	2712	4908	4072
NM_002540	ODF2	0.36	-0.03	1086	1529	2003	1815
NM_015441	OLFML2B	0.05	-0.73	299	372	772	405

Table 6D: Differentially Downregulated Genes in SEN + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001286352	OLFML3	0.06	-0.13	1102	1261	3444	2969
NM_012381	ORC3	0.06	-0.26	167	221	501	355
NM_014321	ORC6	0.00	-0.31	450	419	354	235
NM_017807	OSGEP	0.26	-0.36	263	380	732	497
NM_145260	OSR1	0.00	-0.19	478	533	890	695
NM_012383	OSTF1	0.00	-0.11	1081	1123	2200	1895
NM_000436	OXCT1	0.16	-0.17	473	609	1169	939
NM_000916	OXTR	0.07	-1.20	13965	15094	10394	4346
NM_006191	PA2G4	0.35	-0.50	1583	2177	2375	1555
NM_001114734	PABPC4L	0.00	-0.62	117	101	235	118
NM_019088	PAF1	0.21	-0.05	756	977	1368	1209
NM_002573	PAFAH1B3	0.07	-0.08	314	392	830	697
NM_024516	PAGR1	0.00	-0.01	633	691	884	782
NM_007203	PALM2-AKAP2	0.22	-0.15	8867	10707	24263	21369
NM_001618	PARP1	0.24	-0.36	1308	1681	1682	1201
NM_032789	PARP10	0.00	-0.27	274	306	559	397
NM_001003931	PARP3	0.00	-0.02	594	656	1412	1272
NM_031458	PARP9	0.46	-0.14	146	256	520	405
NM_017915	PARPBP	0.00	-0.23	126	128	200	131
NM_018492	PBK	0.00	-0.48	516	519	401	237
NM_019035	PCDH18	0.49	-0.39	1973	2962	6738	4915
NM_007144	PCGF2	0.00	-0.17	1277	1386	1942	1599
NM_002592	PCNA	0.40	-0.21	1467	2090	1543	1222
NM_002593	PCOLCE	0.10	-0.23	1538	1782	3084	2462
NM_004716	PCSK7	0.40	-0.21	2203	3109	4952	4072
NM_001184917	PCYT2	0.05	-0.05	448	538	1678	1492
NM_014976	PDCD11	0.00	-0.13	1820	1941	2381	2026
NM_004708	PDCD5	0.00	-0.05	188	236	441	362
NM_024065	PDCL3	0.00	-0.28	139	139	289	192
NM_018945	PDE7B	0.00	-0.10	509	471	643	523
NM_022341	PDF	0.00	-0.01	198	247	451	381
NM_002607	PDGFA	0.32	-0.04	612	866	790	682
NM_006206	PDGFRA	0.15	-0.63	3877	4533	5085	3109
NM_001173454	PDHA1	0.18	-0.03	1069	1328	1770	1604
NM_001173468	PDHB	0.00	-0.02	1090	1144	2069	1900
NM_021630	PDLIM2	0.00	-0.03	1881	2005	4074	3773
NM_001080471	PEAR1	0.21	-1.16	1926	2387	510	187
NM_001040152	PEG10	0.14	-0.32	1116	1351	616	425
NM_001135690	PENK	0.60	-1.15	4042	6409	3625	1525

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_000285	PEPD	0.42	-0.23	1234	1795	2797	2238
NM_004813	PEX16	0.00	-0.22	326	378	801	608
NM_012393	PFAS	0.36	-0.47	716	1026	1198	778
NM_002622	PFDN1	0.68	-0.15	484	884	1651	1366
NM_000289	PFKM	0.00	-0.16	1855	1786	4190	3564
NM_033419	PGAP3	0.10	-0.08	118	167	528	431
NM_001100164	PHACTR2	0.00	-0.12	4592	4615	5384	4739
NM_001048183	PHACTR4	0.08	-0.06	620	743	859	732
NM_001281496	PHB	0.05	-0.21	1356	1529	2793	2257
NM_001144831	PHB2	0.13	-0.25	2884	3352	5103	4100
NM_015651	PHF19	0.33	-0.03	1010	1397	1291	1152
NM_005392	PHF2	0.18	-0.02	1074	1334	1778	1614
NM_032758	PHF5A	0.00	-0.20	391	409	528	394
NM_001134438	PHLDB2	0.31	-0.13	783	1079	2263	1928
NM_001100876	PHYHD1	0.48	-0.50	39	85	239	131
NM_058004	PI4KA	0.17	-0.08	2111	2551	6416	5828
NM_001286496	PIF1	0.00	-0.13	167	127	258	189
NM_002642	PIGC	0.00	-0.08	163	160	262	200
NM_004204	PIGQ	0.00	-0.03	434	410	886	773
NM_080476	PIGU	0.39	-0.13	231	367	580	460
NM_001193621	PINLYP	0.07	-0.24	38	64	89	50
NM_001135638	PIP5K1A	0.31	-0.13	1294	1751	1531	1277
NM_014338	PISD	0.10	-0.13	728	875	1321	1100
NM_181805	PKIG	0.25	-0.17	599	809	1275	1028
NM_000929	PLA2G5	0.00	-0.14	91	108	98	61
NM_001288989	PLCE1	0.00	-0.04	185	178	464	384
NM_020904	PLEKHA4	0.00	-0.11	173	216	482	381
NM_022835	PLEKHG2	0.46	-0.51	431	683	1470	939
NM_015432	PLEKHG4	0.22	-0.41	528	704	1414	963
NM_172069	PLEKHH2	0.51	-0.08	48	102	364	287
NM_001164189	PLIN3	0.14	-0.04	7305	8341	16793	15924
NM_005030	PLK1	0.39	-1.00	957	1382	1177	521
NM_014264	PLK4	0.00	-0.34	427	469	291	185
NM_021127	PMAIP1	0.43	-0.26	200	332	204	131
NM_001199653	PMF1	0.01	-0.24	412	486	934	702
NM_001199662	PMF1-BGLAP	0.00	-0.16	371	378	676	529
NM_002676	PMM1	0.43	-0.06	732	1104	2978	2688
NM_001282946	PMPCA	0.03	-0.08	1069	1207	2352	2079
NM_006556	PMVK	0.03	-0.08	370	444	973	824

Table 6D: Differentially Downregulated Genes in SEN + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001077399	PNKD	0.65	-0.37	83	177	487	318
NM_004650	PNPLA4	0.00	-0.53	120	148	258	140
NM_033109	PNPT1	0.00	-0.07	222	192	237	179
NM_001161581	POC1A	0.00	-0.42	389	419	464	292
NM_002689	POLA2	0.62	-0.14	547	950	728	579
NM_001278255	POLE3	0.53	-0.02	782	1257	1229	1100
NM_019896	POLE4	0.00	-0.04	459	496	1036	908
NM_006502	POLH	0.13	-0.08	1379	1641	2244	1978
NM_199420	POLQ	0.00	-0.73	358	388	337	163
NM_015425	POLR1A	0.18	-0.12	1411	1739	3067	2660
NM_001282777	POLR1B	0.00	-0.33	478	498	693	481
NM_002695	POLR2E	0.01	-0.09	2075	2237	3937	3508
NM_021128	POLR2L	0.40	-0.45	2046	2889	5698	3989
NM_176869	PPA2	0.71	-0.22	182	368	1079	834
NM_003713	PPAP2B	0.48	-0.45	1703	2546	2327	1579
NM_203453	PPAPDC2	0.64	-0.17	58	130	260	185
NM_032728	PPAPDC3	0.00	-0.28	172	212	728	523
NM_138712	PPARG	0.00	-0.78	277	283	185	79
NM_006347	PPIH	0.39	-0.19	84	151	252	176
NM_014634	PPM1F	0.23	-0.11	1853	2335	3575	3139
NM_021959	PPP1R11	0.30	-0.01	676	936	2075	1913
NM_138689	PPP1R14B	0.15	-0.22	782	971	1585	1250
NM_145030	PPP1R35	0.03	-0.09	207	262	302	231
NM_178001	PPP2R4	0.48	-0.15	1780	2666	5669	4867
NM_000310	PPT1	0.18	-0.01	1067	1330	2017	1854
NM_003981	PRC1	0.03	-0.98	2695	2934	2502	1170
NM_013237	PRELID1	0.49	-0.06	1259	1927	3151	2850
NM_020820	PREX1	0.00	-0.10	114	111	193	139
NM_001291314	PRH1	0.00	-0.15	182	153	362	270
NM_000947	PRIM2	0.37	-0.14	362	549	460	355
NM_206907	PRKAA1	0.07	-0.02	994	1156	2136	1957
NM_006253	PRKAB1	0.00	-0.03	382	410	678	584
NM_145040	PRKCDBP	0.05	-0.27	975	1117	2261	1743
NM_006904	PRKDC	0.05	-0.04	6452	6943	13025	12318
NM_005044	PRKX	0.00	-0.17	134	128	206	142
NM_014502	PRPF19	0.02	-0.04	2027	2207	2051	1858
NM_002764	PRPS1	0.38	-0.37	2762	3797	4731	3486
NM_001039091	PRPS2	0.00	-0.03	618	690	584	497
NM_018304	PRR11	0.00	-0.78	1439	1460	1633	860
NM_018457	PRR13	0.33	-0.09	395	577	1553	1338

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_016644	PRR16	0.18	-0.21	413	545	424	309
NM_004638	PRRC2A	0.18	-0.12	8554	10007	12164	10817
NM_016307	PRRX2	0.10	-0.27	482	597	776	566
NM_003619	PRSS12	0.00	-0.06	1843	1817	1583	1392
NM_001184825	PSG1	0.36	-0.04	110	187	204	155
NM_021016	PSG3	0.00	-0.05	218	267	343	274
NM_002780	PSG4	0.34	-0.07	1589	2168	3350	3018
NM_002790	PSMA5	0.23	-0.19	1051	1360	1915	1547
NM_001282232	PSMA6	0.34	-0.07	730	1034	1458	1268
NM_002792	PSMA7	0.10	-0.11	3420	3876	6549	5802
NM_002795	PSMB3	0.19	-0.10	1288	1607	3259	2872
NM_001144932	PSMB5	0.37	-0.06	3103	4225	6906	6342
NM_001270481	PSMB6	0.13	-0.05	2176	2554	4586	4218
NM_002799	PSMB7	0.00	-0.07	3400	3560	7530	6909
NM_004159	PSMB8	0.17	-0.19	420	549	861	669
NM_002800	PSMB9	0.00	-1.12	91	124	171	55
NM_002803	PSMC2	0.10	-0.12	880	1046	2063	1760
NM_002804	PSMC3	0.22	-0.21	1655	2085	4143	3397
NM_002807	PSMD1	0.16	-0.01	2277	2720	5162	4882
NM_002817	PSMD13	0.41	-0.05	2208	3125	4723	4344
NM_005047	PSMD5	0.06	-0.06	911	1056	2073	1845
NM_002813	PSMD9	0.06	-0.09	1517	1712	2795	2460
NM_002818	PSME2	0.46	-0.17	131	232	430	322
NM_001267045	PSME3	0.30	-0.05	2495	3266	4166	3811
NM_032302	PSMG3	0.30	-0.37	315	460	510	336
NM_001128592	PSMG4	0.17	-0.01	129	189	212	165
NM_001032291	PSRC1	0.78	-0.66	138	300	304	153
NM_024430	PSTPIP2	0.41	-0.09	237	382	428	340
NM_002819	PTBP1	0.12	-0.04	4837	5496	5499	5122
NM_001284405	PTCD2	0.00	-0.12	156	127	299	224
NM_001166292	PTCH2	1.39	-0.50	1767	4937	3298	2185
NM_000956	PTGER2	0.00	-0.34	61	44	376	246
NM_001136042	PTGES3L-AARSD1	0.33	-0.04	259	391	532	445
NM_002824	PTMS	1.00	-0.05	2432	5150	3406	3107
NM_001010915	PTPLAD2	0.00	-0.03	43	44	125	89
NM_015967	PTPN22	0.00	-0.40	7	12	206	120
NM_016077	PTRH2	0.00	-0.04	416	473	796	684
NM_001282382	PTTG1	0.27	-1.35	389	548	595	192
NM_002852	PTX3	0.51	-0.41	8141	11999	2774	1952

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_013328	PYCR2	0.00	-0.05	1366	1453	1824	1627
NM_023078	PYCRL	0.00	-0.46	192	232	451	275
NM_005051	QARS	0.00	-0.04	2528	2638	4257	3935
NM_014298	QPRT	0.00	-0.27	11	26	651	468
NM_018292	QRSL1	0.03	-0.22	174	224	393	281
NM_006834	RAB32	0.85	-0.08	1109	2178	2263	1987
NM_004283	RAB3D	0.00	-0.10	270	238	572	462
NM_013401	RAB3IL1	0.15	-0.05	256	343	1073	932
NM_006822	RAB40B	0.00	-0.09	122	141	424	335
NM_016154	RAB4B	0.00	-0.09	204	243	657	538
NM_004251	RAB9A	-0.01	-0.02	585	505	838	736
NM_005833	RABEPK	0.00	-0.11	545	606	1225	1030
NM_001173988	RABL6	0.00	-0.02	2179	2117	3683	3449
NM_005052	RAC3	0.00	-0.10	82	94	177	126
NM_001126104	RACGAP1	0.00	-0.55	1187	1254	1237	758
NM_020165	RAD18	0.00	-0.12	681	643	609	488
NM_001270362	RAD23A	0.06	-0.18	3990	4387	6726	5700
NM_002875	RAD51	0.07	-0.44	380	469	297	176
NM_001130862	RAD51AP1	0.00	-0.28	195	205	110	63
NM_001142571	RAD51D	0.00	-0.06	240	247	283	220
NM_012415	RAD54B	0.00	-0.48	116	115	119	59
NM_152663	RALGPS2	0.00	-0.53	707	794	1385	865
NM_005855	RAMP1	0.00	-0.34	36	42	156	91
NM_001278639	RANBP1	0.34	-0.21	347	517	624	468
NM_001278651	RANGAP1	0.00	-0.07	6719	6809	7876	7238
NM_017805	RASIP1	0.29	-0.90	334	482	863	401
NM_178169	RASSF3	0.20	-0.43	903	1148	2117	1449
NM_001204467	RBM10	0.01	-0.12	1571	1713	2061	1756
NM_006047	RBM12	0.06	-0.20	2660	2953	2425	1974
NM_006328	RBM14	0.04	-0.06	1616	1800	1778	1571
NM_001198845	RBM14-RBM4	0.00	-0.03	1303	1253	2200	2009
NM_152945	RBM45	0.00	-0.30	150	133	268	174
NM_001098634	RBM47	0.00	-0.25	57	45	383	268
NM_032120	RBM48	0.00	-0.04	94	111	139	100
NM_001003793	RBMS3	0.00	-0.28	1828	1872	2119	1614
NM_006867	RBPMS	0.00	-0.10	868	949	1081	911
NM_001032279	RCE1	0.00	-0.12	285	327	397	307
NM_025232	REEP4	0.04	-0.21	478	569	616	462
NM_005045	RELN	0.17	-0.29	2490	2989	925	671

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_020385	REXO4	0.00	-0.18	640	642	1102	878
NM_001278791	RFC2	0.21	-0.03	457	611	493	414
NM_002915	RFC3	0.00	-0.49	403	440	308	176
NM_002916	RFC4	0.07	-0.17	422	516	318	231
NM_018339	RFK	0.23	-0.02	374	513	788	688
NM_018124	RFWD3	0.11	-0.18	1265	1495	1346	1081
NM_003721	RFXANK	0.32	-0.26	606	853	1395	1057
NM_001012761	RGMB	0.44	-0.12	6096	8610	9602	8534
NM_001282848	RGN	0.39	-0.49	31	67	195	105
NM_003702	RGS20	0.00	-0.31	48	41	173	105
NM_001282871	RHD	0.00	-0.35	44	54	106	57
NM_014578	RHOD	0.41	-0.21	193	317	670	505
NM_031430	RILP	0.00	-0.05	82	86	283	222
NM_032848	RITA1	0.00	-0.04	305	313	638	542
NM_006397	RNASEH2A	0.00	-0.40	807	755	815	543
NM_032015	RNF26	0.00	-0.39	1620	1637	2196	1553
NM_203387	RNH1	0.25	-0.01	5557	6898	14959	14456
NM_001286076	RPA2	0.23	-0.06	400	547	532	440
NM_032194	RPF2	0.00	-0.04	269	294	395	323
NM_006013	RPL10	0.15	-0.08	4357	5056	9288	8468
NM_007104	RPL10A	0.27	-0.39	1480	1938	3232	2307
NM_000975	RPL11	0.07	-0.12	4723	5204	8961	7965
NM_000976	RPL12	1.00	-0.11	317	741	1013	843
NM_033251	RPL13	0.41	-0.38	4442	6194	10648	7885
NM_012423	RPL13A	0.44	-0.22	2671	3849	5987	4915
NM_001253382	RPL15	0.26	-0.24	6011	7518	14955	12327
NM_000979	RPL18	0.11	-0.29	4194	4757	7699	6039
NM_000980	RPL18A	0.49	-0.41	1354	2065	3525	2503
NM_000981	RPL19	0.64	-0.23	1380	2332	3506	2817
NM_000983	RPL22	0.19	-0.01	1208	1507	2658	2466
NM_001099645	RPL22L1	0.00	-1.05	699	675	759	314
NM_000984	RPL23A	0.24	-0.12	1690	2158	3078	2671
NM_000986	RPL24	1.00	-0.16	345	801	980	784
NM_000987	RPL26	0.31	-0.09	1272	1720	3084	2725
NM_016093	RPL26L1	0.00	-0.05	234	285	553	462
NM_000990	RPL27A	0.12	-0.03	2132	2480	3388	3122
NM_001136134	RPL28	0.69	-0.02	4317	7259	9013	8553
NM_000967	RPL3	0.45	-0.28	6338	8994	11900	9482
NM_001099693	RPL31	0.43	-0.13	380	597	1027	843
NM_001007074	RPL32	0.97	-0.46	3916	8037	68665	49312

Table 6D: Differentially Downregulated Genes in SEN + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_033625	RPL34	0.33	-0.20	374	548	772	593
NM_007209	RPL35	0.07	-0.22	2140	2415	5538	4532
NM_033643	RPL36	0.80	-0.35	822	1579	2196	1593
NM_021029	RPL36A	0.13	-0.52	69	108	166	85
NM_052969	RPL39L	1.09	-0.17	82	234	302	218
NM_000968	RPL4	0.31	-0.31	4844	6298	10964	8527
NM_000969	RPL5	0.22	-0.12	2280	2836	5160	4514
NM_001024662	RPL6	0.00	-0.02	2195	2240	3596	3364
NM_000971	RPL7	0.39	-0.16	506	757	1111	893
NM_000972	RPL7A	0.36	-0.45	2918	3971	7740	5431
NM_001024921	RPL9	1.18	-0.12	389	1013	1096	906
NM_053275	RPLP0	0.31	-0.17	10422	13300	18261	15881
NM_001003	RPLP1	0.70	-0.34	1964	3408	3157	2338
NM_001004	RPLP2	1.11	-0.03	1117	2624	2797	2577
NM_001017	RPS13	0.04	-0.17	752	870	1281	1035
NM_001025070	RPS14	0.87	-0.48	1170	2319	4280	2911
NM_001018	RPS15	0.38	-0.55	1636	2301	4648	3017
NM_001020	RPS16	0.46	-0.24	2732	3995	5147	4159
NM_022551	RPS18	0.90	-0.26	517	1090	1845	1416
NM_002952	RPS2	0.18	-0.35	4327	5142	7042	5303
NM_001025	RPS23	0.60	-0.38	1525	2500	3660	2652
NM_001029	RPS26	0.00	-0.08	258	308	576	471
NM_015920	RPS27L	0.16	-0.13	1071	1313	3228	2773
NM_001260506	RPS3	0.23	-0.35	5032	6168	8541	6445
NM_001007	RPS4X	0.20	-0.17	3478	4204	6929	5928
NM_001009	RPS5	0.54	-0.29	1682	2634	3764	2915
NM_001010	RPS6	0.22	-0.25	9254	11144	18727	15381
NM_021135	RPS6KA2	0.19	-0.20	4011	4813	7445	6236
NM_001006944	RPS6KA4	0.26	-0.32	994	1311	1805	1327
NM_001011	RPS7	0.53	-0.62	972	1548	2452	1477
NM_001012	RPS8	0.24	-0.28	5557	6843	12336	9848
NM_001013	RPS9	0.00	-0.46	1923	1876	2824	1920
NM_002295	RPSA	0.00	-0.14	3931	3743	4311	3708
NM_173659	RPUSD3	0.00	-0.25	493	453	815	606
NM_032795	RPUSD4	0.15	-0.22	615	775	977	749
NM_001271634	RQCD1	0.16	-0.26	1830	2205	2227	1728
NM_001033	RRM1	0.28	-0.11	1840	2399	2573	2224
NM_001034	RRM2	0.00	-0.69	999	967	460	237
NM_016052	RRP15	0.06	-0.03	356	439	451	375
NM_033112	RRP36	0.68	-0.15	522	950	1720	1427

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_015703	RRP7A	0.25	-0.08	892	1180	1539	1338
NM_004704	RRP9	0.35	-0.12	505	734	690	558
NM_018346	RSAD1	0.00	-0.15	833	922	1450	1192
NM_032730	RTN4IP1	0.33	-0.10	35	71	135	92
NM_001105203	RUSC1	0.10	-0.05	970	1148	1809	1614
NM_003707	RUVBL1	0.00	-0.35	842	901	1512	1083
NM_006666	RUVBL2	0.37	-0.23	1628	2263	2928	2342
NM_016104	RWDD1	0.25	-0.06	443	610	973	839
NM_002960	S100A3	0.28	-0.11	50	91	162	113
NM_001400	S1PR1	0.05	-0.14	1060	1212	799	641
NM_005226	S1PR3	0.00	-0.16	650	619	663	518
NM_005500	SAE1	0.38	-0.20	1853	2596	3022	2466
NM_001101676	SAMD12	0.00	-0.24	390	415	287	196
NM_001258275	SAMD3	0.00	-0.42	22	24	121	63
NM_017827	SARS2	0.68	-0.24	168	334	553	403
NM_133491	SAT2	0.30	-0.28	639	890	1325	989
NM_005698	SCAMP3	0.22	-0.14	1598	2012	3818	3286
NM_152540	SCFD2	0.18	-0.56	1264	1559	3440	2189
NM_007281	SCRG1	0.52	-0.14	77	153	44	22
NM_002999	SDC4	0.29	-0.08	2244	2921	3165	2823
NM_138432	SDSL	0.00	-0.40	24	37	295	179
NM_006808	SEC61B	0.91	-0.21	318	701	1125	876
NM_001258289	SELENBP1	0.19	-0.77	36	66	204	89
NM_153617	SEMA6D	0.16	-0.29	234	320	58	28
NM_016955	SEPSECS	0.00	-0.02	109	106	193	148
NM_001018067	SERBP1	0.00	-0.19	2706	2729	3267	2697
NM_004155	SERPINB9	0.24	-0.74	217	315	258	120
NM_002615	SERPINF1	0.34	-0.56	229	353	1210	734
NM_001207014	SERPINH1	0.28	-0.06	8513	10678	10523	9763
NM_012426	SF3B3	0.31	-0.12	3833	4988	6451	5689
NM_005850	SF3B4	0.10	-0.07	1271	1488	1522	1325
NM_031287	SF3B5	0.21	-0.02	1359	1706	2859	2654
NM_005066	SFPQ	0.33	-0.05	2459	3294	2512	2274
NM_003012	SFRP1	0.00	-0.15	1351	1346	4190	3575
NM_001261411	SFSWAP	0.28	-0.17	602	829	952	754
NM_005627	SGK1	0.05	-0.06	8304	8922	3589	3244
NM_001080826	SGK223	0.01	-0.07	561	646	1487	1298
NM_001160033	SGOL2	0.00	-0.13	374	341	385	294
NM_001103161	SH2D5	0.08	-0.50	729	869	738	453
NM_014521	SH3BP4	0.28	-0.06	4207	5375	6443	5944

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_203349	SHC4	0.00	-0.61	1	7	81	33
NM_024745	SHCBP1	0.05	-0.64	929	1066	782	436
NM_138356	SHF	1.28	-2.03	243	699	524	100
NM_001272067	SHISA5	0.12	-0.29	2286	2655	4887	3789
NM_020859	SHROOM3	0.25	-0.21	1335	1723	2408	1939
NM_001135054	SIGIRR	0.00	-0.32	243	194	559	383
NM_012237	SIRT2	0.11	-0.06	862	1036	2057	1837
NM_012241	SIRT5	0.04	-0.32	183	237	489	331
NM_016539	SIRT6	0.43	-0.11	207	341	532	423
NM_006427	SIVA1	0.31	-0.20	410	591	674	512
NM_001039535	SKA1	0.00	-0.49	319	316	225	124
NM_182620	SKA2	0.17	-0.02	338	448	485	410
NM_145061	SKA3	0.00	-0.32	364	405	277	177
NM_005983	SKP2	0.07	-0.45	390	480	539	336
NM_001270622	SLC16A7	0.00	-0.52	787	798	742	451
NM_194255	SLC19A1	0.00	-0.38	245	206	237	142
NM_001270888	SLC25A10	0.00	-0.25	265	285	485	346
NM_024698	SLC25A22	0.29	-0.07	665	918	898	763
NM_013386	SLC25A24	0.14	-0.01	984	1196	1714	1569
NM_213611	SLC25A3	0.24	-0.22	5866	7201	10822	8978
NM_018843	SLC25A40	0.22	-0.03	173	254	287	229
NM_001152	SLC25A5	0.25	-0.46	2798	3536	4390	3018
NM_005094	SLC27A4	0.08	-0.19	934	1093	2874	2357
NM_012254	SLC27A5	0.05	-0.22	34	58	79	44
NM_080670	SLC35A4	0.07	-0.22	1472	1678	2512	2018
NM_198277	SLC37A2	0.00	-0.01	116	119	530	453
NM_001271957	SLC39A1	0.44	-0.22	1202	1783	2593	2079
NM_001278206	SLC43A3	0.00	-0.50	1549	1671	630	384
NM_001287587	SLC50A1	0.00	-0.20	523	583	1190	939
NM_021095	SLC5A6	0.00	-0.11	608	676	830	684
NM_020949	SLC7A14	0.00	-0.68	21	18	198	92
NM_004787	SLIT2	0.22	-0.20	2629	3250	3479	2859
NM_005902	SMAD3	0.42	-0.27	984	1446	2394	1852
NM_022733	SMAP2	0.05	-0.44	1083	1234	2159	1475
NM_003069	SMARCA1	0.04	-0.31	765	885	1770	1312
NM_003073	SMARCB1	0.00	-0.03	1651	1755	2028	1848
NM_058182	SMIM11	0.00	-0.03	149	180	241	189
NM_001124767	SMIM4	0.12	-0.27	132	187	597	427
NM_003068	SNAI2	0.72	-0.20	777	1415	3885	3205
NM_007241	SNF8	0.16	-0.03	516	659	1348	1203

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_004596	SNRPA	0.00	-0.03	743	753	965	848
NM_003091	SNRPB	0.01	-0.19	5364	5663	5415	4543
NM_003092	SNRPB2	0.00	-0.18	410	475	468	351
NM_003093	SNRPC	0.19	-0.03	448	593	851	741
NM_006938	SNRPD1	0.00	-0.12	314	372	387	298
NM_177542	SNRPD2	0.10	-0.02	2155	2468	4706	4427
NM_003095	SNRPF	0.00	-0.62	159	129	277	142
NM_003102	SOD3	0.00	-0.62	149	179	297	153
NM_080627	SOGA1	0.00	-0.11	2506	2469	3238	2817
NM_006461	SPAG5	0.19	-0.74	1406	1748	1310	706
NM_004890	SPAG7	0.00	-0.10	728	707	1524	1299
NM_001142854	SPATC1L	0.00	-0.23	153	172	308	214
NM_182513	SPC24	0.62	-0.83	97	199	235	100
NM_020675	SPC25	0.49	-0.65	87	166	133	59
NM_015330	SPECC1L	0.00	-0.02	2530	2652	4076	3810
NM_182965	SPHK1	0.01	-0.47	5455	5745	7699	5351
NM_001080394	SPIDR	0.07	-0.14	461	559	986	799
NM_144569	SPOCD1	0.10	-0.54	830	995	3261	2103
NM_032641	SPSB2	0.00	-0.30	97	104	412	279
NM_003131	SRF	0.00	-0.02	1689	1742	2132	1957
NM_003130	SRI	0.00	-0.12	578	567	1117	926
NM_005839	SRRM1	0.20	-0.07	1724	2133	2466	2201
NM_003142	SSB	0.00	-0.11	681	706	903	745
NM_018984	SSH1	0.25	-0.09	5186	6444	7975	7198
NM_017857	SSH3	0.29	-0.10	153	238	780	641
NM_003731	SSNA1	0.57	-0.07	722	1197	1926	1693
NM_003145	SSR2	0.29	-0.08	3942	5062	6441	5854
NM_003146	SSRP1	0.19	-0.05	2681	3257	3741	3414
NM_001049	SSTR1	0.00	-1.02	1568	1598	2042	921
NM_213618	ST5	0.17	-0.01	440	572	984	876
NM_175039	ST6GALNAC4	0.78	-0.20	396	782	1572	1251
NM_015136	STAB1	0.69	-0.20	210	412	724	551
NM_001013841	STAP2	0.23	-0.24	57	98	133	81
NM_032016	STARD3NL	0.66	-0.08	347	641	1040	882
NM_007315	STAT1	0.42	-0.20	2776	3945	6961	5798
NM_012449	STEAP1	0.00	-0.10	501	502	1549	1322
NM_207342	STEAP1B	0.21	-0.04	259	363	327	262
NM_182915	STEAP3	0.26	-0.23	849	1128	3350	2682
NM_001282936	STIL	0.02	-0.20	517	604	485	359

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001243313	STK36	0.00	-0.21	249	263	761	580
NM_005563	STMN1	0.10	-0.54	2797	3175	3413	2203
NM_001199214	STMN2	0.54	-1.62	5	26	946	261
NM_015894	STMN3	0.00	-0.77	121	89	218	96
NM_004099	STOM	0.02	-0.50	4540	4816	6430	4331
NM_013442	STOML2	0.14	-0.37	1807	2150	4018	2932
NM_001271006	STRA13	0.23	-0.31	621	826	955	686
NM_001171137	STRBP	0.00	-0.14	76	84	160	109
NM_001039877	STRN4	0.00	-0.10	2120	2221	2980	2615
NM_016930	STX18	0.29	-0.09	201	304	624	510
NM_003848	SUCLG2	0.15	-0.18	509	648	1065	847
NM_001017392	SUGP2	0.21	-0.10	1536	1918	3361	2950
NM_001128205	SULF1	0.13	-0.12	6706	7605	21270	19087
NM_000456	SUOX	0.49	-0.36	211	362	641	433
NM_003599	SUPT3H	0.00	-0.32	127	98	281	181
NM_001278942	SURF6	0.10	-0.08	463	574	693	577
NM_019601	SUSD2	0.00	-0.37	31	30	79	39
NM_001287005	SUSD3	0.00	-0.45	106	139	102	50
NM_003173	SUV39H1	0.11	-0.32	353	448	391	261
NM_014849	SV2A	0.00	-0.32	607	629	857	608
NM_033025	SYDE1	0.31	-0.16	2110	2793	2691	2253
NM_030786	SYNC	0.11	-0.10	2376	2729	6052	5397
NM_001159677	SYNCRIP	0.19	-0.11	1592	1967	2518	2183
NM_015180	SYNE2	0.00	-0.63	329	317	447	240
NM_018373	SYNJ2BP	0.00	-0.03	575	657	1483	1329
NM_001040709	SYPL2	0.00	-0.46	20	19	218	122
NM_001114600	SZRD1	0.37	-0.05	4090	5541	6802	6320
NM_006342	TACC3	0.25	-0.66	815	1078	821	455
NM_016360	TACO1	0.00	-0.33	502	506	703	486
NM_006354	TADA3	0.34	-0.05	1229	1697	3296	3005
NM_014409	TAF5L	0.54	-0.10	370	627	653	532
NM_001190415	TAF6	0.47	-0.13	763	1179	1568	1311
NM_001001522	TAGLN	0.57	-0.44	34290	51712	62715	45611
NM_003564	TAGLN2	-0.01	-0.02	11144	10731	15732	15146
NM_006755	TALDO1	0.09	-0.09	6037	6707	11030	10065
NM_001145909	TANC1	0.24	-0.04	1163	1505	3687	3403
NM_024562	TANGO6	0.57	-0.10	648	1079	1491	1275
NM_000593	TAP1	0.00	-0.11	1499	1493	2439	2116
NM_000544	TAP2	0.00	-0.05	931	1008	1585	1401
NM_145647	TBC1D31	0.00	-0.09	118	150	189	137

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001139466	TBL1X	0.11	-0.04	715	870	1666	1494
NM_006453	TBL3	-0.01	-0.17	1041	932	1452	1181
NM_001006935	TCEAL4	0.00	-0.23	1056	1093	1947	1532
NM_152278	TCEAL7	0.00	-0.06	93	69	356	283
NM_153333	TCEAL8	0.07	-0.10	576	691	1304	1103
NM_007109	TCF19	0.09	-0.37	1654	1905	1316	921
NM_198392	TCF21	1.22	-1.91	17	73	69	6
NM_001134851	TCF7	0.00	-0.13	229	208	1770	1495
NM_031283	TCF7L1	0.00	-0.03	492	492	416	344
NM_018319	TDP1	0.00	-0.04	649	620	678	580
NM_001256661	TEAD2	0.16	-0.10	545	696	1065	895
NM_003213	TEAD4	0.50	-0.39	384	632	233	139
NM_016111	TELO2	0.00	-0.03	619	685	1123	993
NM_170754	TENC1	0.13	-0.08	597	744	1603	1388
NM_017746	TEX10	0.06	-0.16	532	637	1298	1054
NM_007111	TFDP1	0.15	-0.01	1415	1708	1857	1702
NM_015927	TGFB1I1	0.25	-0.16	1804	2303	3088	2590
NM_138350	THAP3	0.17	-0.20	485	629	844	651
NM_000361	THBD	0.30	-0.06	381	547	2575	2307
NM_003247	THBS2	0.26	-0.03	13115	16124	32251	31038
NM_003249	THOP1	0.08	-0.29	1244	1441	1965	1482
NM_018676	THSD1	0.00	-0.05	129	147	362	292
NM_024817	THSD4	0.02	-0.53	790	897	1707	1081
NM_012454	TIAM2	0.20	-0.31	456	607	1483	1091
NM_182919	TICAM1	0.63	-0.38	443	786	961	658
NM_012458	TIMM13	0.00	-0.33	1275	1270	2196	1614
NM_001167947	TIMM17B	0.32	-0.37	239	363	595	397
NM_003258	TK1	0.31	-0.43	1595	2129	1042	688
NM_001135055	TKT	0.06	-0.15	13833	14856	17057	14972
NM_001282748	TLE4	0.01	-0.10	1903	2067	1104	930
NM_015059	TLN2	0.09	-0.10	2058	2352	4839	4309
NM_018352	TMA16	0.00	-0.46	383	363	324	190
NM_015933	TMA7	0.00	-0.16	128	152	331	244
NM_181719	TMCO4	0.63	-0.34	323	586	537	362
NM_032354	TMEM107	1.49	-0.03	1693	5070	5099	4754
NM_181724	TMEM119	0.00	-1.22	65	56	435	150
NM_032928	TMEM141	0.47	-0.12	314	515	1210	1009
NM_017854	TMEM160	0.00	-0.23	51	51	98	57
NM_001161342	TMEM171	0.00	-0.33	222	255	293	187
NM_198282	TMEM173	0.00	-0.60	939	947	1069	627

Table 6D: Differentially Downregulated Genes in SEN + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001105198	TMEM177	0.00	-0.33	89	123	179	107
NM_001142645	TMEM194B	0.00	-0.40	57	73	87	43
NM_053045	TMEM203	0.17	-0.01	639	814	1414	1281
NM_001004313	TMEM220	0.00	-0.38	111	92	177	102
NM_032933	TMEM241	0.00	-0.03	218	250	476	399
NM_152766	TMEM256	0.00	-0.10	171	140	478	379
NM_033428	TMEM261	0.00	-0.18	356	343	632	486
NM_018056	TMEM39B	0.36	-0.05	354	534	711	603
NM_014573	TMEM97	0.40	-0.08	219	353	482	388
NM_001032283	TMPO	0.22	-0.50	619	815	539	323
NM_021109	TMSB4X	0.45	-0.08	10426	14703	30300	28081
NM_032813	TMTC4	0.71	-0.03	171	348	349	283
NM_002160	TNC	0.26	-1.03	3327	4199	13501	6370
NM_021137	TNFAIP1	0.24	-0.18	2185	2763	3569	2981
NM_152362	TNFAIP8L1	0.81	-0.10	54	137	185	133
NM_002546	TNFRSF11B	0.01	-0.49	5506	5798	1795	1168
NM_016639	TNFRSF12A	0.05	-0.10	6207	6707	6863	6142
NM_003820	TNFRSF14	0.00	-0.02	320	331	959	847
NM_001066	TNFRSF1B	0.00	-0.48	237	265	351	205
NM_020243	TOMM22	0.34	-0.34	731	1034	1884	1375
NM_006809	TOMM34	0.00	-0.10	1396	1469	3332	2926
NM_001134484	TOMM5	0.45	-0.04	479	749	911	791
NM_001134493	TOMM6	0.03	-0.08	1043	1174	2389	2107
NM_001067	TOP2A	0.00	-0.76	2346	2513	2562	1401
NM_004881	TP53I3	0.50	-0.40	387	634	2269	1599
NM_022445	TPK1	0.00	-0.24	39	45	89	50
NM_213674	TPM2	0.18	-0.13	16559	19170	30082	26996
NM_001278189	TPM3	0.29	-0.04	4631	5922	9286	8747
NM_001145160	TPM4	0.19	-0.27	26570	30835	63316	51679
NM_012112	TPX2	0.41	-1.02	1714	2454	2354	1068
NM_004593	TRA2B	0.00	-0.04	2176	2086	1824	1634
NM_021138	TRAF2	0.09	-0.15	380	476	422	320
NM_005879	TRAIP	0.54	-0.24	91	178	189	122
NM_001042646	TRAK1	0.25	-0.02	2483	3133	2190	2007
NM_016381	TREX1	0.00	-0.24	416	487	580	423
NM_013381	TRHDE	0.00	-1.11	321	324	152	48
NM_014788	TRIM14	0.00	-0.13	270	284	807	654
NM_016102	TRIM17	0.00	-0.05	59	45	71	44
NM_003141	TRIM21	0.31	-0.23	353	513	684	510
NM_015431	TRIM58	0.00	-0.45	462	453	865	558

Table 6D: Differentially Downregulated Genes in SEN + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_173084	TRIM59	0.00	-0.14	461	442	451	346
NM_001003819	TRIM6-TRIM34	0.08	-0.03	276	352	545	462
NM_173547	TRIM65	0.24	-0.02	410	563	497	421
NM_018073	TRIM68	0.06	-0.14	259	328	433	331
NM_004237	TRIP13	0.00	-0.62	820	884	950	545
NM_003302	TRIP6	0.18	-0.42	1387	1710	2899	2020
NM_001286082	TRMT112	0.38	-0.30	753	1097	1699	1270
NM_001257994	TRMT2A	0.43	-0.04	621	944	1300	1150
NM_024917	TRMT2B	0.00	-0.35	355	346	645	438
NM_017910	TRMT61B	0.25	-0.23	149	226	308	214
NM_005480	TROAP	0.00	-1.46	408	454	291	79
NM_003306	TRPC4	0.30	-1.13	948	1285	1004	399
NM_016113	TRPV2	0.37	-0.33	2156	2966	9808	7508
NM_015679	TRUB2	0.00	-0.05	645	731	1620	1440
NM_000368	TSC1	0.13	-0.08	1217	1458	3363	3009
NM_207346	TSEN54	0.05	-0.05	229	292	220	168
NM_001290212	TSPAN10	0.00	-0.48	7	9	162	85
NM_001256530	TSPO	0.00	-0.05	1794	1699	3467	3153
NM_052841	TSSK3	0.44	-0.08	24	57	48	26
NM_003313	TSTA3	0.03	-0.06	918	1041	1624	1434
NM_001282500	TTC1	0.27	-0.07	710	960	1583	1381
NM_022492	TTC31	0.00	-0.04	374	440	832	719
NM_017931	TTC38	0.00	-0.02	435	482	832	728
NM_003594	TTF2	0.08	-0.20	631	754	728	555
NM_001166691	TTK	0.15	-0.92	255	343	335	140
NM_025250	TTYH3	0.19	-0.32	2562	3105	3136	2364
NM_001270399	TUBA1A	0.67	-0.43	5700	9409	17311	12504
NM_006082	TUBA1B	0.49	-0.64	24029	34465	32484	20447
NM_032704	TUBA1C	0.39	-0.64	15529	20794	21822	13643
NM_178014	TUBB	0.48	-0.35	30537	43320	56651	43657
NM_001069	TUBB2A	0.27	-0.19	2069	2675	4157	3462
NM_178012	TUBB2B	0.56	-0.43	541	903	1657	1126
NM_006086	TUBB3	0.19	-0.39	1065	1341	8198	6004
NM_001289130	TUBB4A	1.77	-0.90	13	89	116	41
NM_006088	TUBB4B	0.30	-0.52	12969	16445	15350	10364
NM_032525	TUBB6	0.42	-0.36	17083	23402	33459	25606
NM_001070	TUBG1	0.75	-0.17	964	1778	2236	1850
NM_000474	TWIST1	0.00	-0.33	312	362	337	220
NM_001002926	TWISTNB	0.10	-0.01	310	396	568	488

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_012473	TXN2	0.23	-0.06	642	853	1587	1401
NM_006440	TXNRD2	0.00	-0.06	335	398	695	584
NM_001071	TYMS	0.00	-0.28	1940	2079	873	638
NM_001025204	U2AF1	0.00	-0.18	698	642	684	527
NM_003968	UBA3	0.00	-0.02	801	856	1389	1253
NM_003335	UBA7	0.00	-0.10	684	725	1304	1107
NM_016172	UBAC1	0.30	-0.05	715	985	1994	1786
NM_018449	UBAP2	0.20	-0.04	1613	2004	2304	2092
NM_014847	UBAP2L	0.08	-0.03	4869	5372	7433	6989
NM_181801	UBE2C	0.00	-0.60	500	428	439	240
NM_015983	UBE2D4	0.11	-0.05	186	252	622	523
NM_004223	UBE2L6	0.00	-0.11	696	728	1718	1469
NM_014501	UBE2S	0.37	-0.50	597	871	761	468
NM_014176	UBE2T	0.18	-0.41	255	350	297	179
NM_024292	UBL5	0.00	-0.14	388	386	799	640
NM_020131	UBQLN4	0.00	-0.03	844	891	1223	1085
NM_001261450	UCK1	0.10	-0.06	461	572	977	843
NM_003358	UGCG	0.00	-0.08	783	782	921	778
NM_001048201	UHRF1	0.15	-0.71	1218	1481	547	283
NM_001080419	UNK	0.66	-0.21	225	430	672	506
NM_001003684	UQCR10	0.10	-0.29	792	952	1955	1471
NM_003366	UQCRC2	0.22	-0.01	1675	2101	3250	3039
NM_014825	URB1	0.00	-0.14	2551	2630	2999	2554
NM_001265582	URM1	0.33	-0.36	925	1282	2562	1863
NM_003368	USP1	0.00	-0.04	979	1001	586	494
NM_001272075	USP10	0.03	-0.01	1256	1401	2250	2081
NM_003940	USP13	0.00	-0.18	1038	1125	1628	1322
NM_018218	USP40	0.05	-0.10	483	577	1510	1294
NM_006649	UTP14A	0.34	-0.25	273	415	526	379
NM_032175	UTP15	0.11	-0.15	320	410	534	412
NM_016001	UTP18	0.35	-0.16	171	274	416	314
NM_014503	UTP20	0.03	-0.16	862	978	1356	1107
NM_006634	VAMP5	0.00	-0.07	568	541	992	847
NM_003370	VASP	0.47	-0.20	1454	2178	3876	3200
NM_020927	VAT1L	0.00	-0.21	69	92	595	444
NM_015873	VILL	0.00	-0.15	92	110	156	105
NM_032353	VPS25	0.00	-0.12	909	978	1657	1397
NM_001271087	VPS72	0.07	-0.28	892	1042	1352	1011
NM_004913	VPS9D1	0.00	-0.17	342	324	717	560
NM_016440	VRK3	0.39	-0.14	439	664	1029	839

Table 6D: Differentially Downregulated Genes in SEN + IL-2							
RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_006370	VTI1B	0.00	-0.05	657	743	1343	1185
NM_152559	WBSCR27	0.15	-0.47	62	100	164	87
NM_020830	WDFY1	0.16	-0.16	2012	2405	3664	3098
NM_017883	WDR13	0.00	-0.06	665	751	1497	1314
NM_024100	WDR18	0.18	-0.40	293	397	626	410
NM_052844	WDR34	0.48	-0.43	276	459	969	641
NM_001260474	WDR4	0.22	-0.14	445	598	510	396
NM_017588	WDR5	0.14	-0.20	616	769	994	776
NM_017706	WDR55	0.00	-0.03	892	928	1298	1157
NM_018031	WDR6	0.00	-0.05	3465	3598	4964	4586
NM_001083961	WDR62	0.49	-0.16	439	710	462	351
NM_024102	WDR77	0.33	-0.06	746	1049	1911	1702
NM_133330	WHSC1	0.10	-0.26	4227	4755	3920	3096
NM_032387	WNK4	0.12	-0.18	3386	3883	2441	2007
NM_001080436	WTIP	0.45	-0.04	684	1050	821	710
NM_001100119	XRCC3	0.00	-0.23	538	579	493	359
NM_021141	XRCC5	0.06	-0.13	5681	6182	9774	8660
NM_022167	XYLT2	0.24	-0.03	1661	2111	2818	2588
NM_006761	YWHAE	0.34	-0.06	6442	8456	13305	12358
NM_139121	YY1AP1	0.00	-0.35	1724	1821	3379	2495
NM_133646	ZAK	0.00	-0.04	2997	3039	5026	4664
NM_032799	ZDHHC12	0.00	-0.11	528	549	934	773
NM_024721	ZFHX4	0.00	-0.13	4031	3981	3978	3455
NM_003407	ZFP36	0.01	-0.41	1190	1319	1102	745
NM_032527	ZGPAT	0.00	-0.30	420	478	767	547
NM_003412	ZIC1	0.29	-0.28	188	285	437	303
NM_019103	ZMAT5	0.00	-0.07	219	268	651	542
NM_003434	ZNF133	0.25	-0.23	244	351	510	372
NM_006963	ZNF22	0.00	-0.18	338	397	418	309
NM_001099282	ZNF239	0.37	-0.02	52	100	214	166
NM_005773	ZNF256	0.00	-0.30	82	111	162	98
NM_014487	ZNF330	0.26	-0.04	747	1003	990	863
NM_001282933	ZNF341	0.33	-0.03	147	236	160	118
NM_153695	ZNF367	0.00	-0.24	594	663	241	161
NM_144689	ZNF420	0.00	-0.05	81	63	143	102
NM_152355	ZNF441	0.00	-0.03	105	130	254	200
NM_005815	ZNF443	0.00	-0.06	60	47	98	65
NM_021224	ZNF462	0.19	-0.19	513	671	1410	1128
NM_001006656	ZNF473	0.19	-0.03	210	295	318	257
NM_032752	ZNF496	0.00	-0.09	445	462	553	449

Table 6D: Differentially Downregulated Genes in SEN + IL-2

RefSeq ID	Gene Symbol	SR GFOLD	SEN GFOLD	SR IL-2 -	SR IL-2 +	SEN IL-2 -	SEN IL-2 +
NM_001271318	ZNF512	0.00	-0.03	291	317	562	477
NM_133444	ZNF526	0.13	-0.05	758	930	1183	1037
NM_001042474	ZNF565	0.02	-0.49	75	108	173	91
NM_022752	ZNF574	0.41	-0.15	508	772	886	708
NM_001145347	ZNF576	0.00	-0.08	216	257	449	360
NM_016089	ZNF589	0.00	-0.03	121	118	185	140
NM_133374	ZNF618	0.05	-0.03	1493	1678	2710	2484
NM_001080417	ZNF629	0.16	-0.07	833	1036	1788	1571
NM_024804	ZNF669	0.00	-0.34	112	100	158	92
NM_145271	ZNF688	0.00	-0.11	79	86	187	133
NM_001282795	ZNF7	0.00	-0.05	206	246	376	303
NM_025069	ZNF703	0.21	-0.16	285	396	433	327
NM_001010880	ZNF780A	0.00	-0.06	70	96	220	166
NM_001195605	ZNF865	0.22	-0.02	185	269	283	227
NM_014205	ZNHIT2	0.96	-0.14	48	137	220	157
NM_001278786	ZNRD1	0.00	-0.10	374	341	437	344
NM_001042697	ZSWIM7	0.00	-0.10	122	152	339	261
NM_001287821	ZWILCH	0.26	-0.21	310	440	497	366
NM_032997	ZWINT	0.47	-0.53	607	947	819	497

able 7: Proteins Expression With and Without IL-2 treatment in SR and SEN hADSCs

aw data protein microarray (normalized values against negative)

		SR			SR + IL2			SEN			SEN + IL2		
Protein Name	**10% PRP**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**
Acrp30	1.9906	1.7267	0.0000	1.9846	1.3016	2.3799	1.3797	1.4034	1.6601	1.2449	1.1842	2.1786	2.7266
Activin A	5.5127	3.8425	7.0180	3.5865	2.6392	7.2831	5.8653	4.8911	8.4566	2.2450	3.2213	6.7031	2.7259
AgRP	2.1403	2.0670	1.1545	2.3200	1.4000	2.5571	1.4548	1.4184	1.3673	0.0000	1.2969	1.9093	2.8466
ALCAM	5.2309	4.1953	7.6635	3.5971	2.3671	7.2204	5.4144	5.1089	7.8102	2.4079	3.0986	5.3750	2.7221
ANG	0.0000	0.0000	0.0000	1.5127	0.0000	0.0000	1.1264	1.1170	0.0000	0.0000	1.1488	0.0000	0.0000
ANGPT2	2.1696	1.9598	0.0000	2.1267	1.6403	2.2390	1.3215	1.2514	1.4214	1.2900	1.1470	1.8578	2.8152
AREG	1.8281	1.6344	0.0000	1.9837	1.2505	1.9108	1.1054	0.0000	0.0000	0.0000	1.1028	1.2819	1.8805
Axl	1.7897	1.4567	0.0000	1.7697	0.0000	1.6622	0.0000	0.0000	0.0000	1.1594	1.0313	1.1653	1.5707
b-NGF	1.4432	1.2653	0.0000	1.4735	0.0000	1.4234	0.0000	1.1838	0.0000	1.3909	1.3112	1.1327	1.7046
BDNF	0.0000	1.3009	1.5763	2.2460	1.1868	1.4820	1.5919	1.7004	1.3962	0.0000	1.7874	2.1395	1.7741
bFGF	2.0525	1.6365	1.1390	1.8419	1.3603	1.7292	0.0000	1.1812	1.2779	1.5579	1.4446	1.6634	2.5339
BLC (CXCL13)	0.0000	0.0000	1.1843	1.5858	0.0000	0.0000	0.0000	1.2457	0.0000	0.0000	1.4209	1.3900	0.0000
BMP 5	4.8192	5.1370	8.6495	3.7048	1.4304	7.1869	6.1152	5.9347	11.7418	3.2899	3.6011	7.1250	3.4143
BMP 7	4.1543	4.9228	7.1538	3.5586	0.0000	6.1955	5.2938	5.5754	8.4778	2.9665	3.1606	4.5625	3.2136
BMP4	0.0000	0.0000	1.3010	1.6810	0.0000	0.0000	1.1395	1.3177	1.4824	0.0000	1.8827	2.1601	1.2792
BMP6	0.0000	0.0000	0.0000	1.3908	0.0000	0.0000	0.0000	1.1172	1.1257	0.0000	1.9253	1.8054	0.0000
BTC	1.2327	1.2265	1.2349	1.4869	0.0000	1.3380	0.0000	1.1707	1.3156	1.5758	1.5331	1.1887	2.0910
CCL23	0.0000	0.0000	1.4156	1.7443	0.0000	1.1108	1.3719	1.6100	1.6595	0.0000	3.0483	2.5000	1.2505
CCL28	0.0000	0.0000	1.1480	1.6428	0.0000	0.0000	1.6927	0.0000	1.1613	1.1350	0.0000	1.2443	2.5985
CD14	3.1727	4.6425	7.4476	4.3188	0.0000	5.7709	4.8656	6.7465	8.4355	3.8385	4.4048	5.5625	3.4105
CD80	4.2398	3.3165	7.9128	3.3382	1.5886	6.5427	5.1120	5.2037	8.0751	2.6430	2.9403	5.0625	2.6128
CNTF	0.0000	0.0000	1.3880	1.5508	0.0000	1.1316	1.2175	1.6206	1.6156	0.0000	3.3783	2.8787	1.5144
CT-1	3.6318	4.8724	7.7881	4.4073	0.0000	6.5615	5.5979	6.7356	9.8767	3.6226	4.1365	7.0938	3.7065
CTACK (CCL27)	5.9157	8.2865	1.6690	4.5118	11.2803	6.6482	4.0186	3.7664	10.6590	2.8290	3.9831	5.8344	7.8050
CXCL16	1.4312	2.6425	5.4889	3.4248	0.0000	3.4910	2.8627	5.1182	3.8786	2.9027	3.9219	2.3125	2.5887
DR6 (TNFRSF21)	1.1811	3.2283	7.4088	4.6902	0.0000	4.4782	24.8942	6.0855	10.5125	4.3387	5.4060	7.5000	4.1333

able 7: Proteins Expression With and Without IL-2 treatment in SR and SEN hADSCs

aw data protein microarray (normalized values against negative)

		SR			SR + IL2			SEN			SEN + IL2		
Protein Name	**10% PRP**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**
Dtk (TYRO)	2.5474	2.5898	0.0000	1.8760	2.4431	3.2288	2.1533	2.1400	2.4860	0.0000	2.3962	2.7945	1.9706
E selectin	3.9643	4.6929	8.5605	4.0955	2.7215	7.5927	5.8635	4.7247	7.9374	2.2535	3.1821	10.5625	2.9482
EGF	0.0000	0.0000	1.2835	1.4322	0.0000	0.0000	1.2638	1.4882	1.8373	0.0000	3.5073	2.6390	1.3703
EGFR	2.2096	2.0563	0.0000	1.6972	1.5212	2.7657	1.8194	2.0575	1.9257	0.0000	1.9208	2.1894	1.5882
ENA-78 (CXCL5)	2.3239	2.1126	0.0000	2.0400	1.4142	3.0456	1.9233	2.2308	1.8874	0.0000	2.0352	2.0060	2.1837
Endoglin	8.0299	9.2661	13.1501	4.0926	7.0000	12.8678	9.3310	6.7481	23.0173	3.6180	5.1092	24.7188	4.2247
Eotaxin 1 (CCL11)	0.0000	0.0000	1.1909	1.5127	0.0000	0.0000	2.4429	1.2626	1.4283	0.0000	3.3451	2.0151	1.9433
Eotaxin 2 (CCL24)	1.3070	1.1844	1.2730	2.2540	1.4237	1.2616	1.8056	1.5405	2.5752	1.2580	1.4635	2.3263	1.6947
Eotaxin 3 CCL26)	1.2536	1.2052	1.4199	2.2715	1.3567	1.3012	1.7425	1.5603	1.8755	1.1319	1.6620	1.7742	1.5389
ErbB3	6.2568	7.8142	12.1552	4.5574	5.6392	11.7007	8.1198	5.6967	15.8112	3.1470	4.3441	22.2031	3.8487
Fas	2.4938	2.4572	0.0000	2.1110	1.3889	3.1952	1.7997	2.3597	1.9900	0.0000	2.3167	2.2383	1.8808
Fas ligand	5.2372	3.9402	8.6851	4.3178	2.2215	7.7056	5.3060	5.4386	10.0568	2.3741	3.3074	5.6563	2.5277
FGF-4	2.2505	2.0995	0.0000	2.0520	1.1243	2.9649	1.5879	2.0905	1.6439	0.0000	1.8951	1.8751	1.7765
FGF-6	1.2219	1.2272	1.4400	2.2757	1.3695	1.2044	1.5075	1.6746	1.7251	1.1717	1.8035	2.3610	1.8691
FGF-7	0.0000	0.0000	1.1132	1.8267	0.0000	0.0000	1.2607	1.2692	1.3712	0.0000	1.2963	1.7545	1.5419
FGF-9	2.8139	2.6479	1.3408	2.6706	1.7241	3.5488	1.8125	2.2538	2.2583	1.4065	2.1909	2.2993	2.9721
Flt-3 Ligand	0.0000	0.0000	1.1708	1.8777	0.0000	1.1343	1.1448	1.3154	1.1395	0.0000	1.3677	1.3139	1.2909
Fractalkine (CX3CL1)	0.0000	0.0000	0.0000	1.7596	0.0000	1.1105	1.1444	1.2833	0.0000	0.0000	1.3101	1.2827	1.2385
G-CFS (CSF3)	3.2969	3.6056	0.0000	1.9394	2.2853	2.6573	1.3552	2.2872	1.9620	0.0000	2.1202	1.6272	1.2719
GCP-2 (CXCL6)	0.0000	0.0000	1.2054	1.7991	0.0000	1.1592	1.2924	1.4153	0.0000	0.0000	1.4873	1.4507	1.2751
GDNF	1.1058	1.2071	1.3212	1.8110	1.1124	1.1926	1.3473	1.3364	1.6682	1.1385	1.6584	2.0279	1.5048
GITR	2.2719	2.1740	1.2024	2.0871	1.6620	2.4562	1.3362	1.7997	1.3507	1.1715	1.8460	1.4030	1.7477
GITR ligand	2.2175	2.3456	1.1608	1.6428	1.6049	2.6509	1.6927	1.9125	1.3618	1.1350	1.9824	1.6455	2.5985

Table 7: Proteins Expression With and Without IL-2 treatment in SR and SEN hADSCs

Raw data protein microarray (normalized values against negative)

		SR			SR + IL2			SEN			SEN + IL2		
Protein Name	**10% PRP**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**
GM CSF (CSF2)	0.0000	0.0000	0.0000	1.5127	0.0000	0.0000	2.4429	0.0000	0.0000	0.0000	1.4081	1.1090	1.9433
GRO	2.7029	2.9214	1.4072	2.4796	2.1248	2.5889	1.3419	2.3881	2.0397	1.4234	2.7892	1.7303	1.9509
GRO alpha (CXCL1)	2.8341	2.2512	1.2201	1.7872	2.3741	1.9669	0.0000	2.1295	2.0200	1.6963	3.0249	1.9727	2.3982
HCC-4 (CCL16)	2.1082	1.6714	1.2824	1.7032	1.8196	1.8947	0.0000	1.4507	1.5859	1.4496	2.6994	1.4501	2.0235
HGF	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	1.3151	1.2064	1.1948	1.3155
I-309 (CCL1)	0.0000	1.1716	0.0000	1.3749	0.0000	0.0000	0.0000	1.2270	0.0000	0.0000	1.8541	1.1163	0.0000
I-TAC (CXCL11)	1.7773	2.4167	0.0000	1.1429	1.9403	2.4790	1.6060	2.0923	4.4408	1.1135	1.9897	2.8718	2.1238
ICAM 2	7.7260	5.1717	10.6862	5.1954	2.9367	11.5585	7.0205	8.4510	21.9788	4.0921	5.0098	17.6250	4.3301
ICAM-1	2.2744	2.7507	0.0000	1.3208	2.4726	2.2341	1.4577	2.3083	3.6382	1.1280	2.3291	3.0441	2.4095
ICAM-3	2.6613	2.2837	0.0000	1.4283	2.0152	3.2082	1.9390	1.8424	2.4951	0.0000	2.1678	2.6968	1.8250
IFN gamma	0.0000	1.3137	0.0000	1.3248	0.0000	0.0000	1.1216	1.3209	1.1836	0.0000	2.0549	2.2996	1.2292
IGF 1	1.2639	1.1234	0.0000	1.7804	1.5034	1.6790	1.7504	1.5738	2.4959	0.0000	1.3921	2.0765	1.7998
IGF-1 sR	2.3210	2.1679	0.0000	1.8193	1.1657	3.8612	1.8814	2.1052	2.0054	1.1465	2.0784	2.2369	1.7936
IGF-2	7.8210	5.3984	13.3460	5.3629	3.4114	13.2883	7.4609	8.4417	18.6936	3.7455	5.2313	13.0938	3.9503
IGFBP 1	0.0000	1.4184	1.2150	1.3997	0.0000	0.0000	1.3760	1.5956	1.7953	1.2422	2.5289	2.1571	1.1460
IGFBP 2	0.0000	1.3743	1.3597	1.5149	0.0000	1.1398	1.4701	1.6614	2.1925	1.3702	2.9630	3.7437	1.5504
IGFBP 3	2.8931	2.1995	0.0000	1.5877	1.8361	3.2348	1.9069	1.9777	2.8991	1.2437	2.2331	3.0895	1.9370
IGFBP 4	0.0000	0.0000	1.1015	1.4862	0.0000	0.0000	0.0000	1.1592	1.5931	1.2422	2.7576	2.5841	0.0000
IGFBP 6	2.6328	2.0586	0.0000	1.6428	1.5540	3.6886	1.6927	1.9589	2.4686	1.1350	2.1048	2.6761	2.5985
IL 1 beta	1.2030	1.1404	1.1401	1.6718	1.2215	1.2587	1.4024	1.3315	1.1020	0.0000	1.4070	1.8535	1.5430
IL 1ra	1.4787	1.4602	1.5494	2.0854	1.6168	1.5486	1.7840	1.6918	1.6712	1.1120	1.7498	2.6571	1.9368
IL-1 alpha	0.0000	0.0000	0.0000	1.4987	1.2027	1.1183	1.1942	1.1610	0.0000	0.0000	1.1988	1.4154	1.3277
IL-1 R1	1.8982	1.7219	0.0000	1.7535	0.0000	3.4568	1.5748	1.6351	1.5707	0.0000	1.7159	1.6807	1.5087
IL-1 R4	3.5852	4.2726	1.7262	3.0683	2.2333	5.9276	2.2413	3.3577	3.4899	1.7249	4.1825	3.5853	2.9641
IL-10	0.0000	0.0000	0.0000	1.4609	1.2651	1.2192	1.2172	1.2012	1.9078	0.0000	1.1018	1.7283	1.7007

able 7: Proteins Expression With and Without IL-2 treatment in SR and SEN hADSCs

aw data protein microarray (normalized values against negative)

		SR			SR + IL2			SEN			SEN + IL2		
Protein Name	**10% PRP**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**
IL-10 R beta	4.2176	2.0724	6.9379	2.8859	1.2468	6.4507	4.4566	4.9829	8.2023	2.4840	2.9986	6.1719	2.6166
IL-11	1.7938	1.7272	0.0000	1.6827	1.2060	2.9873	1.4332	1.7263	1.4346	0.0000	1.7404	1.4698	1.3806
IL-12 p40 (IL12b)	2.2191	2.2428	1.3027	2.2102	1.7044	3.5189	1.7550	2.0841	1.7512	1.3740	2.5586	1.6757	2.0308
IL-12 p70 (IL12a)	2.2645	2.4740	1.2300	1.9482	1.9702	2.8214	1.6628	1.8080	1.7086	1.3278	2.3665	1.6441	1.8878
IL-13	0.0000	0.0000	0.0000	1.4879	1.1238	1.1229	0.0000	1.1386	1.2390	0.0000	0.0000	1.1181	1.3577
IL-13 R alpha 2	4.5248	2.3811	7.9506	13.7069	1.3987	7.6889	24.8942	5.9393	10.0674	10.9439	3.4112	7.7500	18.0928
IL-15	0.0000	0.0000	1.1631	1.5127	1.3185	1.3656	2.4429	1.4099	1.3914	0.0000	1.3143	1.7417	1.9433
IL-16	0.0000	0.0000	1.1357	1.7959	1.3020	1.2950	1.3526	1.2798	1.3054	0.0000	1.2625	2.0206	1.8628
IL-17	2.2418	2.3619	0.0000	1.5032	2.1217	1.9841	1.3163	1.7896	2.0121	1.2222	2.0095	1.4174	1.5038
IL-18 BP alpha	3.0904	1.6630	6.0565	3.1044	0.0000	5.0158	3.7960	5.2131	6.5491	2.4993	2.9264	5.2500	2.3956
IL-18 R beta	4.4583	2.5134	8.1398	4.7816	1.1519	7.1012	5.5612	7.3950	14.0732	3.7855	4.5409	9.6563	3.0637
IL-1R 2	4.7686	3.2220	7.3541	3.0255	1.5728	7.1200	4.3168	5.5334	9.2091	2.5308	3.3827	7.3438	2.8186
IL-2	0.0000	1.1072	0.0000	1.2525	1.1035	0.0000	1.1067	0.0000	1.0095	0.0000	1.2570	1.9272	1.3422
IL-2 beta	2.0328	2.0031	5.7894	3.8280	0.0000	4.6163	3.0567	5.0653	6.6551	3.0717	4.1858	6.5313	2.4540
IL-21 R	8.9735	11.7008	13.9870	4.8471	4.4430	15.6644	9.3886	7.5070	21.6821	4.1674	5.6212	22.4688	3.7522
IL-2R alpha	2.9958	2.7251	1.1476	1.5468	2.8307	1.8495	1.0695	2.6661	2.2709	1.4120	3.4867	1.7784	1.8648
IL-2R gamma	1.3045	1.8961	6.9868	4.1725	0.0000	4.6728	2.6250	5.1058	9.2408	2.8873	4.8788	8.3125	2.8821
IL-3	1.1011	1.2907	0.0000	1.3258	1.1775	1.1401	1.2611	1.3045	1.6659	0.0000	1.5734	3.1692	1.9542
IL-4	0.0000	1.3943	0.0000	1.2039	0.0000	0.0000	1.1511	1.3160	1.2914	0.0000	1.6728	1.5556	0.0000
IL-5	1.1291	1.4900	1.1305	1.1746	0.0000	0.0000	1.1690	1.2913	1.7102	1.1760	1.8514	2.2417	1.2944
IL-5 R alpha	4.2683	7.0835	7.8727	3.8540	1.6203	8.2097	4.6996	4.0544	7.8844	2.3564	3.0745	9.8594	2.6166
IL-6	1.1682	1.5695	1.2615	1.5127	1.1780	1.1444	2.4429	1.2190	1.6850	0.0000	1.6620	2.3157	1.9433
IL-6R	2.3560	2.0135	1.1477	1.6428	2.5712	1.6563	1.6927	1.6988	1.7804	1.1350	2.8486	1.5573	2.5985
IL-7	0.0000	1.1716	0.0000	1.3876	0.0000	0.0000	0.0000	0.0000	1.5363	1.1676	0.0000	2.4300	0.0000
IL-8	0.0000	1.1393	0.0000	1.9613	1.4520	1.3270	0.0000	0.0000	1.8381	2.1195	1.8577	1.5563	2.4861
IL-9	4.0340	4.8063	6.7442	3.8011	1.0190	6.9234	4.5056	3.9440	8.9653	2.3180	2.9429	8.4063	2.6065

able 7: Proteins Expression With and Without IL-2 treatment in SR and SEN hADSCs

aw data protein microarray (normalized values against negative)

		SR			SR + IL2			SEN			SEN + IL2		
Protein Name	**10% PRP**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**
IP-10 (CXCL10)	5.0377	4.9197	8.5583	13.7069	1.4114	9.4689	24.8942	4.9673	13.4692	10.9439	3.4745	10.9688	18.0928
L Selectin	5.8958	2.4315	7.8482	3.6086	1.6804	9.4815	6.0278	6.0855	16.1079	3.7632	4.4776	13.1563	3.5312
LAP (TGF b1)	5.2942	3.9591	7.4721	3.9233	1.2595	9.5400	4.9198	5.0311	11.8266	3.1224	3.4517	10.0313	3.1641
Leptin	1.1812	1.1291	1.1443	1.7150	1.5761	1.8687	1.5569	1.3935	2.5268	0.0000	1.3439	1.7122	1.9316
Leptin R	7.8368	5.3795	10.9243	4.5776	2.6203	12.8511	6.7601	7.9487	21.3642	4.0821	4.9288	14.9375	3.7928
LIF	4.5659	2.2646	6.5506	2.9504	1.2342	7.3563	4.4042	4.8414	9.4422	2.6891	3.3099	6.5938	2.6192
LIGHT (TNFSF14)	1.3757	1.3005	1.4893	1.9354	1.7565	2.0072	1.5816	1.5204	2.2014	0.0000	1.4663	2.3087	2.5589
M-CSF (CSF1)	1.4403	1.2881	1.4465	1.7755	1.4197	1.5868	1.5603	1.7082	1.6379	0.0000	1.6473	2.5690	1.9209
M-CSF R (CSF1R)	7.6278	3.5591	12.3711	5.0751	3.2342	13.9597	9.1562	9.5568	27.8179	5.3521	6.1984	18.9219	4.1117
MCP-1 (CCL2)	1.2320	1.4263	1.6123	3.3764	1.5828	2.2230	1.5260	1.4099	1.6576	0.0000	1.3597	2.2346	2.4159
MCP-2 (CCL8)	1.1270	1.1287	1.1030	1.6005	1.3047	1.5253	1.2381	1.3177	1.5346	0.0000	1.2708	1.9635	1.9084
MCP-3 (CCL7)	1.1107	0.0000	0.0000	1.3730	1.1270	1.3022	0.0000	1.1747	1.1412	0.0000	1.1329	1.3170	1.3534
MCP-4 (CCL13)	1.1581	0.0000	0.0000	1.4008	1.1299	1.2833	1.1590	1.2178	0.0000	0.0000	1.1745	1.4451	1.3498
MDC (CCL22)	1.2655	1.1861	1.3001	1.5127	1.3103	1.3770	2.4429	1.4027	1.3767	0.0000	1.3528	2.0833	1.9433
MIF	2.1597	2.1795	0.0000	1.8483	1.6636	4.6365	2.5650	2.1712	2.3463	1.3275	2.1213	2.6968	2.4719
MIG (CXCL9)	1.1859	1.1170	0.0000	1.2173	1.1761	1.2199	1.2101	1.1147	0.0000	0.0000	0.0000	1.5816	0.0000
MIP-1 alpha (CCL3)	2.4060	2.1377	0.0000	1.9708	1.6713	4.3292	2.3397	2.2547	2.3589	1.4853	2.2950	2.8582	2.6981
MIP-1 beta (CCL4)	2.2925	2.1884	1.1355	1.9657	1.4562	4.2223	2.2441	2.2207	2.5274	1.6386	2.2041	2.9260	3.0404

able 7: Proteins Expression With and Without IL-2 treatment in SR and SEN hADSCs

aw data protein microarray (normalized values against negative)

		SR			SR + IL2			SEN			SEN + IL2		
Protein Name	**10% PRP**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**
MIP-1 delta (CCL15)	1.1882	1.1553	0.0000	1.1814	1.1814	1.2850	1.2868	1.2058	1.2023	0.0000	1.1628	1.6067	0.0000
MIP-3 alpha (CCL20)	1.2230	1.2933	1.1993	1.2213	1.2494	1.2286	1.3463	1.2933	1.2335	1.1105	1.2473	1.5692	1.1384
MIP-3 beta (CCL19)	1.6491	1.8158	0.0000	1.5196	0.0000	3.4060	1.7735	1.8004	1.7130	1.1557	1.7639	1.9080	1.5432
MMP 1	3.2550	0.0000	7.0447	3.2391	0.0000	6.7937	4.8499	4.8212	8.8911	3.1985	3.3213	8.0000	2.4960
MMP 13	4.0308	1.3165	7.1004	3.4623	0.0000	7.1618	4.8866	5.4572	9.7071	3.7133	3.7485	8.2813	2.4667
MMP 3	4.3474	3.5780	9.0012	5.6564	0.0000	7.8855	5.4633	7.0731	14.0308	4.3687	4.9143	15.0156	3.7077
MMP 9	3.1980	1.1780	6.3658	3.3045	0.0000	6.0030	3.5391	5.1462	10.7987	3.4759	3.9074	7.3438	2.1936
MPIF-1	2.8972	1.2945	7.4209	13.7069	0.0000	7.0510	24.8942	5.3281	13.3844	10.9439	5.1244	12.1250	18.0928
MSP alpha (HGF like)	1.5158	1.5849	0.0000	1.4188	0.0000	3.1234	1.6842	1.5789	1.4513	0.0000	1.5278	1.3833	1.3102
NAP-2	1.3355	1.6746	1.5684	1.4006	1.4223	1.3801	1.6883	1.5784	2.6414	1.8530	1.5222	3.8348	2.1190
NGFR	0.0000	0.0000	3.9620	2.0131	0.0000	2.5434	1.1675	2.8227	3.8786	1.5059	3.3074	2.8438	1.5420
NT-3	1.4553	1.8727	1.7590	1.4913	1.6149	1.3835	1.6577	1.7653	2.9707	2.0114	1.7024	6.5136	2.7886
NT-4	1.7015	1.7823	0.0000	1.6428	1.1224	3.1103	1.6927	1.7011	1.5498	1.1350	1.7016	1.2623	2.5985
OPG	1.9588	2.0288	1.2671	1.9805	1.3503	3.1937	2.0473	1.8625	1.6066	1.3444	2.1143	1.5444	1.9144
OSM	2.9682	3.0088	1.5496	2.1498	2.5752	3.1750	2.0925	2.2717	2.2816	1.8480	2.8324	2.2654	3.5391
PARC (CCL18)	1.4146	1.8942	1.8088	1.5028	1.6723	1.5219	1.4773	1.9464	2.2464	1.4573	1.8771	3.9748	2.1256
PDGF AA	4.3728	7.2819	5.8806	2.9061	0.0000	9.9312	4.9390	4.1586	6.0934	2.0829	2.9321	8.0313	2.1721
PDGF AB	4.3474	7.3953	6.6908	3.5759	0.0000	9.7576	5.3602	4.3733	8.7746	2.8182	3.7947	8.4375	2.6395
PDGF BB	1.1755	1.1456	1.2772	2.1257	1.8991	1.9970	1.9589	1.9444	3.4659	0.0000	1.8752	2.4537	3.1652
PDGF R alpha	2.6218	4.0220	4.1601	2.6213	0.0000	5.3358	3.4010	2.2862	3.3276	1.9000	2.3809	3.8125	1.9993
PDGF R beta	2.7991	1.9717	3.3721	2.3615	0.0000	4.5682	2.9152	2.2333	2.9884	1.8701	2.1214	2.2500	1.5865
PECAM 1	3.5242	2.0472	5.2218	2.6925	0.0000	6.5657	3.8869	3.6330	7.3545	2.6653	2.6562	4.1563	2.0831
PLGF	1.9995	2.1042	1.2736	1.4493	1.9781	2.0050	1.5313	2.0033	1.8854	1.2553	2.0916	1.5373	2.1870
PRL	4.8002	2.3811	7.5433	3.0255	0.0000	9.0485	4.7852	4.8072	9.9615	3.1424	3.3080	8.3281	2.5328

able 7: Proteins Expression With and Without IL-2 treatment in SR and SEN hADSCs

aw data protein microarray (normalized values against negative)

		SR			SR + IL2			SEN			SEN + IL2		
Protein Name	**10% PRP**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**	**24h**	**48h**	**72h**
RANTES (CCL5)	1.3096	1.2135	1.6016	2.1810	1.7488	2.1340	1.7569	1.8236	3.6534	1.2143	1.7586	3.3439	3.7305
SCF	1.2204	1.1268	1.3764	1.5127	1.3769	1.8305	2.4429	1.5836	1.8959	0.0000	1.5272	1.9418	1.9433
SCF R	4.9364	1.8457	7.9796	3.3844	1.1329	10.1508	5.4878	5.3686	12.3565	3.5988	3.7536	8.7031	2.8834
SDF-1 alpha	1.3057	1.1283	1.3137	1.6077	1.3562	1.8259	1.2496	1.7122	1.6701	0.0000	1.6512	1.9230	1.9613
SDF-1 beta	4.2619	0.0000	6.3080	13.7069	0.0000	7.6826	24.8942	4.7605	9.9827	10.9439	3.4973	8.0313	18.0928
sgp130 (IL6ST)	2.2686	2.3484	1.4306	1.4705	2.5113	1.7665	1.3003	2.3061	1.7749	1.3635	2.6473	1.6322	2.2869
Siglec 5	2.5299	0.0000	4.7655	2.4182	0.0000	5.4111	3.5740	3.4557	6.3796	2.9173	2.8220	4.0938	2.1276
sTNFRI (TNFRSF1A)	0.0000	0.0000	1.1578	0.0000	1.4643	0.0000	0.0000	0.0000	1.2100	1.6022	1.7870	1.8964	2.3271
sTNFRII (TNFRSF1B)	1.9044	1.9186	1.4867	1.4075	2.6485	1.5852	1.0310	1.7671	1.7607	1.5579	2.6495	1.7601	2.3271
TARC (CCL17)	1.3270	1.1513	1.2954	1.6107	1.2686	1.6083	1.1221	1.6134	1.7633	1.1083	1.5560	2.3620	1.8573
TECK (CCL25)	1.1900	2.0126	0.0000	1.3492	1.2024	2.7107	2.0992	1.5479	3.3719	0.0000	1.7041	1.7530	1.8681
TGF alpha	2.0360	0.0000	4.4116	2.2402	0.0000	4.1582	3.0532	3.0140	4.3025	2.6146	2.4005	1.9688	1.5979
TGF beta 1	1.2030	0.0000	1.1813	1.5739	0.0000	1.4450	0.0000	1.4940	1.5380	0.0000	1.4408	1.6989	1.4131
TGF beta 2	3.9168	0.0000	6.9535	3.1688	0.0000	6.1578	3.6003	4.6998	10.9470	3.4282	3.7264	6.3438	2.2800
TGF beta 3	1.3716	1.1878	1.3123	1.6893	1.1931	1.5166	1.2988	1.5534	1.4329	0.0000	1.4981	1.7555	1.3785
THPO	1.6967	1.2428	0.0000	1.4502	1.2371	2.8090	1.9955	1.3720	1.9699	1.2798	1.3259	1.8384	1.6889
TIE-1	3.4260	0.0000	6.7108	3.1987	0.0000	6.3795	3.4971	4.6781	12.2505	3.5942	3.7327	5.9375	2.2889
TIE-2	3.3437	0.0000	8.8410	3.4287	0.0000	8.2160	4.4549	6.0062	16.0655	4.4463	5.2440	11.1250	2.8415
TIMP-1	1.6136	9.7600	7.0577	14.7773	4.6085	24.4847	15.5688	2.9073	7.2915	2.6604	3.3255	4.3043	5.6560
TIMP-2	1.1656	1.5467	1.1132	1.6428	1.2063	4.0519	1.6927	1.2993	1.6808	1.1350	1.2203	1.5861	2.5985
TIMP-4	1.4439	0.0000	7.1471	2.0362	0.0000	5.3609	3.0130	3.7558	11.1696	3.4805	4.3137	8.5625	2.6852
TNF alpha	1.2282	0.0000	1.1371	1.3016	0.0000	1.2323	0.0000	0.0000	1.1535	0.0000	0.0000	1.4096	1.1837
TNF beta	1.3485	1.1618	1.3546	1.4087	1.2383	1.3726	1.1619	1.2614	1.5829	0.0000	1.2165	2.1747	1.5305

Table 7: Proteins Expression With and Without IL-2 treatment in SR and SEN hADSCs

(raw data protein microarray (normalized values against negative)

Protein Name	10% PRP	SR			SR + IL2			SEN			SEN + IL2		
		24h	48h	72h	24h	48h	72h	24h	48h	72h	24h	48h	72h
TRAIL R3 (TNFRSD10C)	1.4030	1.4235	0.0000	1.5132	0.0000	2.7369	2.1068	1.3606	1.3436	0.0000	1.2645	1.3823	1.3020
TRAIL R4 (TNFRSF10D)	1.2073	1.4240	0.0000	1.4843	0.0000	2.4524	2.0421	1.4239	1.2442	0.0000	1.2353	1.1666	0.0000
uPAR	1.2991	1.5921	0.0000	1.7088	0.0000	2.5193	2.1857	1.4108	1.2572	0.0000	1.1521	1.1368	0.0000
VE Cadherin	2.9669	4.3591	2.8824	1.7976	0.0000	7.7307	4.3098	1.7449	2.7341	1.5712	1.9955	3.2969	1.8583
VEGF	1.6355	1.6877	0.0000	1.6013	1.3020	2.1407	1.8824	1.4757	1.9375	1.3938	1.1928	1.6292	1.3449
VEGF R2	4.0593	5.0457	3.9375	2.1459	0.0000	9.0108	4.9163	2.4588	5.5530	2.1928	2.6074	6.1406	2.2254
VEGF R3	8.6854	9.4142	9.9049	13.7069	0.0000	15.7355	24.8942	6.2240	18.9056	10.9439	4.7200	18.5156	18.0928
VEGF-D	1.7188	1.8505	1.2501	1.7738	1.2923	2.2446	2.0839	1.6580	1.6986	1.3904	1.4664	1.4556	1.6349
XCL1	2.3969	2.7051	0.0000	1.7291	0.0000	4.6858	2.3568	2.3074	3.3162	1.3284	2.4838	3.8532	2.6120
Array 6													
Mean positive	3.1982	3.5238	4.1985	4.4906	2.8622	3.0507	3.7518	3.6569	3.5047	4.4157	3.9684	4.3600	4.0705
Mean negative	0.9894	0.9930	0.9932	0.9928	0.9825	0.9880	0.9972	0.9898	0.9956	1.0073	0.9894	0.9919	0.9947
Array 7													
Mean positive	2.4540	3.5311	3.2874	3.6983	2.9950	3.2025	2.4273	4.5576	3.0852	2.3917	5.6725	2.9576	4.4572
Mean negative	0.9675	0.9729	0.9906	0.9920	0.9707	0.9879	0.9650	0.9788	0.9930	0.9979	0.9787	0.9786	0.9736
Array 8													
Mean positive	5.6484	3.8376	6.8396	7.6892	3.9872	5.6337	4.8771	4.9257	4.5014	6.6287	5.2075	4.0405	3.7488
Mean negative	0.9030	0.7308	0.8919	0.9719	1.0128	0.8939	0.9503	0.9263	0.8167	0.9445	0.9649	0.7984	0.9817

[0433] From the foregoing it will be appreciated that, although specific variations of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

What is claimed is:

1. A method of treating a disease or disorder in an individual comprising delivering one or more factors produced by a population of stem cells to the individual or to a biological fluid from the individual.

2. The method of claim 1, wherein the stem cells comprise mesenchymal stem cells (MSCs).

3. The method of claim 1, wherein the stem cells comprise self-renewing (SR) cells and senescent (SEN) cells.

4. The method of claim 1, wherein the population of stem cells comprise at least 50% SR cells.

5. The method of claim 1, wherein the population of stem cells comprise at least 50% SEN cells.

6. The method of claim 1, wherein the stem cells have been induced to produce the factors upon exposure to an inducing agent.

7. The method of claim 6, wherein the exposure is for about 24 hours.

8. The method of claim 6, wherein the inducing agent comprises IL-2.

9. The method of claim 6, wherein the stem cells comprise at least 50% SR cells.

10. The method of claim 6, wherein the stem cells comprise at least 50% SEN cells.

11. The method of claim 1, wherein the factors are secreted from the cells.

12. The method of claim 7, wherein the factors are delivered 24, 48 or 72 hours post-induction.

13. The method of claim 1, wherein the disease or disorder is cancer, an autoimmune disease, a cardiovascular disease, diabetes, a skin disease, a neurodegenerative disease, osteoporosis, osteoarthritis, a spinal cord injury, a disease of the liver, a disease of the

kidney, an age-related pathology, hair loss, a burn, a condition in need of a skin graft, or a skin lesion.

14. The method of claim 1, wherein the stem cells are adipose derived stem cells (ADSCs).

15. The method of claim 1, wherein the stem cells are from a vesicular stromal fraction.

16. The method of claim 1, wherein the delivery comprises use of a transdermal patch, a plasmapheresis system, a microneedle-based system, a cream, or a dermaroller.

17. The method of claim 1, wherein the factors are autologous to the individual.

18. The method of claim 1, wherein the factors are allogeneic to the individual.

19. The method of claim 1, wherein the factors are produced in a factor production unit.

20. The method of claim 1, wherein the factors comprise Interleukin 1 beta (IL1b), Interleukin 3 (IL3), Interleukin-13 Receptor subunit alpha-2 (IL13Rα2), Interleukin 1 receptor alpha (IL1Rα), Probetacellulin (BTC), Colony stimulating factor (CSF1), Fibroblast growth factor 6 (FGF6), Glial cell line-derived neurotrophic factor (GDNF), insulin-like growth factor 1 (IGF-1), Leptin, platelet-derived growth factor B beta (PDGF BB), Brain-derived neurotrophic factor (BDNF), Bone morphogenetic protein 4 (BMP4), Bone morphogenetic protein 6 (BMP6), Ciliary neurotrophic factor (CNTF), Epidermal growth factor (EGF), Fibroblast growth factor 7 (FGF7), insulin-like growth factor-binding protein-4 (IGFBP4), Stem cell factor/c-kit ligand (SCF), Stromal Cell-Derived Factor-1 alpha (SDF1a), Stromal Cell-Derived Factor-1 beta (SDF1b), Angiotensin (ANG), colony stimulating factor 2 (CSF2), Transforming growth factor beta 1 (TGFb1), Transforming growth factor beta 3 (TGFb3), tumor necrosis factor superfamily member 14 (TNFSF14), Chemokine (C-C motif) ligand 2 (CCL2), Chemokine (C-C motif) ligand 5 (CCL5), Chemokine (C-C motif) ligand 7 (CCL7), Chemokine (C-C motif) ligand 8 (CCL8), Chemokine (C-C motif) ligand 11 (CCL11), Chemokine (C-C motif) ligand 13 (CCL13), Chemokine (C-C motif) ligand 22 (CCL22), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C motif) ligand 24 (CCL24), CXC Chemokine ligand 10 (CXCL10), Chemokine (C-X-C motif) ligand 13 (BLC), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C motif) ligand 28 (CCL28), chemokine (C-C motif) ligand

11 (Eotaxin 1), Chemokine (C-X-C motif) ligand 6 (GCP-2), FLT3LG (Fms-Related Tyrosine Kinase 3 Ligand), and Fractalkine (CX3CL1).

21. The method of claim 1, wherein the factors are delivered to a biological fluid from the individual.

22. The method of claim 21, wherein the factors are delivered to plasma from the individual.

23. The method of claim 21, wherein the delivery of the factors to the plasma induces production of regulatory T cells in the blood.

24. The method of claim 23, further comprising introducing the blood back into the individual.

25. A method of producing one or more factors in a factor production unit comprising adding an inducing agent to a population of stem cells to induce the production of factors, whereby producing the one or more factors.

26. The method of claim 25, wherein the stem cells comprise mesenchymal stem cells (MSCs).

27. The method of claim 25, wherein the stem cells are adipose derived stem cells (ADSCs).

28. The method of claim 25, wherein the stem cells are from a vesicular stromal fraction.

29. The method of claim 25, wherein the stem cells comprise self-renewing (SR) cells and senescent (SEN) cells.

30. The method of claim 25, wherein the population of stem cells comprise at least 50% SR cells.

31. The method of claim 25, wherein the population of stem cells comprise at least 50% SEN cells.

32. The method of claim 25, wherein the stem cells have been induced to produce the factors upon exposure to an inducing agent.

33. The method of claim 32, wherein the inducing agent comprises IL-2.

34. The method of claim 25, wherein the factors are secreted from the cells.

35. The method of claim 32, wherein the factors are obtained 24, 48 or 72 hours post-induction.

36. The method of claim 25, wherein the population of stem cells is from a single individual.

37. The method of claim 25, wherein the population of stem cells is from a plurality of individuals.

38. The method of claim 25, wherein the factors comprise Interleukin 1 beta (IL1b), Interleukin 3 (IL3), Interleukin-13 Receptor subunit alpha-2 (IL13Rα2), Interleukin 1 receptor alpha (IL1Rα), Probetacellulin (BTC), Colony stimulating factor (CSF1), Fibroblast growth factor 6 (FGF6), Glial cell line-derived neurotrophic factor (GDNF), insulin-like growth factor 1 (IGF-1), Leptin, platelet-derived growth factor B beta (PDGF BB), Brain-derived neurotrophic factor (BDNF), Bone morphogenetic protein 4 (BMP4), Bone morphogenetic protein 6 (BMP6), Ciliary neurotrophic factor (CNTF), Epidermal growth factor (EGF), Fibroblast growth factor 7 (FGF7), insulin-like growth factor-binding protein-4 (IGFBP4), Stem cell factor/c-kit ligand (SCF), Stromal Cell-Derived Factor-1 alpha (SDF1a), Stromal Cell-Derived Factor-1 beta (SDF1b), Angiotensin (ANG), colony stimulating factor 2 (CSF2), Transforming growth factor beta 1 (TGFb1), Transforming growth factor beta 3 (TGFb3), tumor necrosis factor superfamily member 14 (TNFSF14), Chemokine (C-C motif) ligand 2 (CCL2), Chemokine (C-C motif) ligand 5 (CCL5), Chemokine (C-C motif) ligand 7 (CCL7), Chemokine (C-C motif) ligand 8 (CCL8), Chemokine (C-C motif) ligand 11 (CCL11), Chemokine (C-C motif) ligand 13 (CCL13), Chemokine (C-C motif) ligand 22 (CCL22), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C motif) ligand 24 (CCL24), CXC Chemokine ligand 10 (CXCL10), Chemokine (C-X-C motif) ligand 13 (BLC), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C motif) ligand 28 (CCL28), chemokine (C-C motif) ligand 11 (Eotaxin 1), Chemokine (C-X-C motif) ligand 6 (GCP-2), FLT3LG (Fms-Related Tyrosine Kinase 3 Ligand), and Fractalkine (CX3CL1).

39. The method of claim 38, wherein the factors are useful for derma-cosmetic applications.

40. The method of claim 25, wherein the factors are useful for the treatment of cancer, an autoimmune disease, a cardiovascular disease, diabetes, a skin disease, a neurodegenerative disease, osteoporosis, osteoarthritis, a spinal cord injury, a disease of the liver, a disease of the kidney, an age-related pathology, hair loss, a burn, a condition in need of a skin graft, or a skin lesion.

41. A method of producing one or more factors suitable for derma-cosmetic applications comprising, incubating a population of stem cells with 10% PRP, whereby producing one or more factors suitable for derma-cosmetic applications.

42. A factor composition comprising factors collected from SR-hADSCs 72 hours following incubation with IL-2.

43. A method of increasing the number of regulatory T cells in a sample comprising contacting a sample comprising T cells with a factor composition, wherein the factor composition comprises factors collected from SR-hADSCs 72 hours following incubation with IL-2.

44. The method of claim 43, wherein the sample comprises blood.

45. The method of claim 43, wherein the sample comprises plasma.

46. A factor production unit comprising a substrate and a population of input stem cells.

47. The factor production unit of claim 42, wherein the substrate comprises a polymer material.

48. The factor production unit of claim 42, wherein the input stem cells comprise MSCs.

49. The factor production unit of claim 42, wherein the substrate is a 3-dimensional substrate.

50. The factor production unit of claim 47, wherein the polymer material comprises a biodegradable polymer.

51. The factor production unit of claim 47, wherein the polymer material comprises a non-biodegradable polymer.

52. The factor production unit of claim 47, wherein the polymer material comprises a polyethylene terephthalate, a polyester, a polymethylmethacrylate, polyacrylonitrile, a silicone, a polyurethane, a polycarbonate, a polyether ketone ketone, a polyether ether ketone, a polyether imide, a polyamide, a polystyrene, a polyether sulfone, a polysulfone, a polycaprolactone (PCL), a polylactic acid (PLA), a polyglycolic acid (PGA), a polyglycerol sebacic, a polydiol citrate, a polyhydroxy butyrate, a polyether amide, a polydiaxanone, fibronectin, collagen, gelatin, hyaluronic acid, chitosan, and combinations, blends, or copolymers thereof.

53. The factor production unit of claim 42, wherein the substrate comprises a plurality of electrospun nanofibers or 3-D printed nanofibers.

54. The factor production unit of claim 53, wherein the nanofibers are electrospun with the stem cells.

55. The factor production unit of claim 53, wherein the plurality of electrospun fibers are configured as an artificial extracellular matrix.

56. The factor production unit of claim 42, wherein the population of stem cells is disposed on a surface of the substrate.

57. The factor production unit of claim 42, wherein the population of stem cells is disposed within a polymer material of the substrate.

58. The factor production unit of claim 42, wherein the stem cells comprise self-renewing (SR) cells and senescent cells (SEN).

59. The factor production unit of claim 42, wherein the population of stem cells comprise at least 50% SR cells.

60. The factor production unit of claim 59, wherein the stem cells are induced SR cells.

61. The factor production unit of claim 42, wherein the population of stem cells comprise at least 50% SEN cells.

62. The factor production unit of claim 61, wherein the stem cells are induced SR cells.

63. The factor production unit of claim 42, wherein the factor production unit is part of an aphereisis system.

64. The factor production unit of claim 63, wherein the apheresis system is a plasmapheresis system.

65. The factor production unit of claim 42, wherein factors are produced and the factors are used for modulation of immune cells.

66. The factor production unit of claim 65, wherein factors are produced and used to increase production of regulatory T cells.

67. The factor production unit of claim 42, wherein factors are produced and the factors are used for treatment of autoimmune diseases , cancer, diabetes, a skin disease, a neurodegenerative disease, osteoporosis, osteoarthritis, a disease of the liver, a disease of the kidney, an age-related pathology, a condition in need of a skin graft, or a skin lesion.

68. A factor composition comprising Interleukin 1 beta (IL1b), Interleukin 3 (IL3), Interleukin-13 Receptor subunit alpha-2 (IL13Rα2), Interleukin 1 receptor alpha (IL1Rα), Probetacellulin (BTC), Colony stimulating factor (CSF1), Fibroblast growth factor 6 (FGF6), Glial cell line-derived neurotrophic factor (GDNF), insulin-like growth factor 1 (IGF-1), Leptin, platelet-derived growth factor B beta (PDGF BB), Brain-derived neurotrophic factor (BDNF), Bone morphogenetic protein 4 (BMP4), Bone morphogenetic protein 6 (BMP6), Ciliary neurotrophic factor (CNTF), Epidermal growth factor (EGF), Fibroblast growth factor 7 (FGF7), insulin-like growth factor-binding protein-4 (IGFBP4), Stem cell factor/c-kit ligand (SCF), Stromal Cell-Derived Factor-1 alpha (SDF1a), Stromal Cell-Derived Factor-1 beta (SDF1b), Angiotensin (ANG), colony stimulating factor 2 (CSF2), Transforming growth factor beta 1 (TGFb1), Transforming growth factor beta 3 (TGFb3), tumor necrosis factor superfamily member 14 (TNFSF14), Chemokine (C-C motif) ligand 2 (CCL2), Chemokine (C-C motif) ligand 5 (CCL5), Chemokine (C-C motif) ligand 7 (CCL7), Chemokine (C-C motif) ligand 8 (CCL8), Chemokine (C-C motif) ligand 11 (CCL11), Chemokine (C-C motif) ligand 13 (CCL13), Chemokine (C-C motif) ligand 22 (CCL22), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C motif) ligand 24 (CCL24), CXC Chemokine ligand 10

(CXCL10), Chemokine (C-X-C motif) ligand 13 (BLC), Chemokine (C-C motif) ligand 23 (CCL23), Chemokine (C-C motif) ligand 28 (CCL28), chemokine (C-C motif) ligand 11 (Eotaxin 1), Chemokine (C-X-C motif) ligand 6 (GCP-2), FLT3LG (Fms-Related Tyrosine Kinase 3 Ligand), and Fractalkine (CX3CL1).

69. The factor composition of claim 68 further formulated in the form of a cream or lotion.

70. The factor composition of claim 68 further formulated on a patch comprising microneedles.

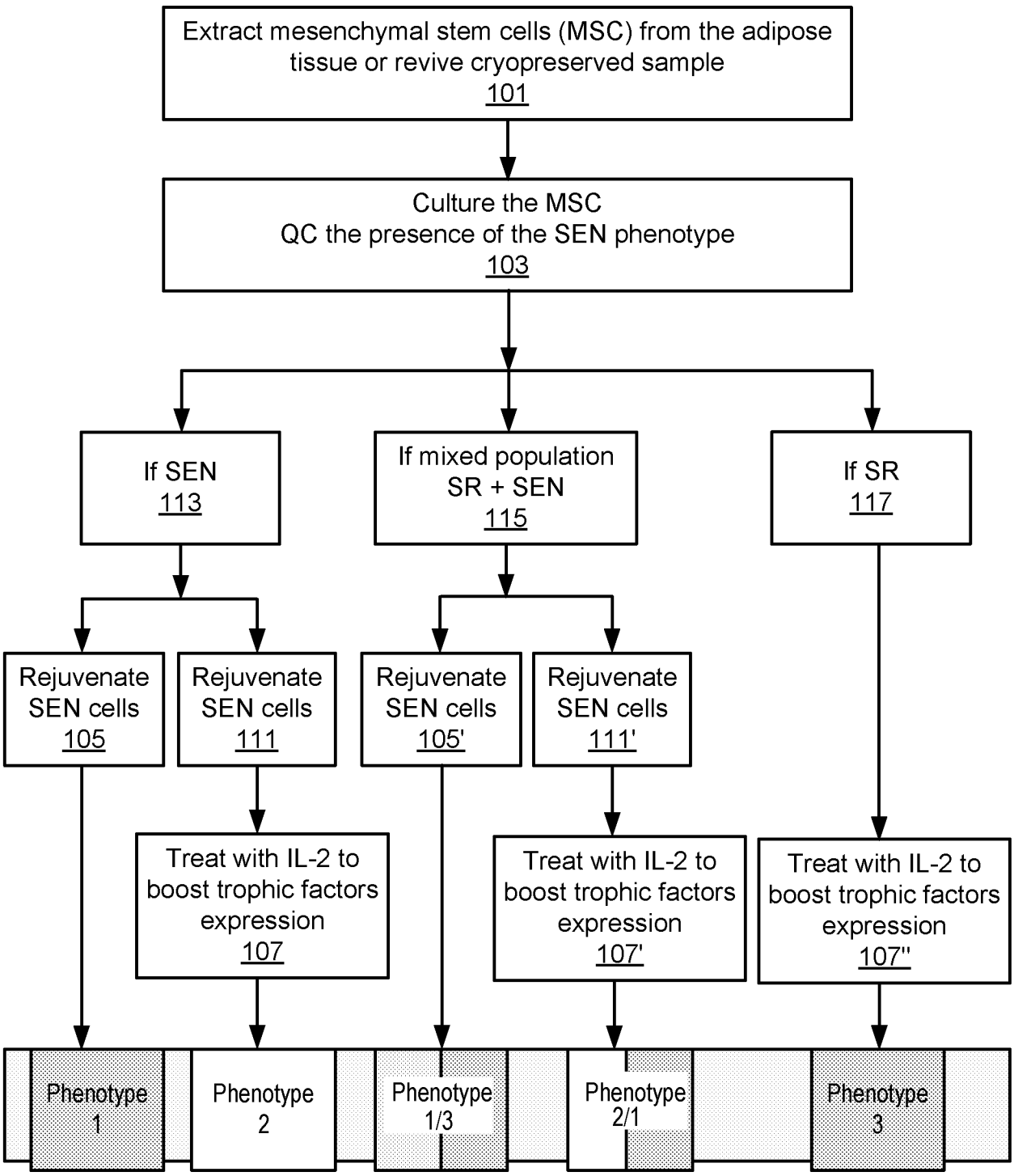
71. The factor composition of claim 68 further formulated to be combined with a dermaroller-based delivery system.

72. A kit comprising the factor composition of claim 68.

73. A method of inducing senescence in a SR-stem cell comprising transfecting into the cell one or microRNAs (miRNAs) selected from the group consisting of miR-17-5p, miR-18a-5p, miR-20a-5p, mir-92a1-5p, mir-19a-3p, mir-125b1-5p, mir100-5p, and mir-let7a-2-3p.

74. The method of claim 73, wherein the SR-stem cell is a SR-hADSC.

FIG. 1A



Specialized Expression of the Factors

FIG. 1B

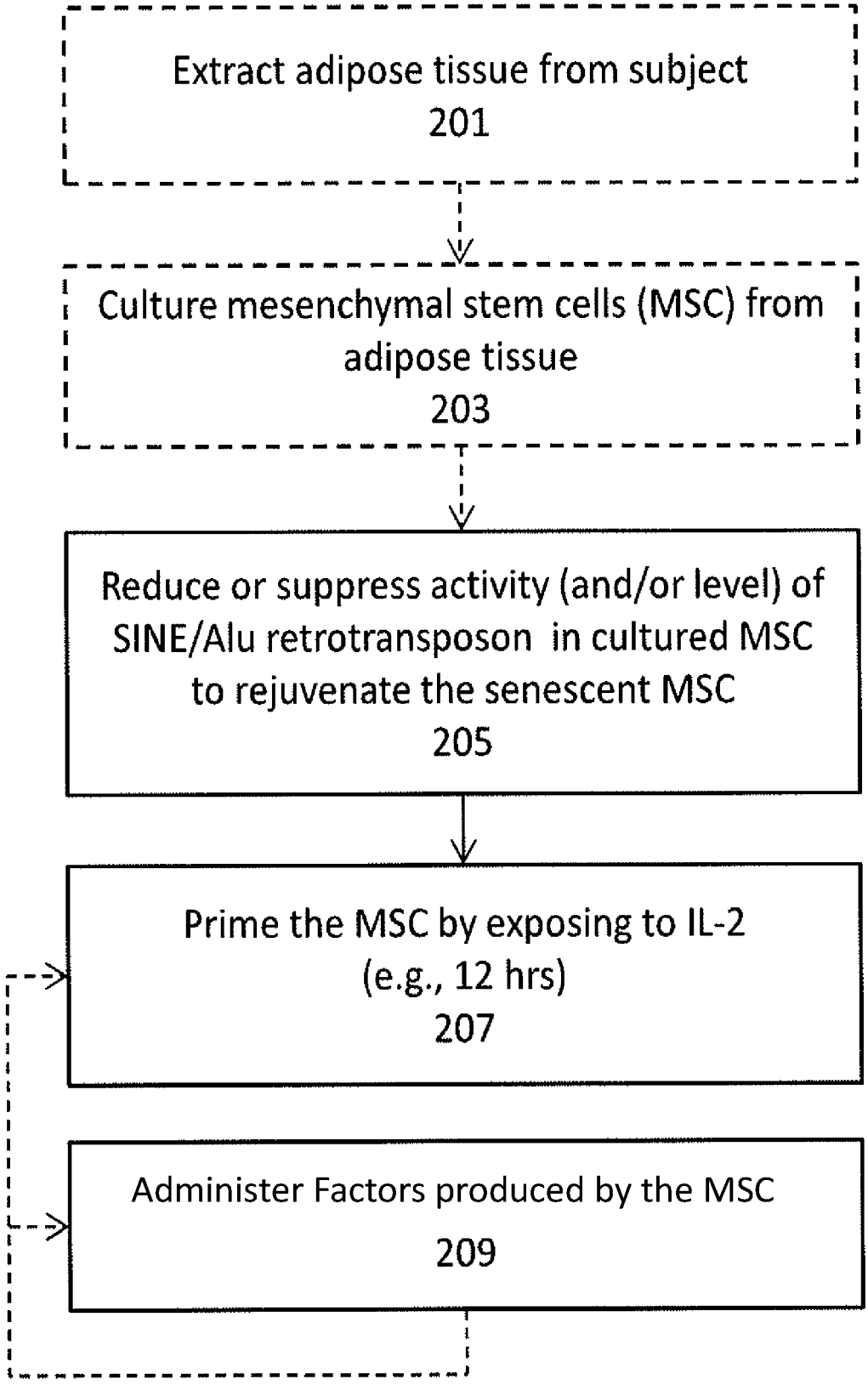

Extract adipose tissue from subject
201
Culture mesenchymal stem cells (MSC) from adipose tissue
203
Reduce or suppress activity (and/or level) of SINE/Alu retrotransposon in cultured MSC to rejuvenate the senescent MSC
205
Prime the MSC by exposing to IL-2 (e.g., 12 hrs)
207
Administer Factors produced by the MSC
209

FIG. 1C

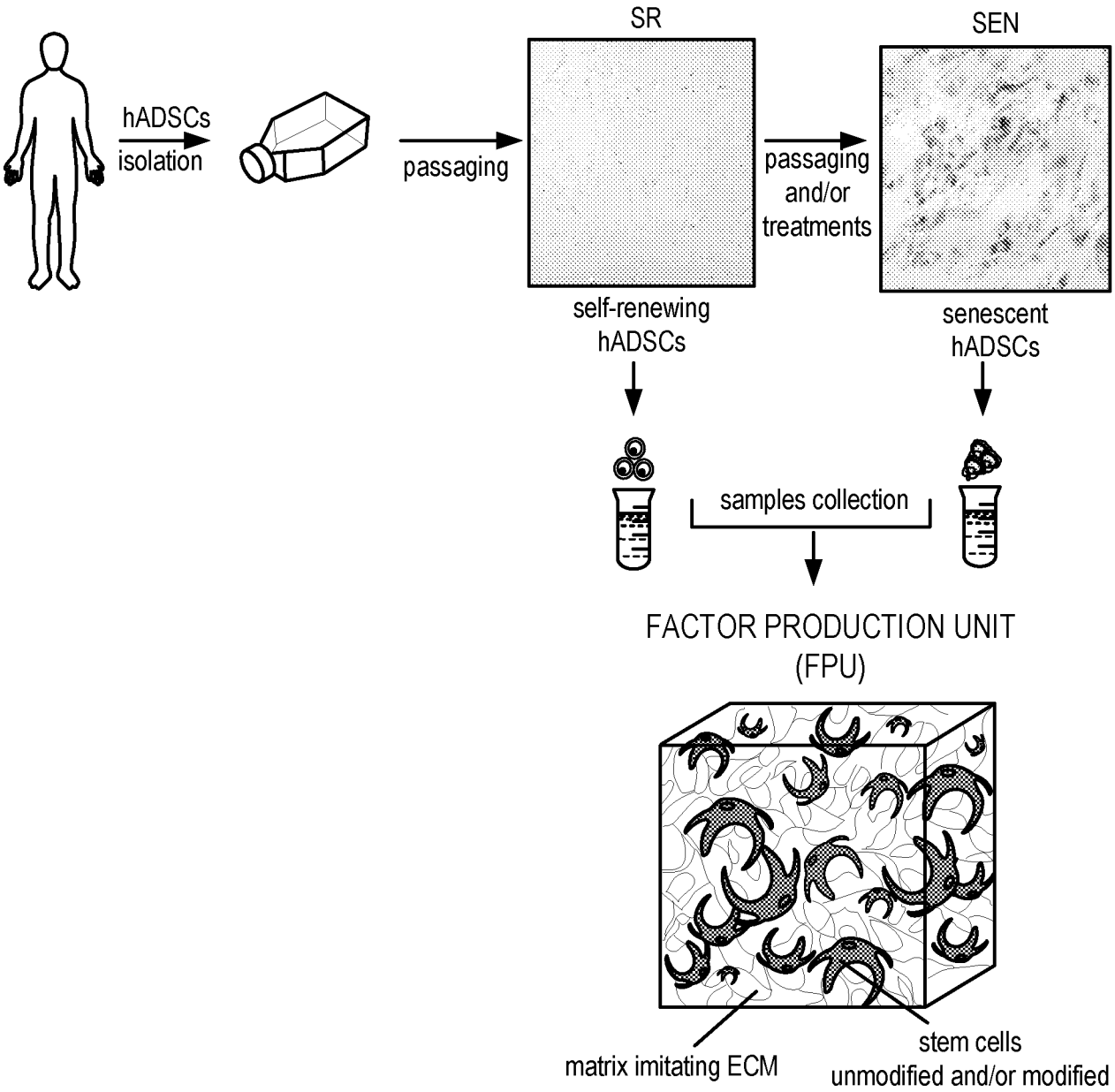

hADSCs
isolation
passaging
SR
self-renewing
hADSCs
passaging
and/or
treatments
SEN
senescent
hADSCs
samples collection
FACTOR PRODUCTION UNIT
(FPU)
matrix imitating ECM
stem cells
unmodified and/or modified

FIG. 2A

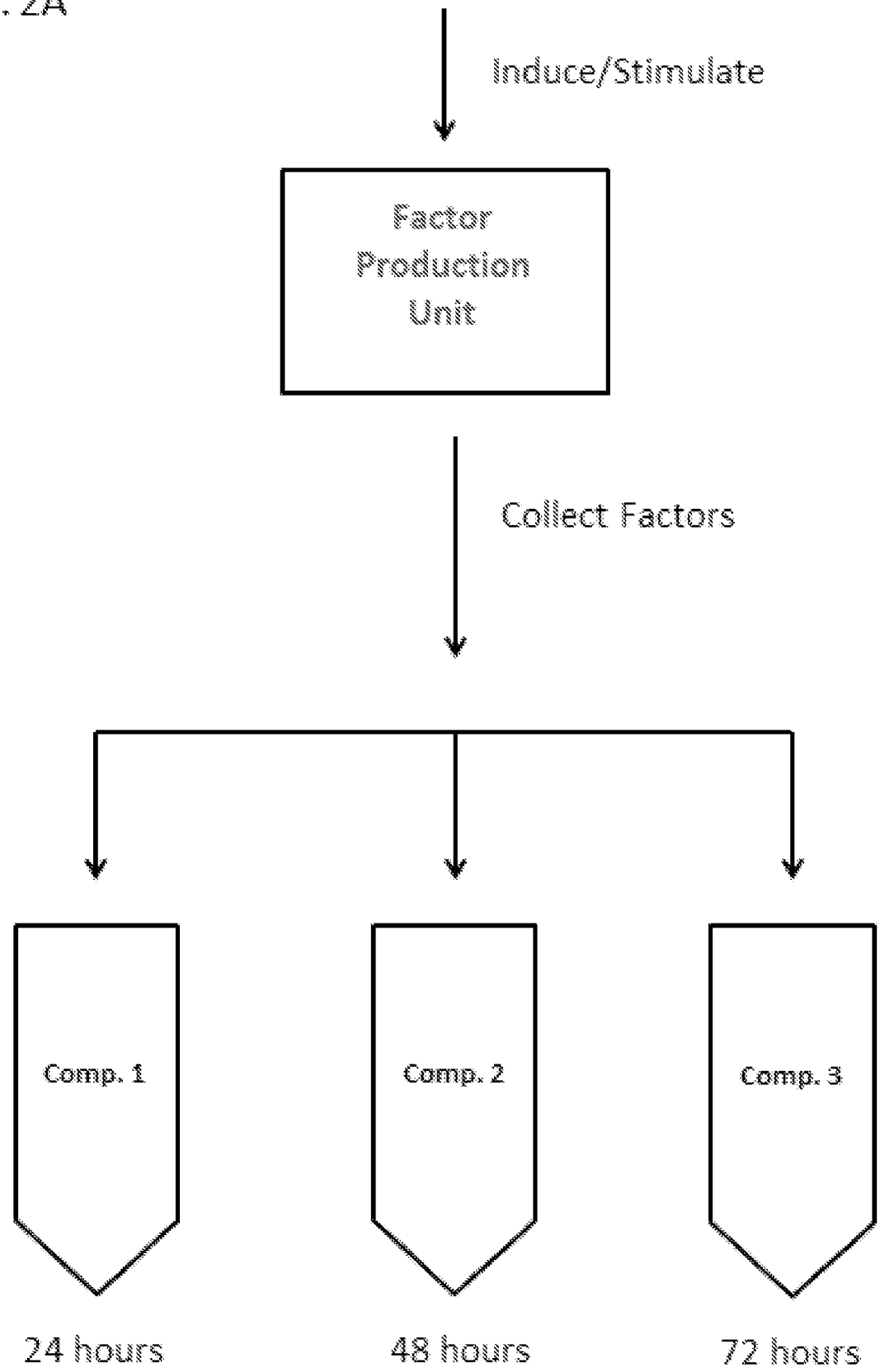

Induce/Stimulate
Factor Production Unit
Collect Factors
Comp. 1
Comp. 2
Comp. 3
24 hours
48 hours
72 hours

FIG. 2B Factor Production Units A-E

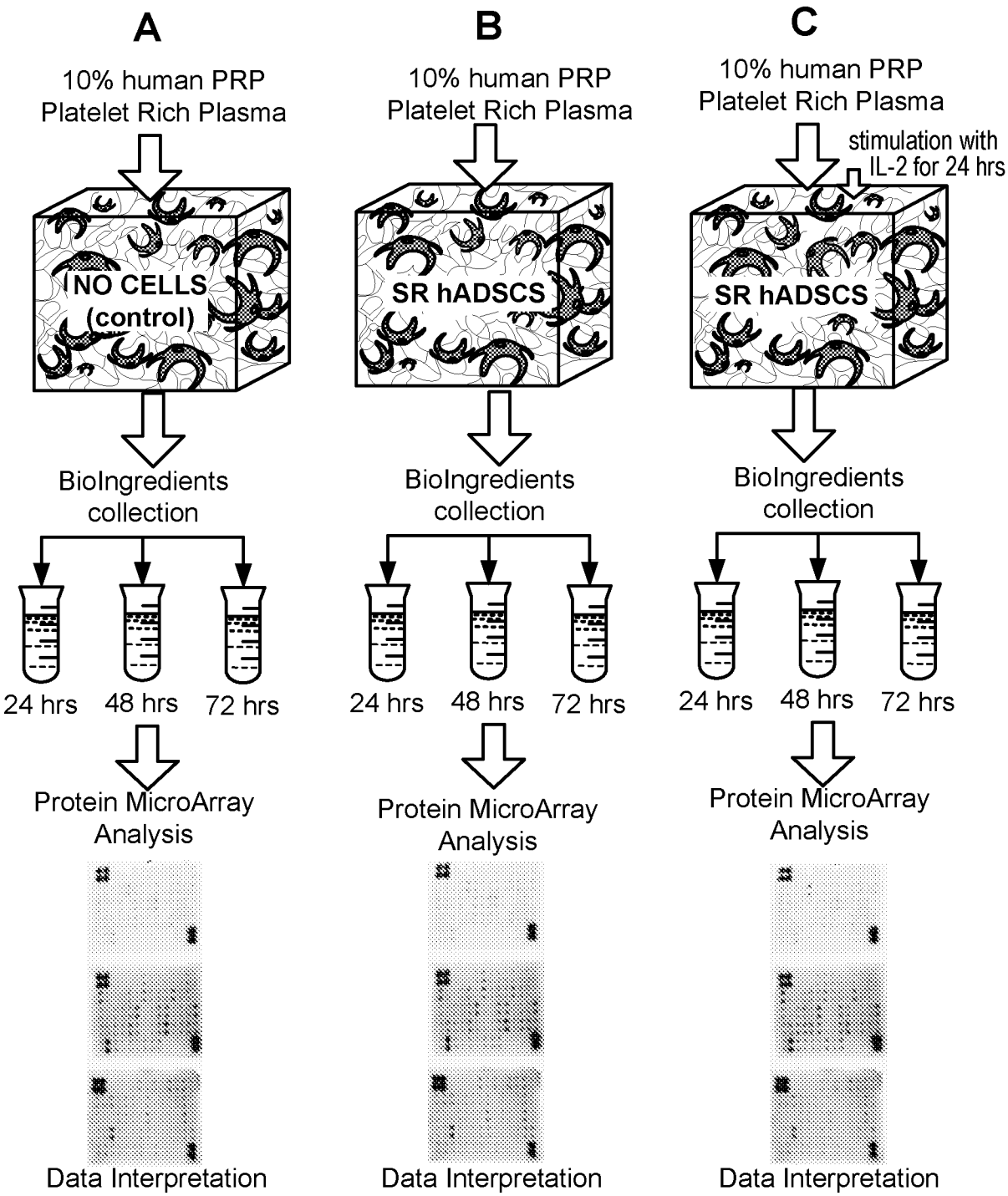
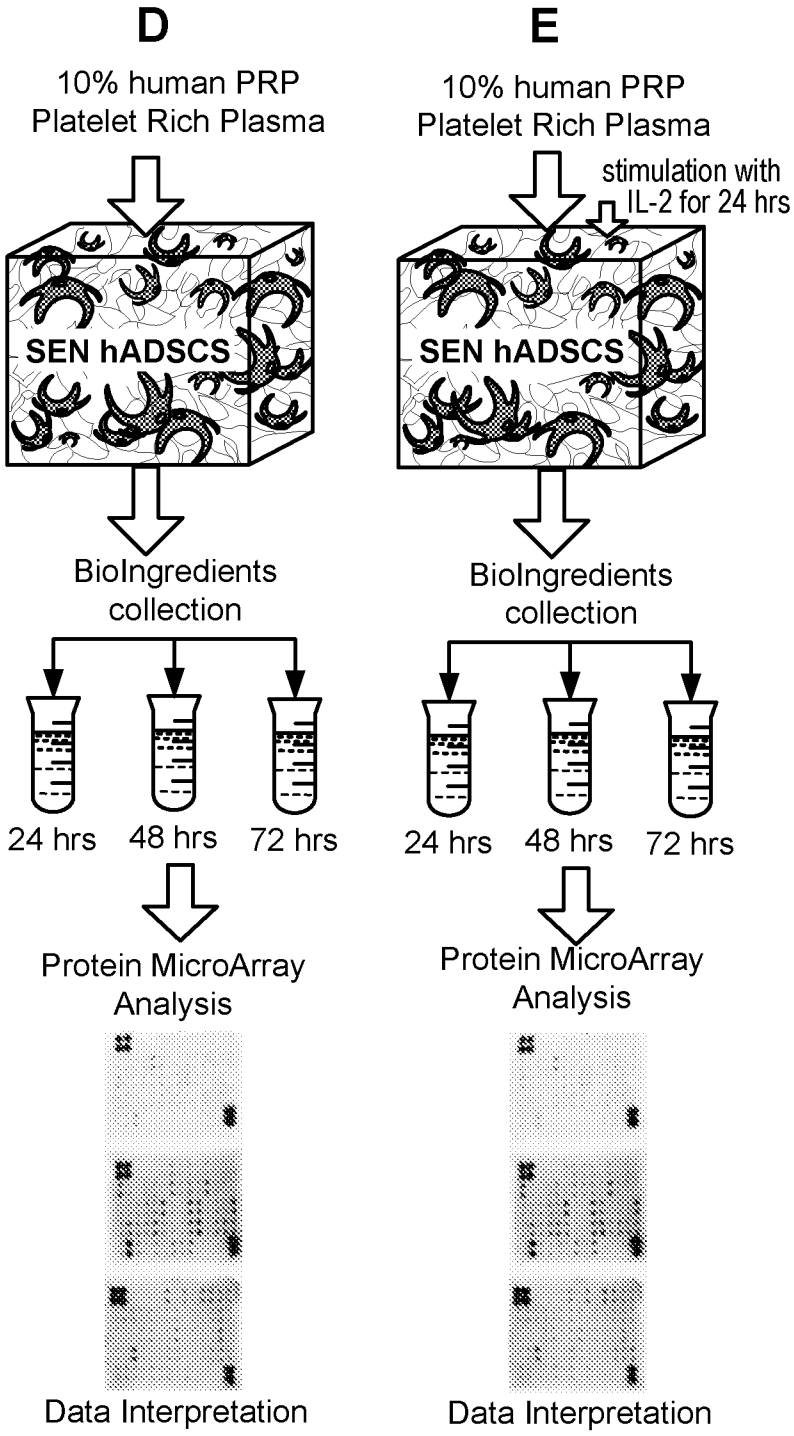


FIG. 2B (Continued)

Factor Production Units A-E



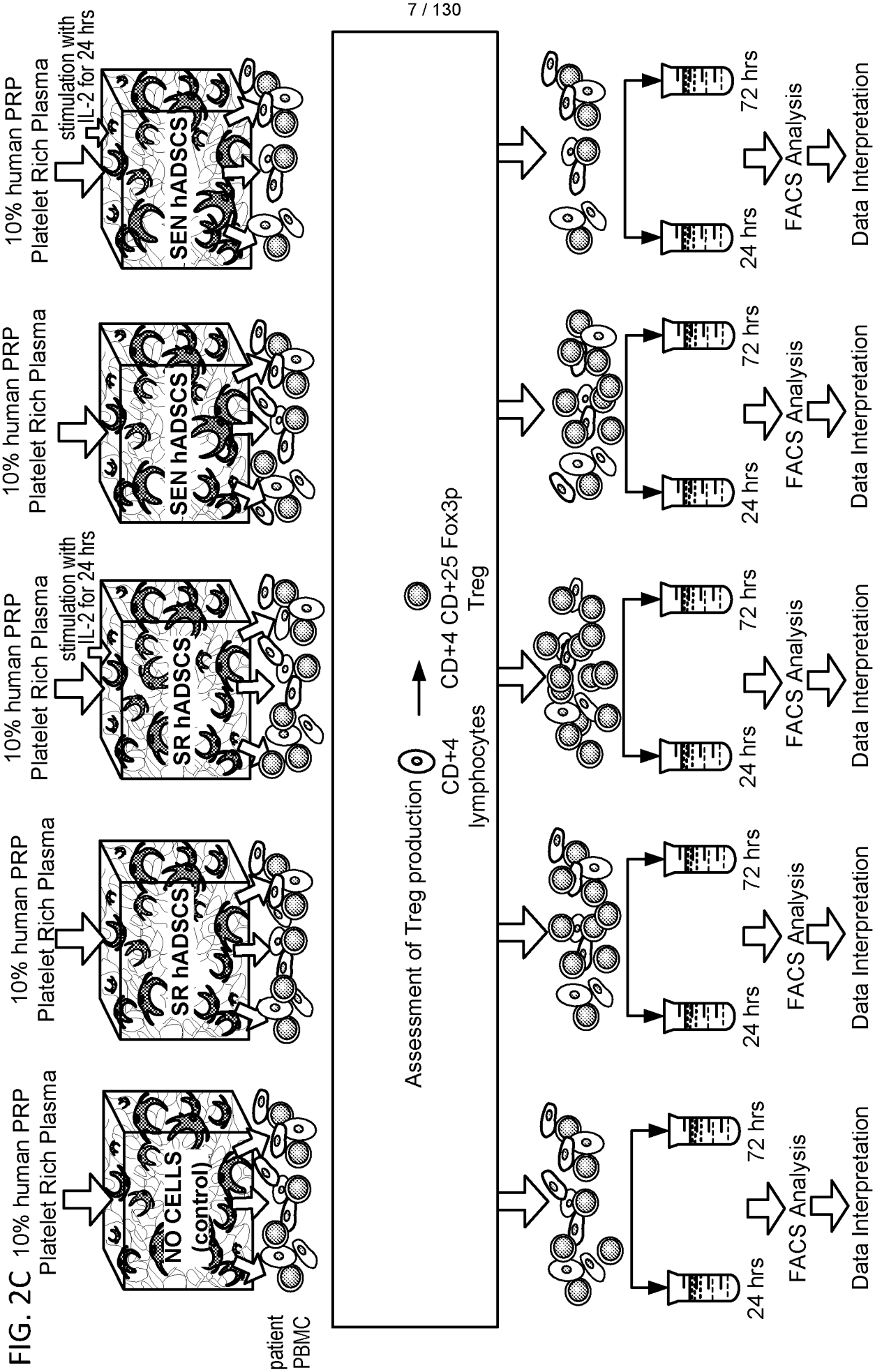

10% human PRP
Platelet Rich Plasma
NO CELLS
(control)
SR hADSCS
SEN hADSCS
stimulation with
IL-2 for 24 hrs
patient
PBMC
Assessment of Treg production
CD+4
lymphocytes
CD+4 CD+25 Fox3p
Treg
24 hrs
72 hrs
FACS Analysis
Data Interpretation

FIG. 2C

FIG. 2D

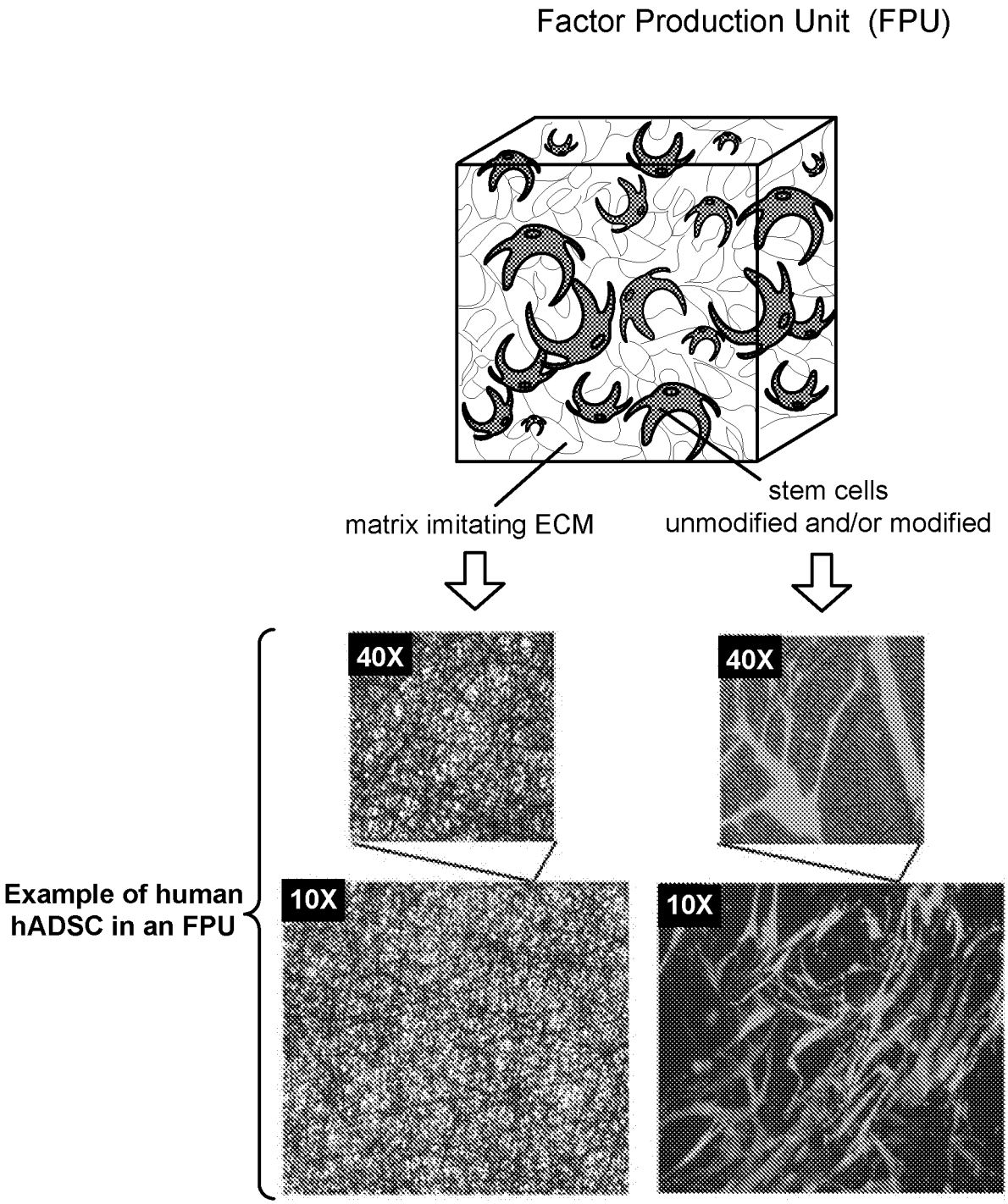

Factor Production Unit (FPU)
matrix imitating ECM
stem cells
unmodified and/or modified
40X
40X
10X
10X
Example of human
hADSC in an FPU

FIG. 3A

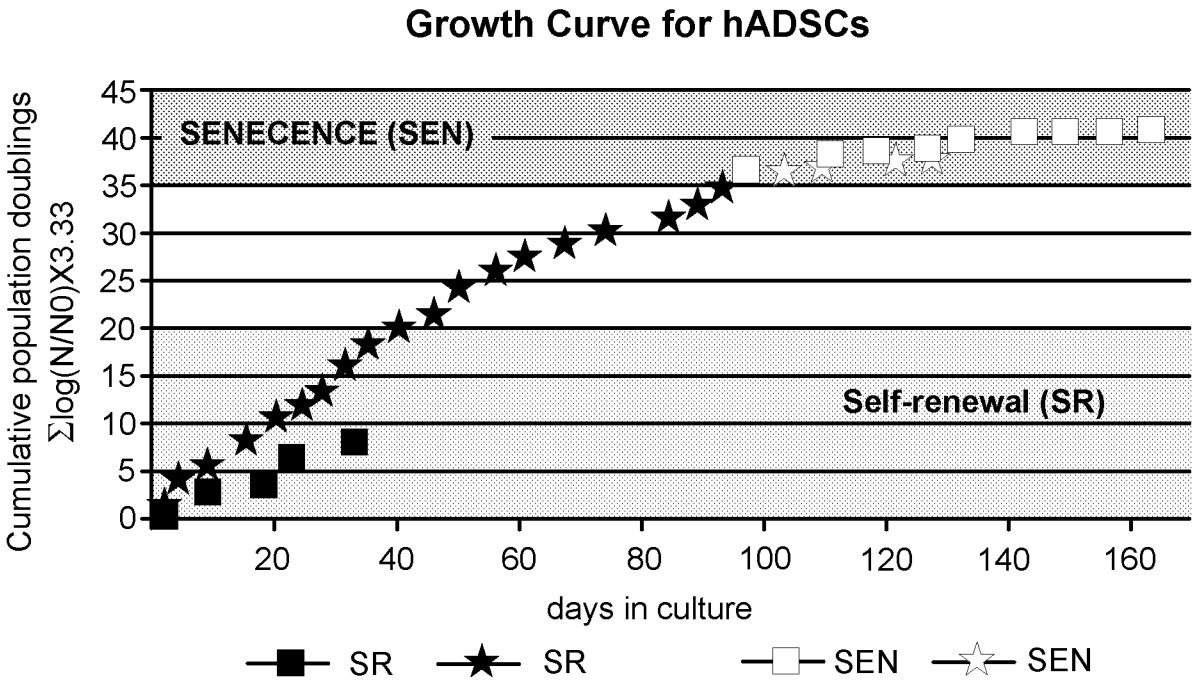


FIG. 3B

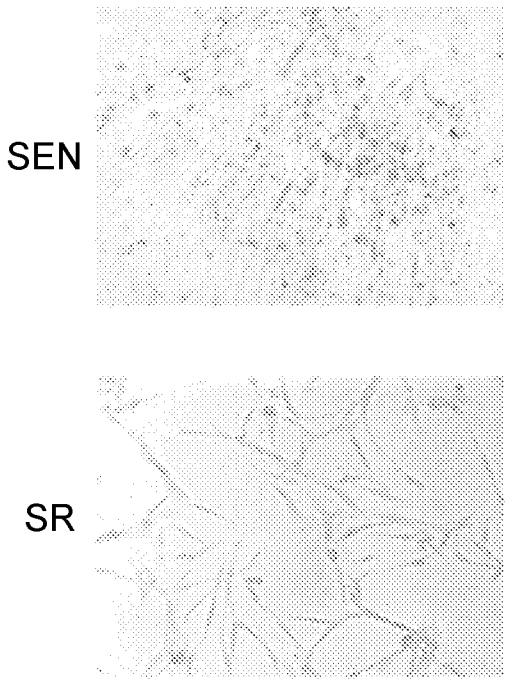


FIG. 3C

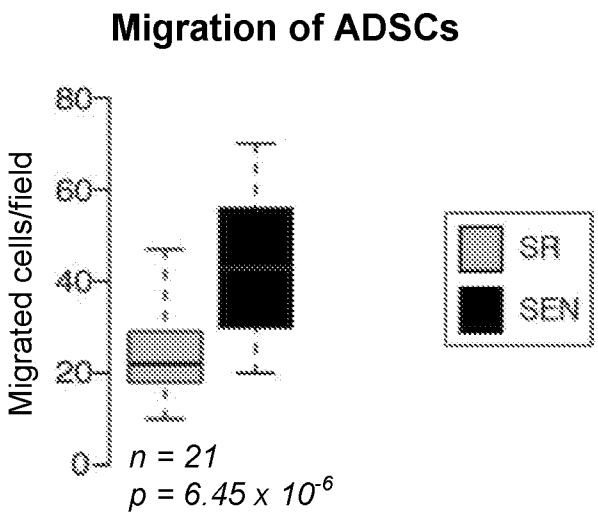
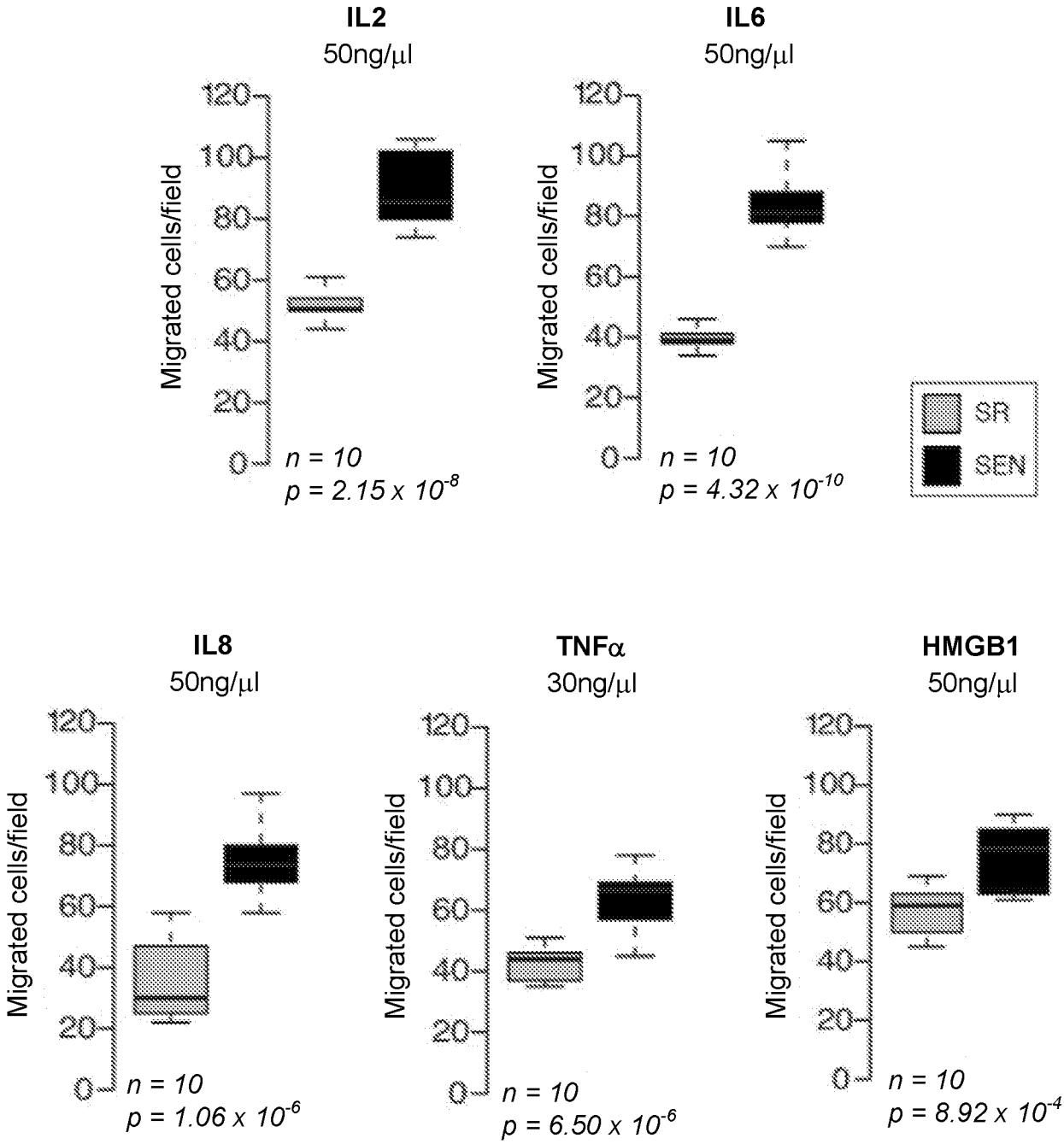


FIG. 3D **Migration in prescence of various cytokines**



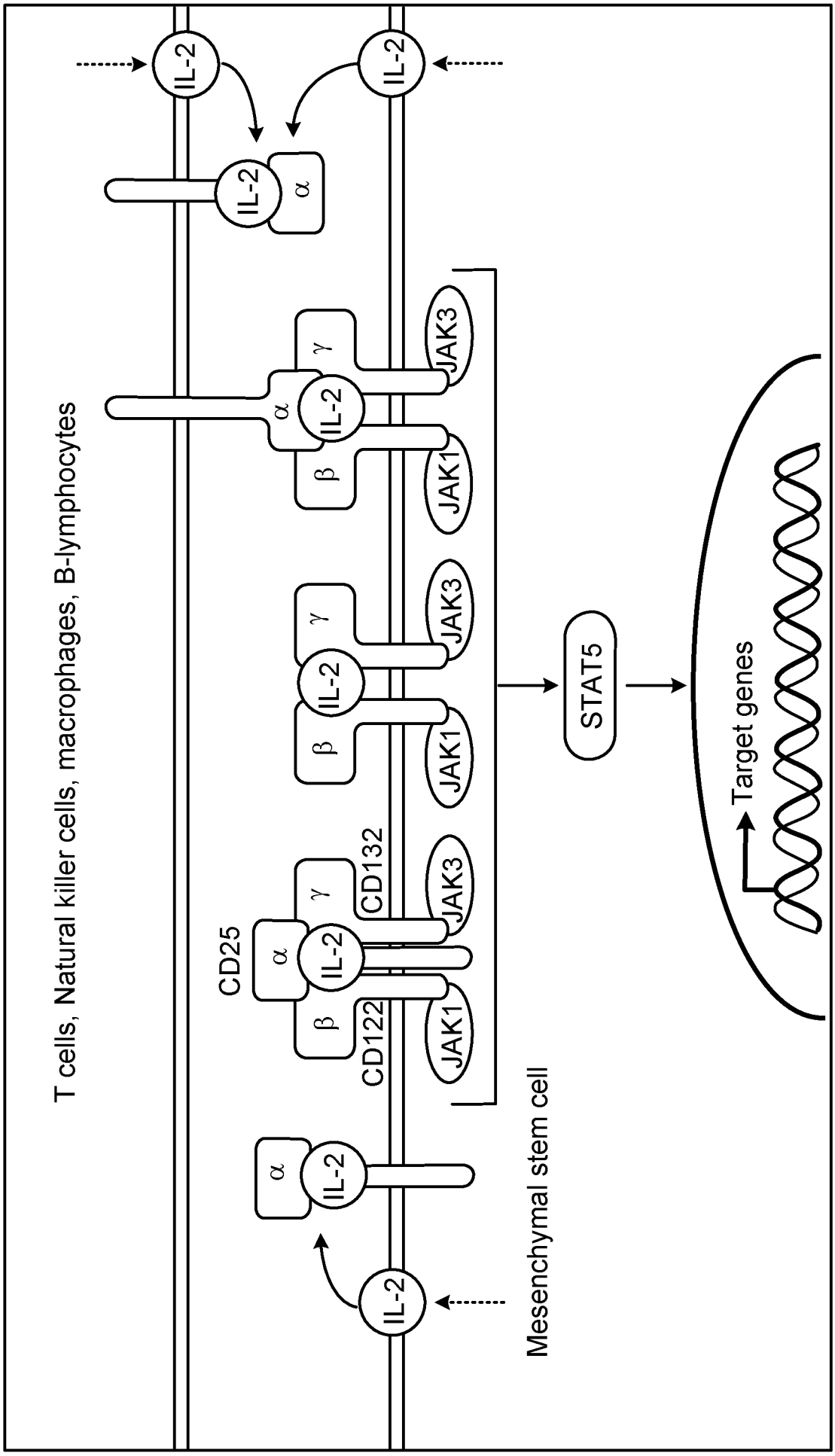

T cells, Natural killer cells, macrophages, B-lymphocytes
Mesenchymal stem cell
IL-2
α
β
γ
CD25
CD132
CD122
JAK1
JAK3
STAT5
Target genes

FIG. 4A

FIG. 4B

qPCR

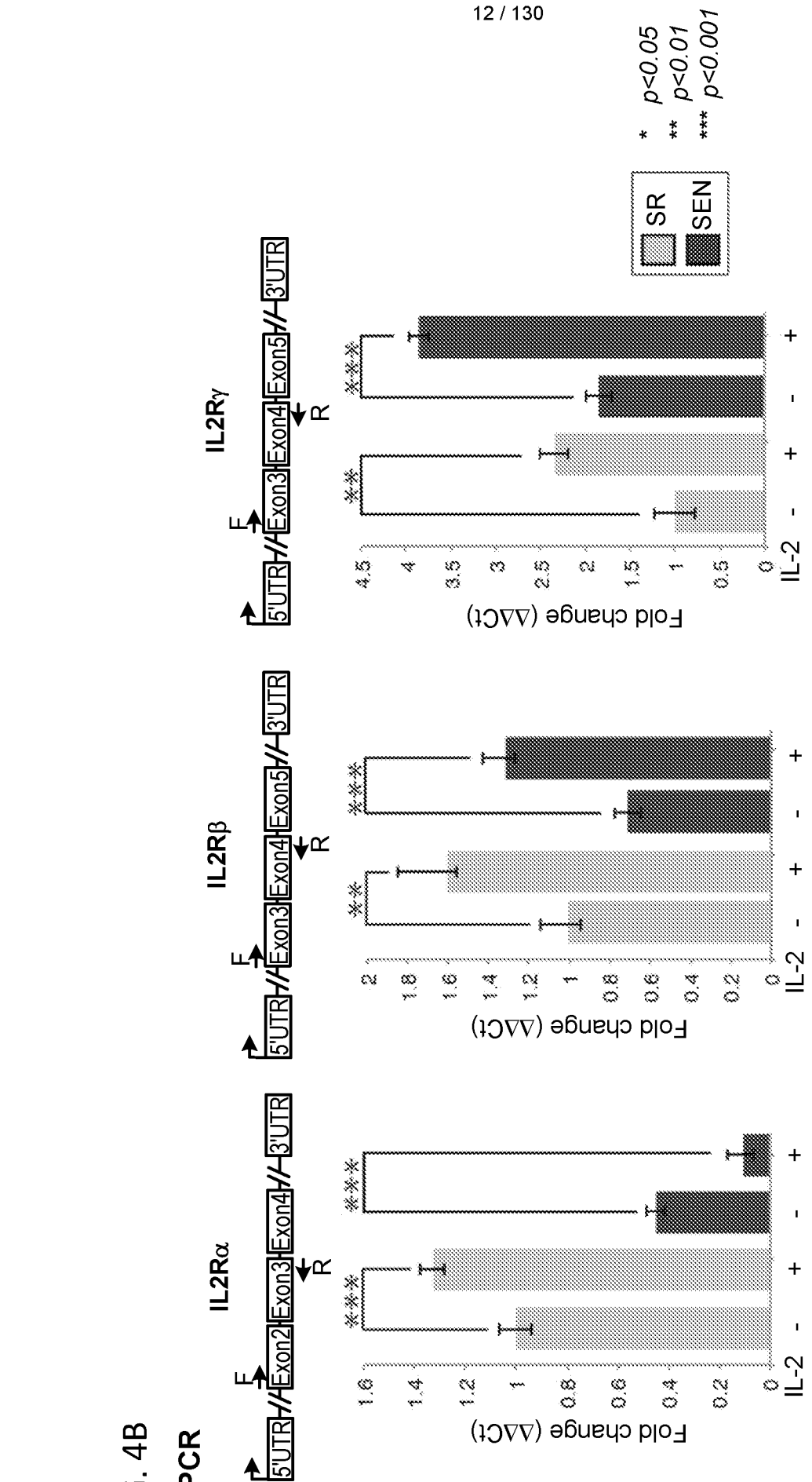

IL2Rα
IL2Rβ
IL2Rγ
5'UTR
Exon2
Exon3
Exon4
Exon5
3'UTR
F
R
Fold change (ΔΔCt)
IL-2
SR
SEN
* p<0.05
** p<0.01
*** p<0.001

FIG. 4C

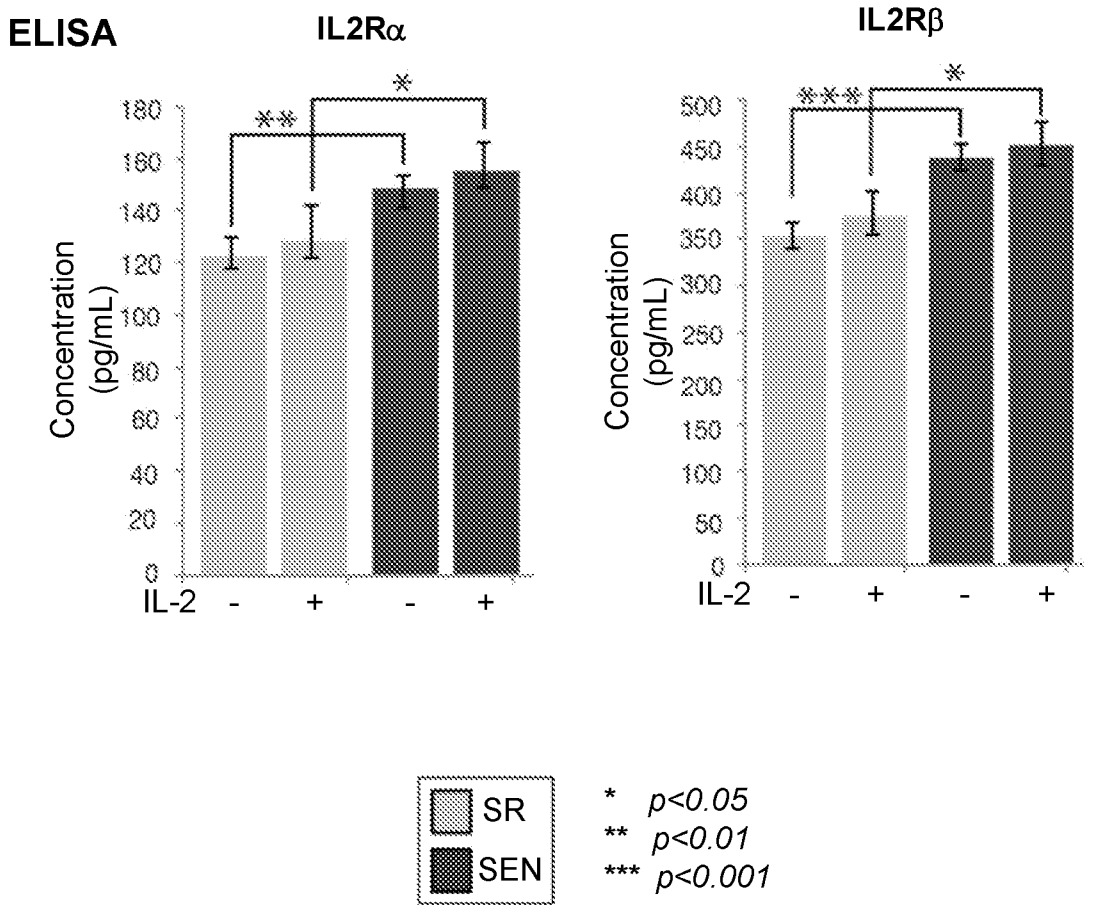

ELISA
IL2Rα
IL2Rβ
Concentration (pg/mL)
IL-2
SR
SEN
* p<0.05
** p<0.01
*** p<0.001

FIG. 5

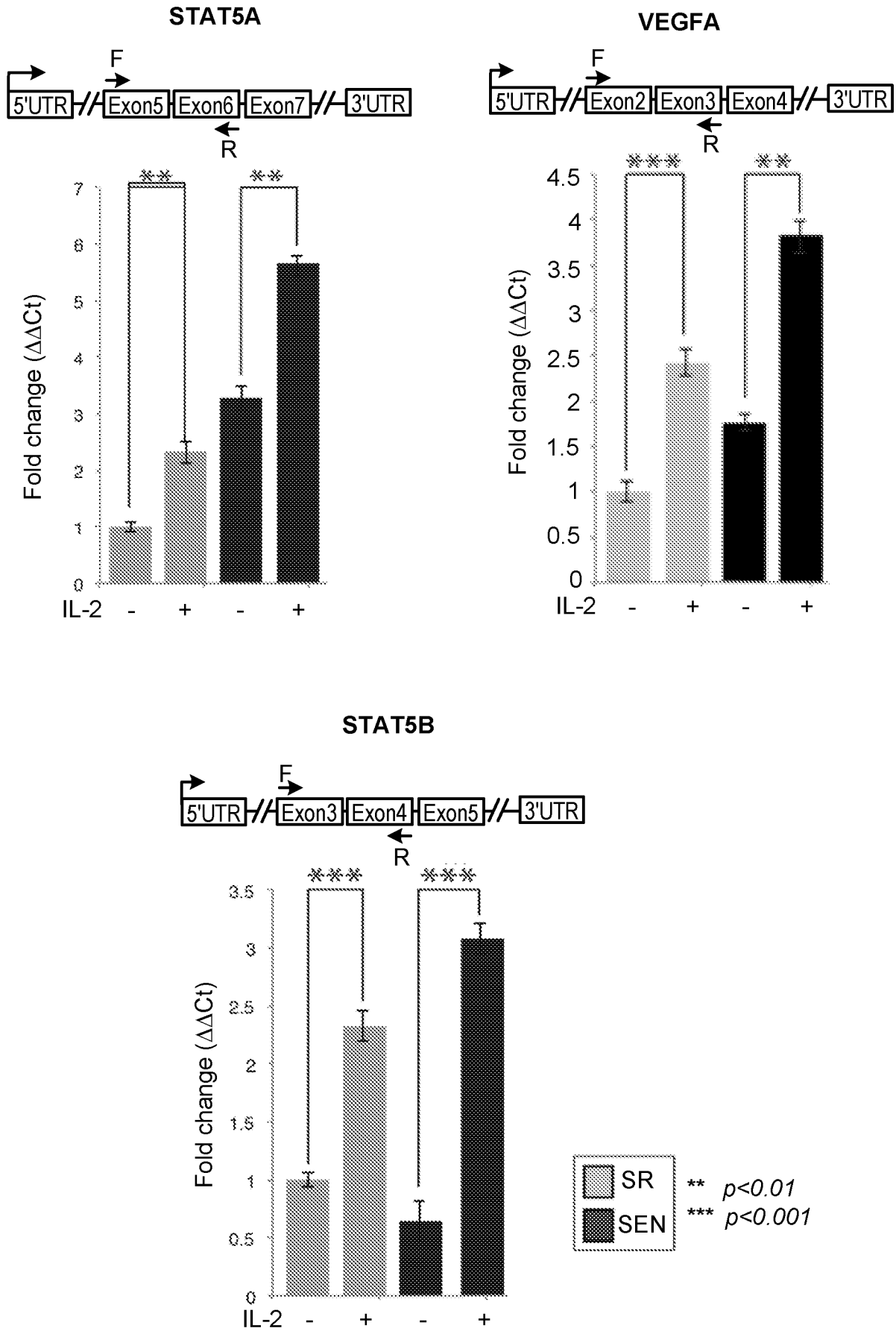

STAT5A
F
5'UTR
Exon5
Exon6
Exon7
3'UTR
R
Fold change (ΔΔCt)
IL-2 - + - +
VEGFA
F
5'UTR
Exon2
Exon3
Exon4
3'UTR
R
Fold change (ΔΔCt)
IL-2 - + - +
STAT5B
F
5'UTR
Exon3
Exon4
Exon5
3'UTR
R
Fold change (ΔΔCt)
IL-2 - + - +
SR
SEN
** p<0.01
*** p<0.001

FIG. 6A

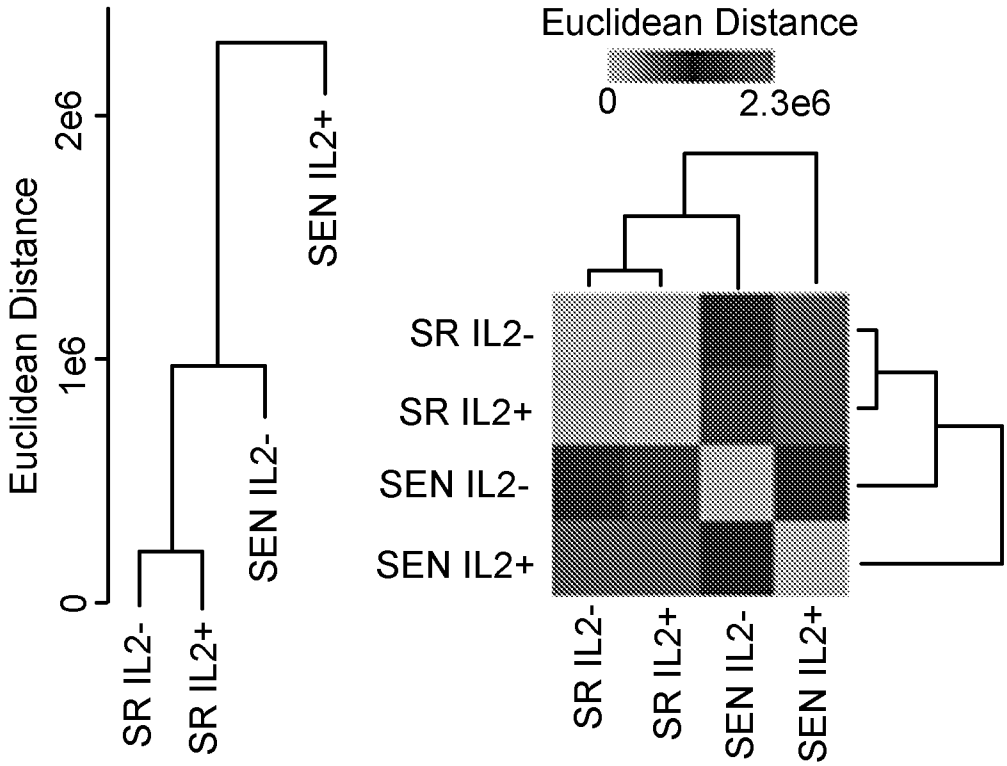

Euclidean Distance
2e6
1e6
0
SR IL2-
SR IL2+
SEN IL2-
SEN IL2+
Euclidean Distance
0
2.3e6
SR IL2-
SR IL2+
SEN IL2-
SEN IL2+
SR IL2-
SR IL2+
SEN IL2-
SEN IL2+

FIG. 6B

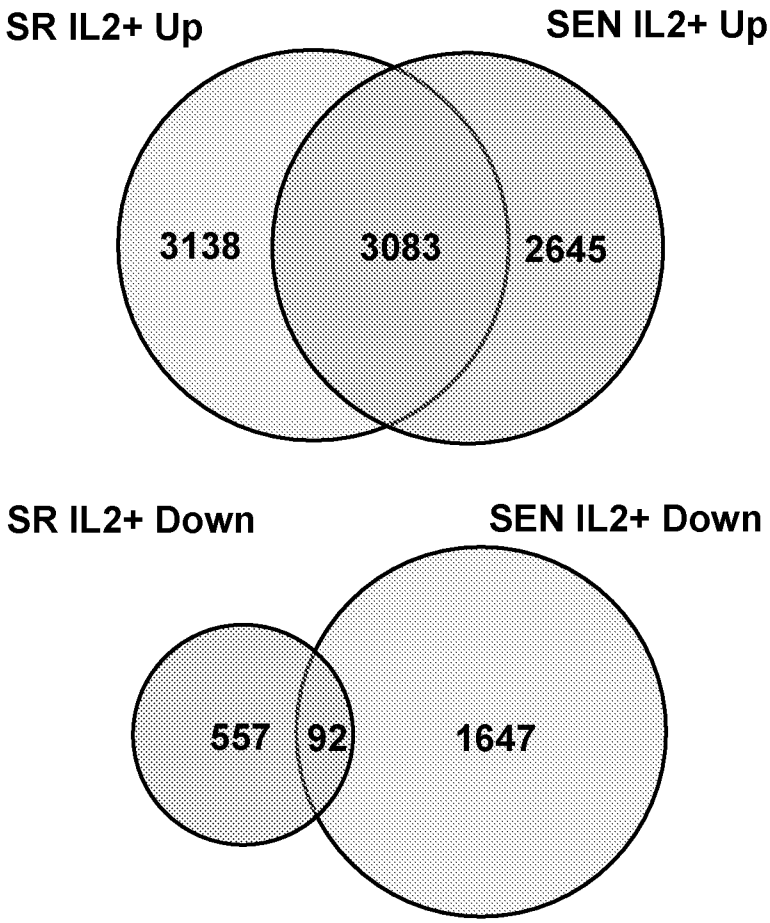

SR IL2+ Up
SEN IL2+ Up
3138
3083
2645
SR IL2+ Down
SEN IL2+ Down
557
92
1647

FIG. 6C

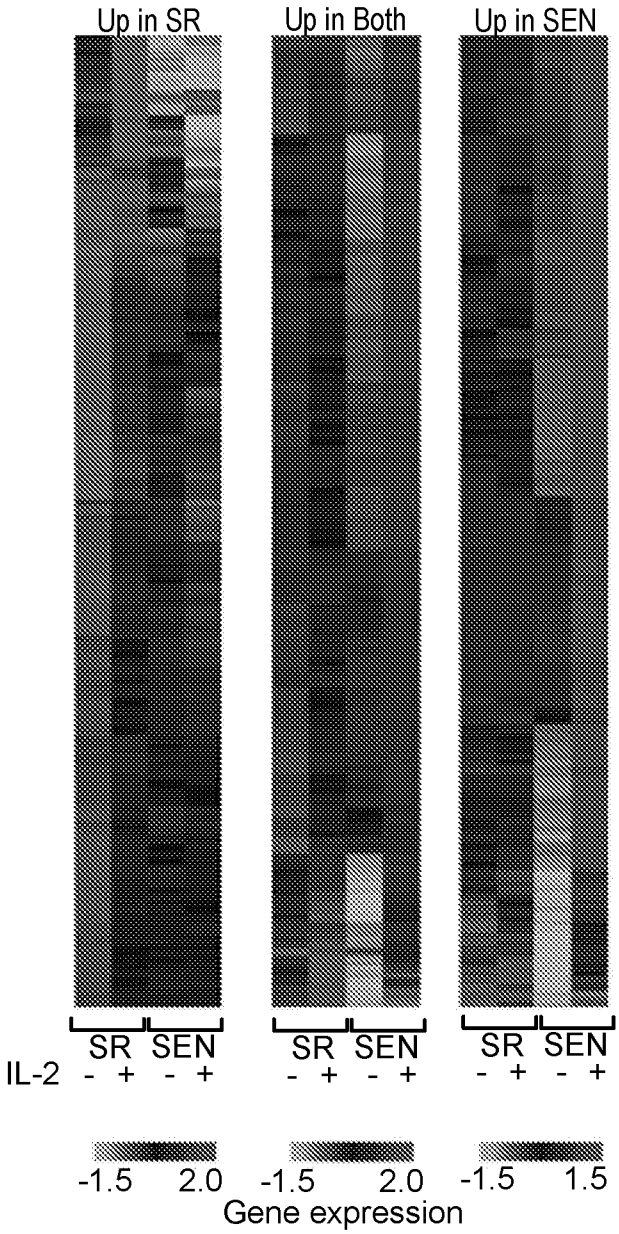

Up in SR
Up in Both
Up in SEN
SR SEN
IL-2 - + - +
-1.5 2.0
-1.5 2.0
-1.5 1.5
Gene expression

FIG. 6D

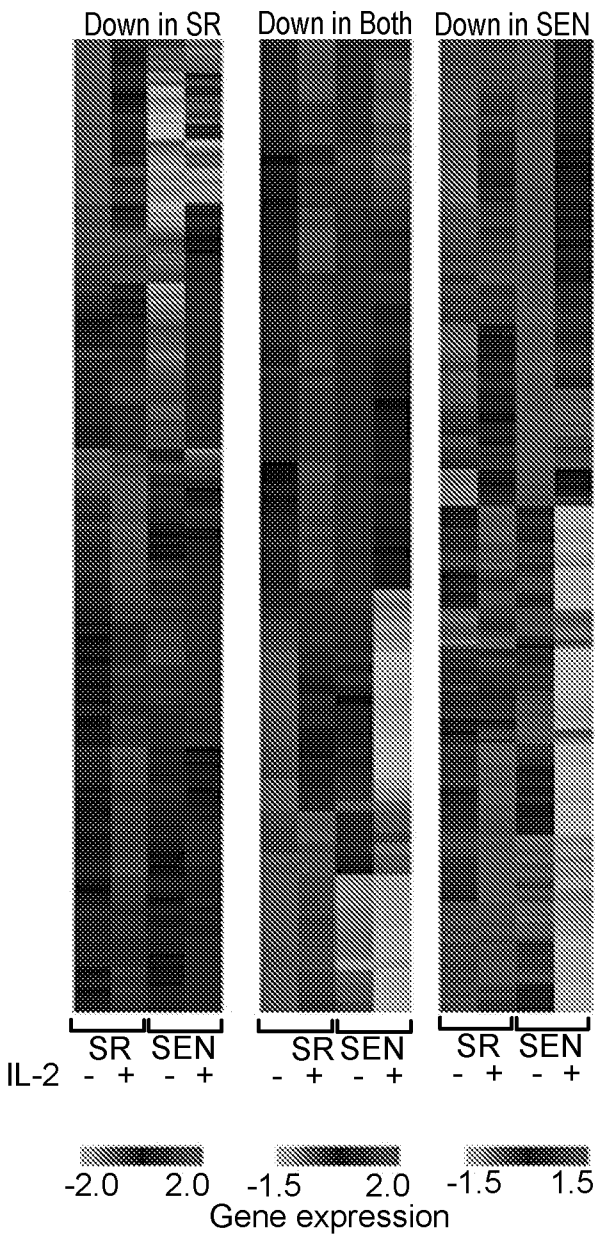

Down in SR
Down in Both
Down in SEN
SR SEN
IL-2 - + - +
-2.0 2.0
-1.5 2.0
-1.5 1.5
Gene expression

FIG. 7A

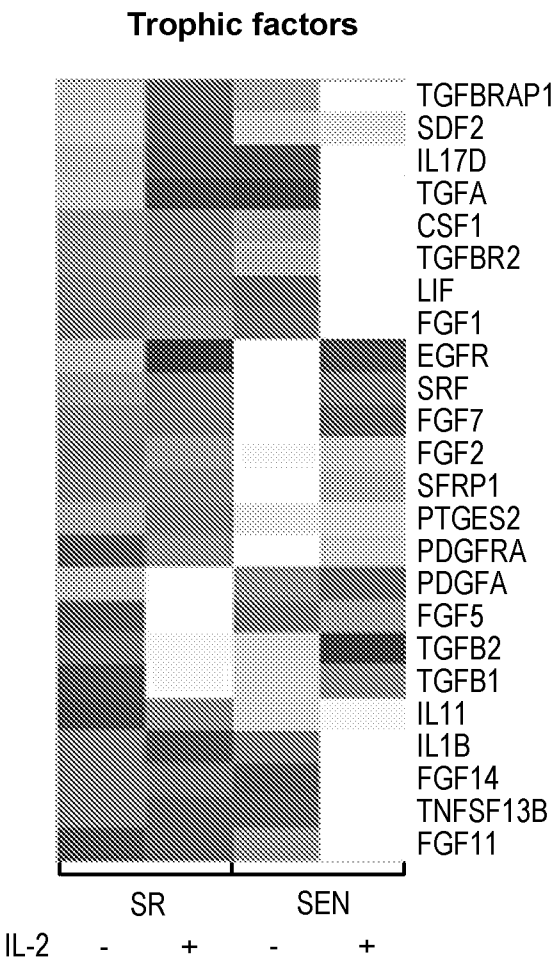


FIG. 7B

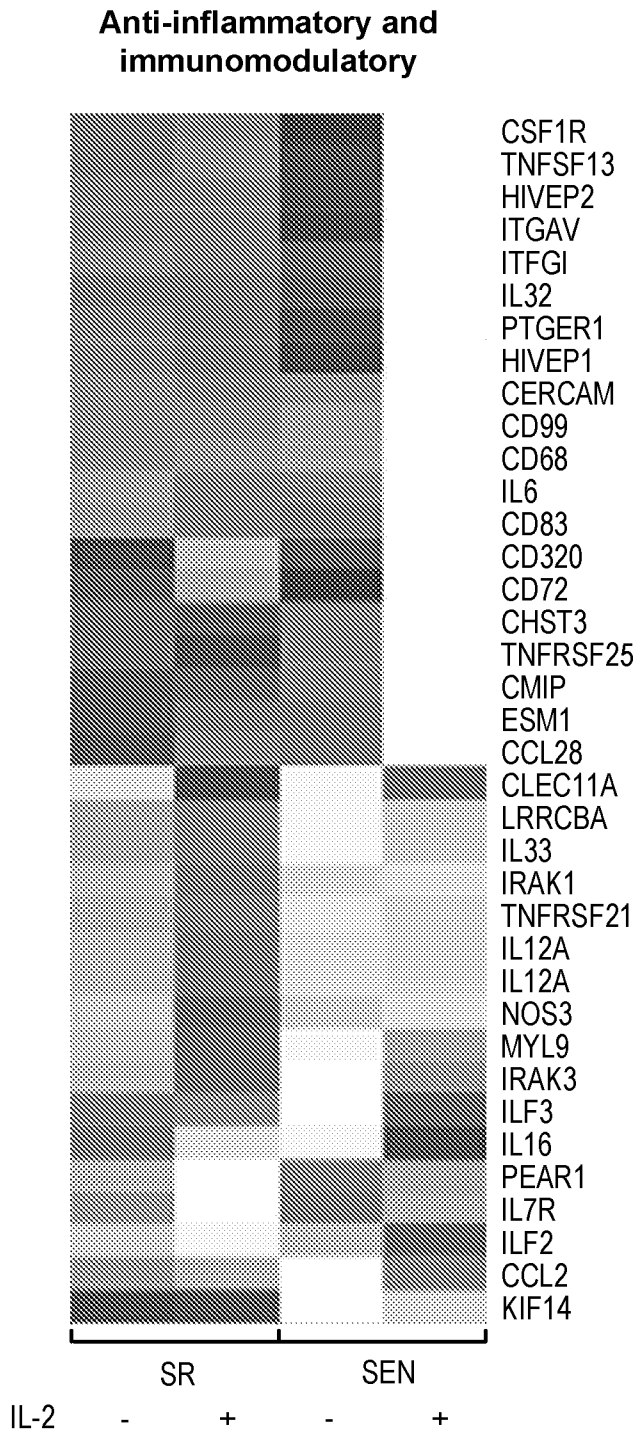


FIG. 7C

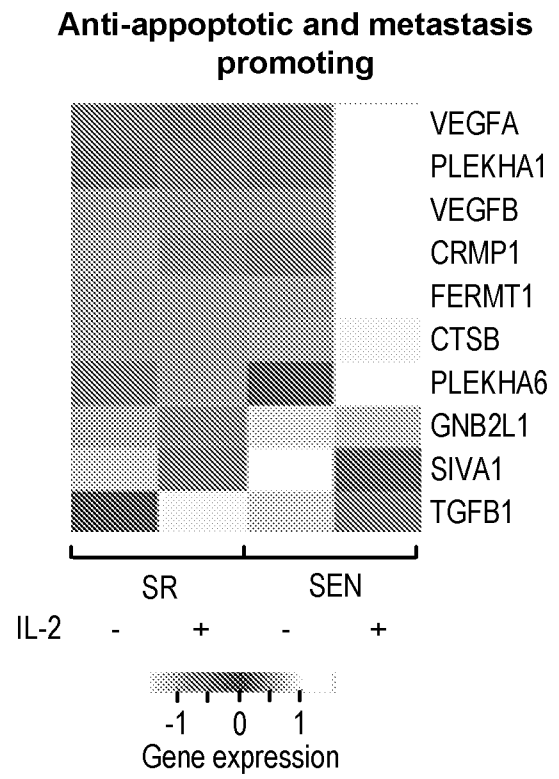


FIG. 7D

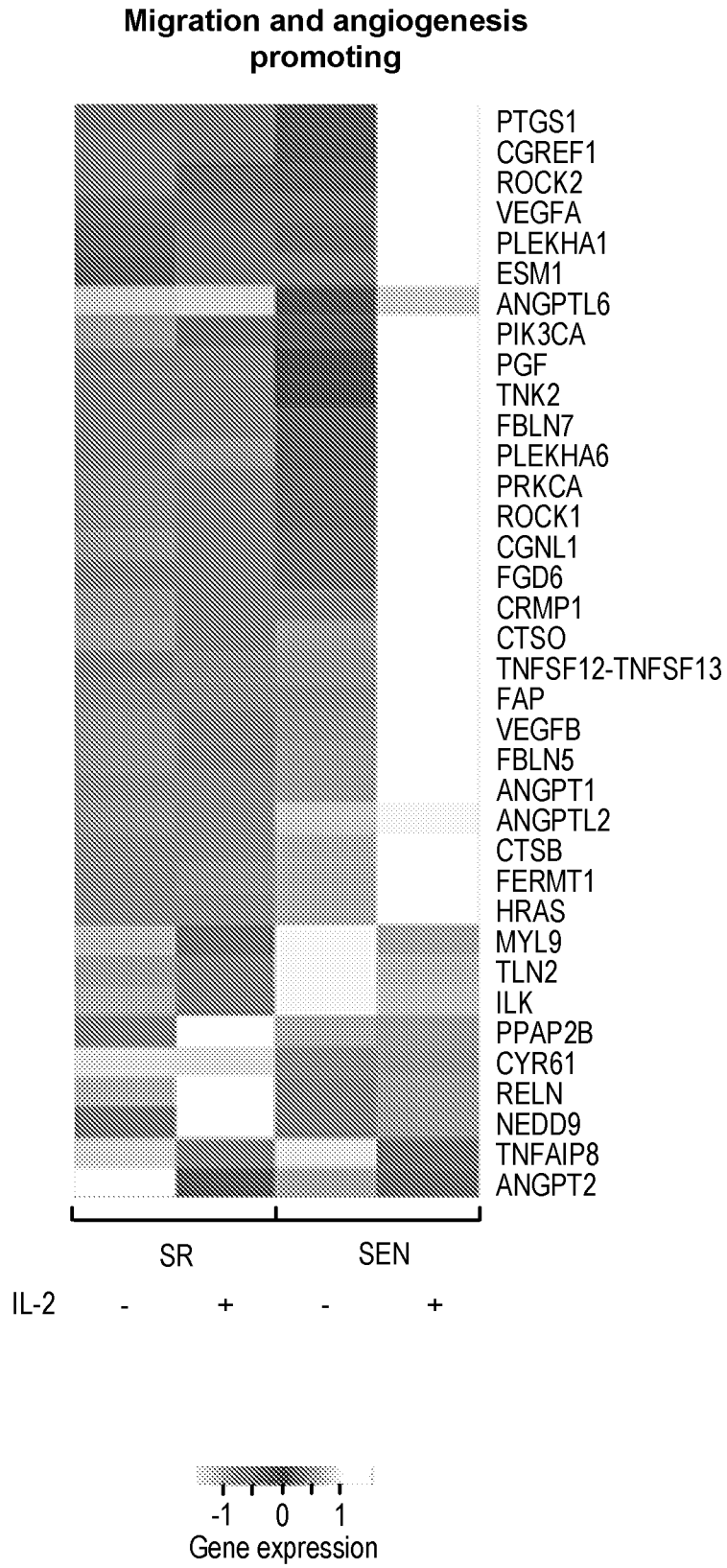

Migration and angiogenesis promoting
PTGS1
CGREF1
ROCK2
VEGFA
PLEKHA1
ESM1
ANGPTL6
PIK3CA
PGF
TNK2
FBLN7
PLEKHA6
PRKCA
ROCK1
CGNL1
FGD6
CRMP1
CTSO
TNFSF12-TNFSF13
FAP
VEGFB
FBLN5
ANGPT1
ANGPTL2
CTSB
FERMT1
HRAS
MYL9
TLN2
ILK
PPAP2B
CYR61
RELN
NEDD9
TNFAIP8
ANGPT2
SR
SEN
IL-2 - + - +
-1 0 1
Gene expression

FIG. 8A

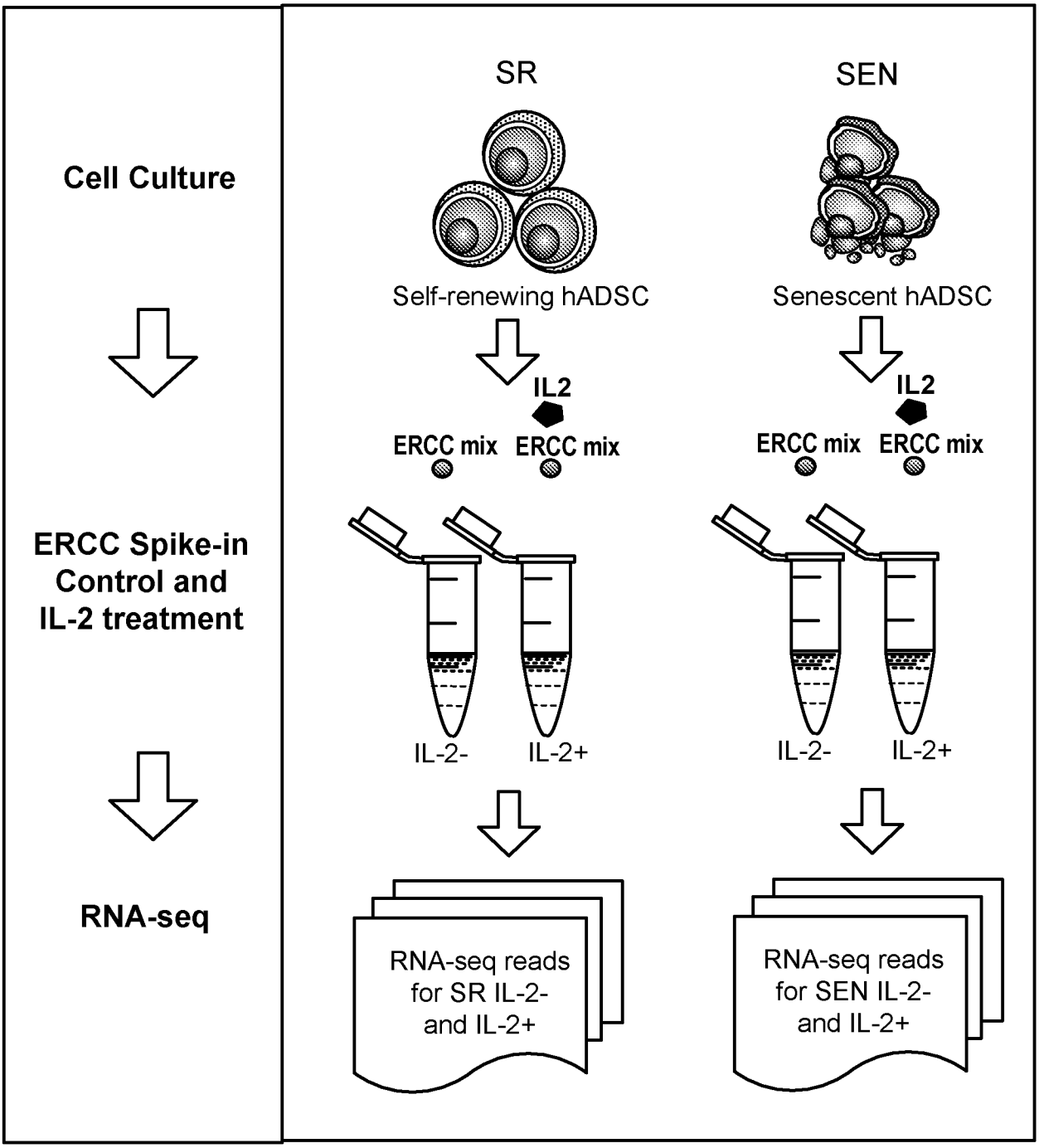

Cell Culture
ERCC Spike-in Control and IL-2 treatment
RNA-seq
SR
SEN
Self-renewing hADSC
Senescent hADSC
IL2
ERCC mix
ERCC mix
IL2
ERCC mix
ERCC mix
IL-2-
IL-2+
IL-2-
IL-2+
RNA-seq reads for SR IL-2- and IL-2+
RNA-seq reads for SEN IL-2- and IL-2+

FIG. 8B

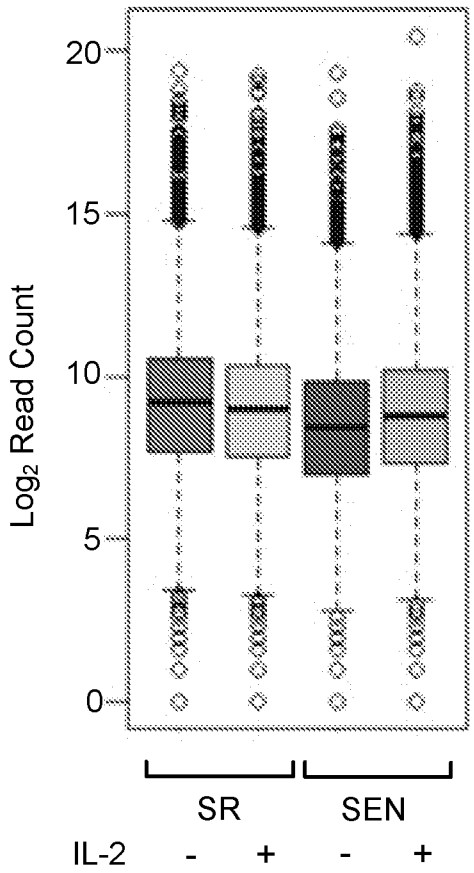


FIG. 8C

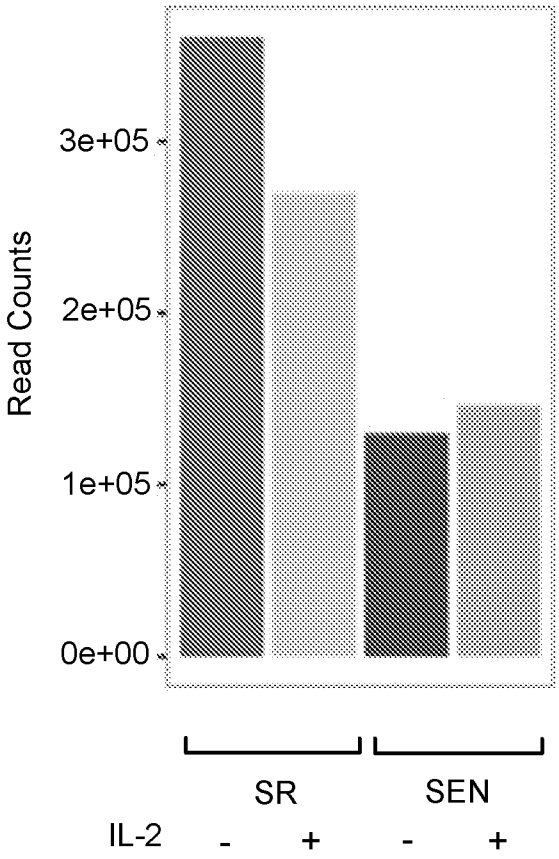


FIG. 8D

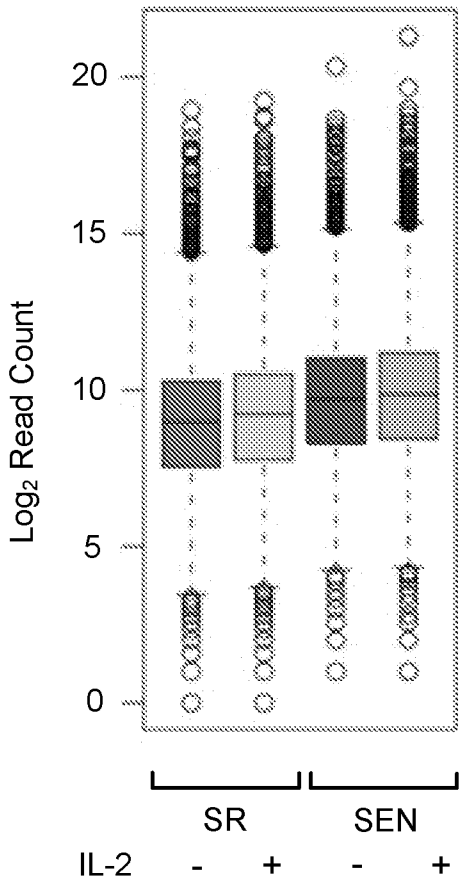
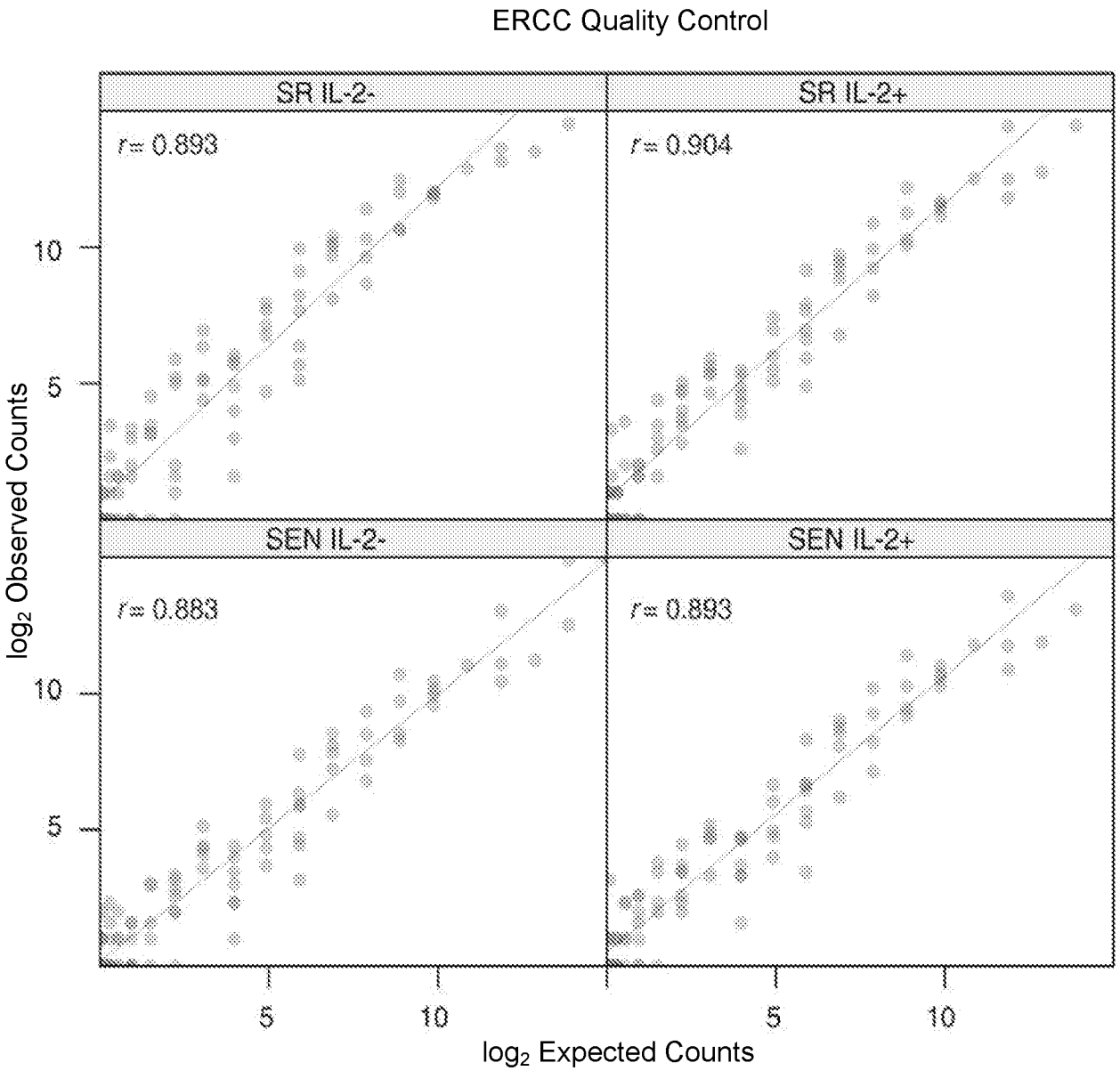


FIG. 9


ERCC Quality Control
SR IL-2-
SR IL-2+
SEN IL-2-
SEN IL-2+
r = 0.893
r = 0.904
r = 0.883
r = 0.893
log2 Observed Counts
log2 Expected Counts
5
10

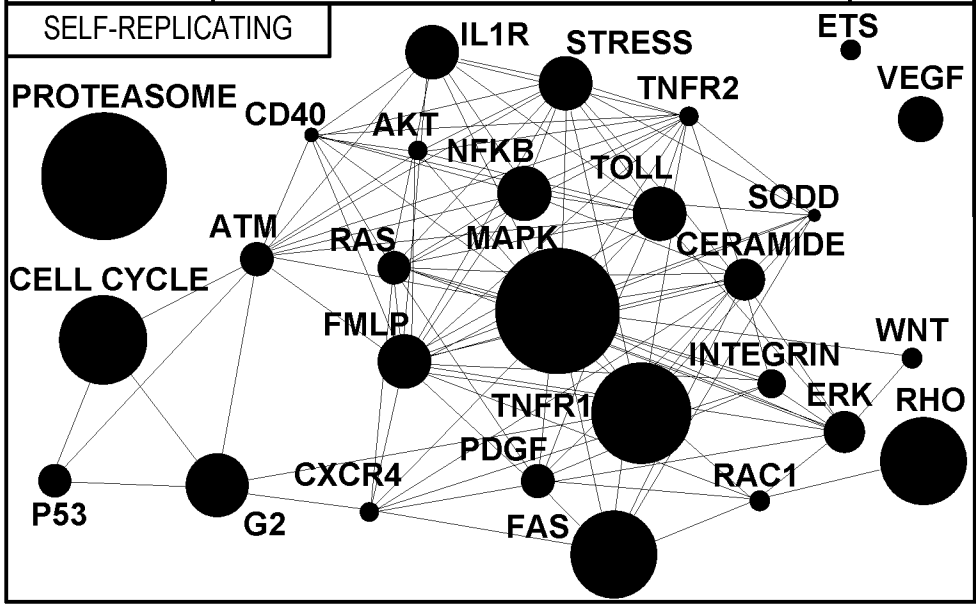
SUBSTITUTE SHEET (RULE 26)

FIG. 10A

BIOLOGICAL PATHWAYS UPREGULATED UPON IL-2 TREATMENT

PATHWAY	SELF-REPLICATING	FDR q-value
ATM	CHEK2, CDKN1A, RAD51, MRE11A, NFKBIA	2.62 e-2
PDGF	ELK1, PDGFA, RAF1, PDGFRA, STAT1	1.07 e-1
AKT	CHUK, BAD, HSP90AA1, NFKBIA	1.06 e-1
VEGF	NOSS, EIF2S3, HIF1A, EIF2S1, EIF2B2, EIF2B3	2.94 e-2
INTEGRIN	ZYX, ACTA1, BCAR1, RAF1, CAPN1	1.64 e-1
RAS	CDC42, ELK1, CHUK, RAF1, BAD	4.27 e-2
IL1R	IL1RAP, MYD88, CHUK, IRAK1, MAP3K14, IRAK3, NFKBIA	1.57 e-2
RHO	PIP5K1A, ARPC1A, ARPC5, ARHGAP1, DIAPH1, ARHGEF5, CFL1, ARPC4, ACTR3, ARHGEF1	2.34 e-4
WNT	CTBP1, MYC, HDAC1, TLE1	1.51 e-1

SELF-REPLICATING



PATHWAY	SELF-REPLICATING	FDR q-value
PROTEASOME	PSMB5, PSMB6, PSMD11, PSMD6, PSMA6, PSMA1, PSMA2, PSMA5, PSMA7, PSMB1, PSMB2, PSMB3, PSMB4, PSMC2, PSMC3, PSMC4	1 e-10
CELL CYCLE	CDK4, CCNH, CDKN1A, CDKN2C, CDK1, CDC25A, CDK2, CDKN1B,TFDP1, CCNB1	1.54 e-5
TNFR1	CASP8, CASP2, PAK2, PAK1, LMNA, PARP1, CRADD, TNFRSF1A, TRAF2, DFFA, PRKDC	1.75 e-5
FAS	CASP8, PAK2, DAXX, PAK1, LMNA, PARP1, FAS, CASP7, DFFA, PRKDC	1.36 e-4
MAPK	RPS6KA4, ELK1, PAK1, DAXX, MAPKAPK3, CHUK, MAP3K11, MYC, PAK2, RAF1, MAP3K14, MAP3K6, MAPKAPK2, STAT1, NFKBIA, RPS6KA2, TRAF2	2.42 e-4
G2	CHEK2, PLK1, ATR, CCNB1, CDC25A, CDKN1A, CDK1, PRKDC	5.94 e-4
NFKB	TNFRSF1A, MYD88, CHUK, IRAK1, TLR4, MAP3K14, NFKBIA	2.63 e-3
STRESS	TNFRSF1A, CHUK,CRADD, MAP3K14, NFKBIA, TRAF2, CASP2	4.3 e-3
CERAMIDE	TNFRSF1A, CASP8, AIFM1, RAF1, BAD,TRAF2	9.96 e-3
P53	CDK4, CDKN1A, CDK2, PCNA, APAF1	1.18 e-2
ERK	ELK1, MYC,NGFR, RAF1, EGFR, PDGFRA	2.62 e-2
TOLL	MAP3K14, ELK1, MYD88, IRAK1, CHUK, NFKBIA, TLR4	2.63 e-2
FMLP	FPR1, RAF1, PAK1, NFATC1, ELK1, CALM3, NFKBIA	3.41 e-2
SODD	CASP8, TNFRSF1A, TRAF2	6.41 e-2
ETS	E2F4, ETS2, DDX20, ETS1	6.57 e-2
TNFR2	MAP3K14, CHUK, TRAF2, NFKBIA	6.57 e-2
RAC1	CDK5, PAK1, CFL1, PDGFRA	1.17 e-1
CXCR4	RAF1, GNAI1, BCAR1, CXCL12	1.3 e-1
CD40	MAP3K14, CHUK, NFKBIA	1.34 e-1

FIG. 10A (Continued)

PATHWAY	SENESCENT	FDR q-value
ATM	JUN, GADD45A, MDM2, NBN, MAPK8, ATM, RBBP8, ABL1, RAD50	8.15 e-5
PDGF	RASA1, JUN, FOS, PRKCA, PIK3CA, MAPK8, STAT5A, HRAS, STAT4	6.86 e-4
AKT	FOXO4, CASP9, PIK3CA, AKT1, PDPK1, FOXO1, FOXO3	1.6 e-3
VEGF	VEGFA,EIF2S2, EIF1AX, PRKCA, PIK3CA, EIF2B4, HRAS	5.24 e-3
INTEGRIN	JUN, RAP1A, MAPK8, ROCK1, CSK, HRAS, SRC, PPP1R12B	5.55 e-3
RAS	RALA, FOXO4, CASP9, PIK3CA, AKT1, HRAS	6.57 e-3
IL1R	JUN, IL1RN, IRAK2, TRAF6, MAPK8, IL6	2.51 e-2
RHO	ARHGAP5, BAIAP2, ROCK1, SRC, PPP1R12B, OPHN1	2.34 e-2
WNT	GSK3B, BTRC, SMAD4, APC, AXIN1	3.37 e-2
EGF	RASA1, JUN, FOS, EGF, PRKCA, PIK3CA, MAPK8, STAT5A, HRAS, STAT4	2.33 e-4
LONGEVITY	SOD2, IGF1R, PIK3CA, AKT1, SOD1, FOXO3, HRAS	2.53 e-4
IL2	JUN, FOS, JAK3, MAPK8, STAT5A, HRAS	5.55 e-3
IL6	JUN, CEBPB, FOS, JAK3, IL6, HRAS	5.55 e-3
IL7	PTK2B, JAK3, EP300, PIK3CA, STAT5A	8.47 e-3
TGFB	TGFBR1, SKIL, EP300, SMAD4, APC	1.25 e-2
IL2RB	FOS, JAK3, PIK3CA, STAT5A, AKT1, CBL, HRAS	1.51 e-2
B-CELL SURVIVAL	FOS, PIK3CA, XIAP, AKT1	2.76 e-2
LEPTIN	LEP, PRKAB2, PRKAA2	5.08 e-2
IL12	JUN, ETV5, MAPK8, STAT4	7.39 e-2
NOS1	PRKACB, GRIN2D, PRKCA, DLG4	8.32 e-2

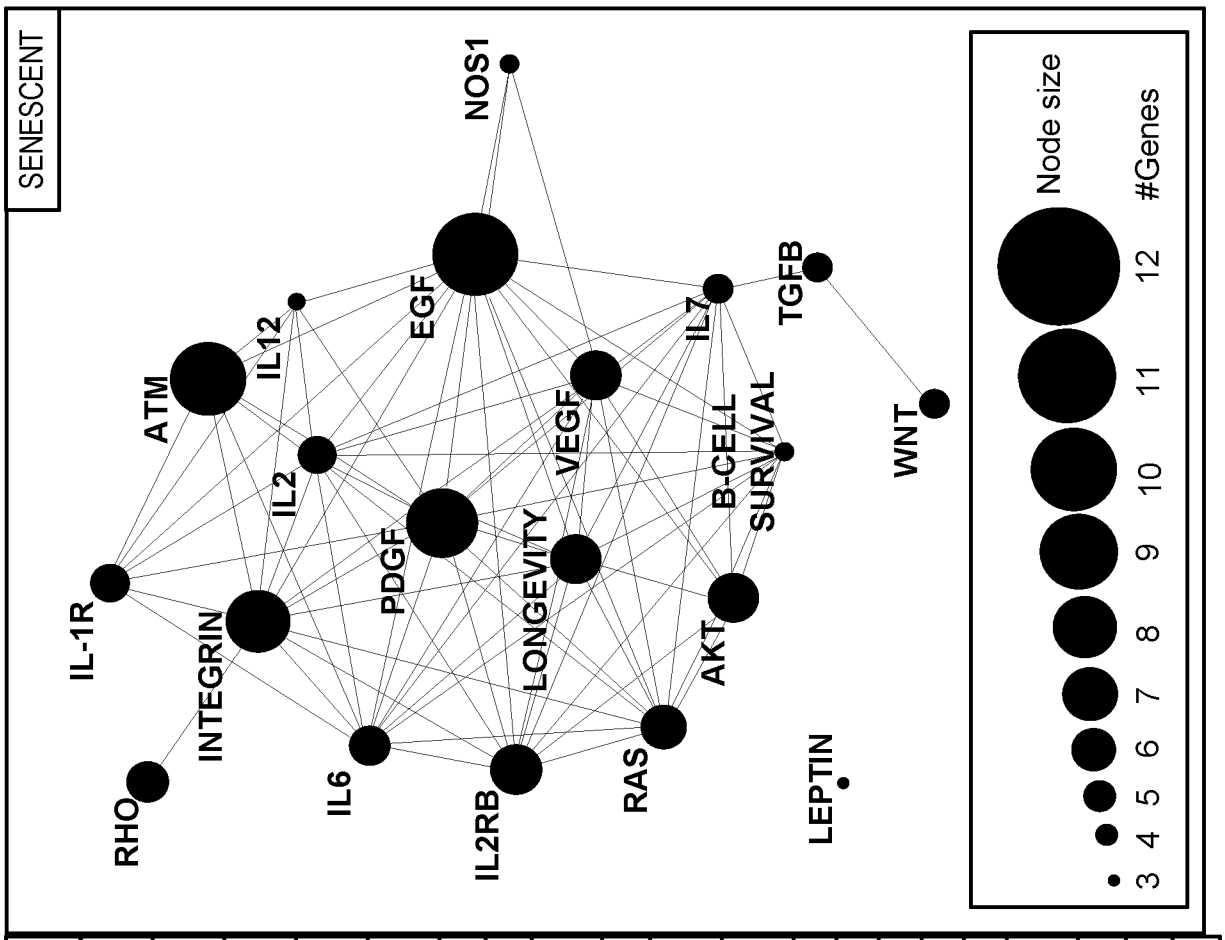


FIG. 10B **BIOLOGICAL PATHWAYS DOWNREGULATED UPON IL-2 TREATMENT**

PATHWAY	SELF-REPLICATING	FDR q-value
G2	GADD45A, CDKN2D	5.35 e-1
P53	GADD45A, BAX	5.35 e-1
MTOR	EIF3A, FKBP1A	5.35 e-1
ETS	NCOR2, CSF1R	5.35 e-1

FIG. 10B
(Continued)

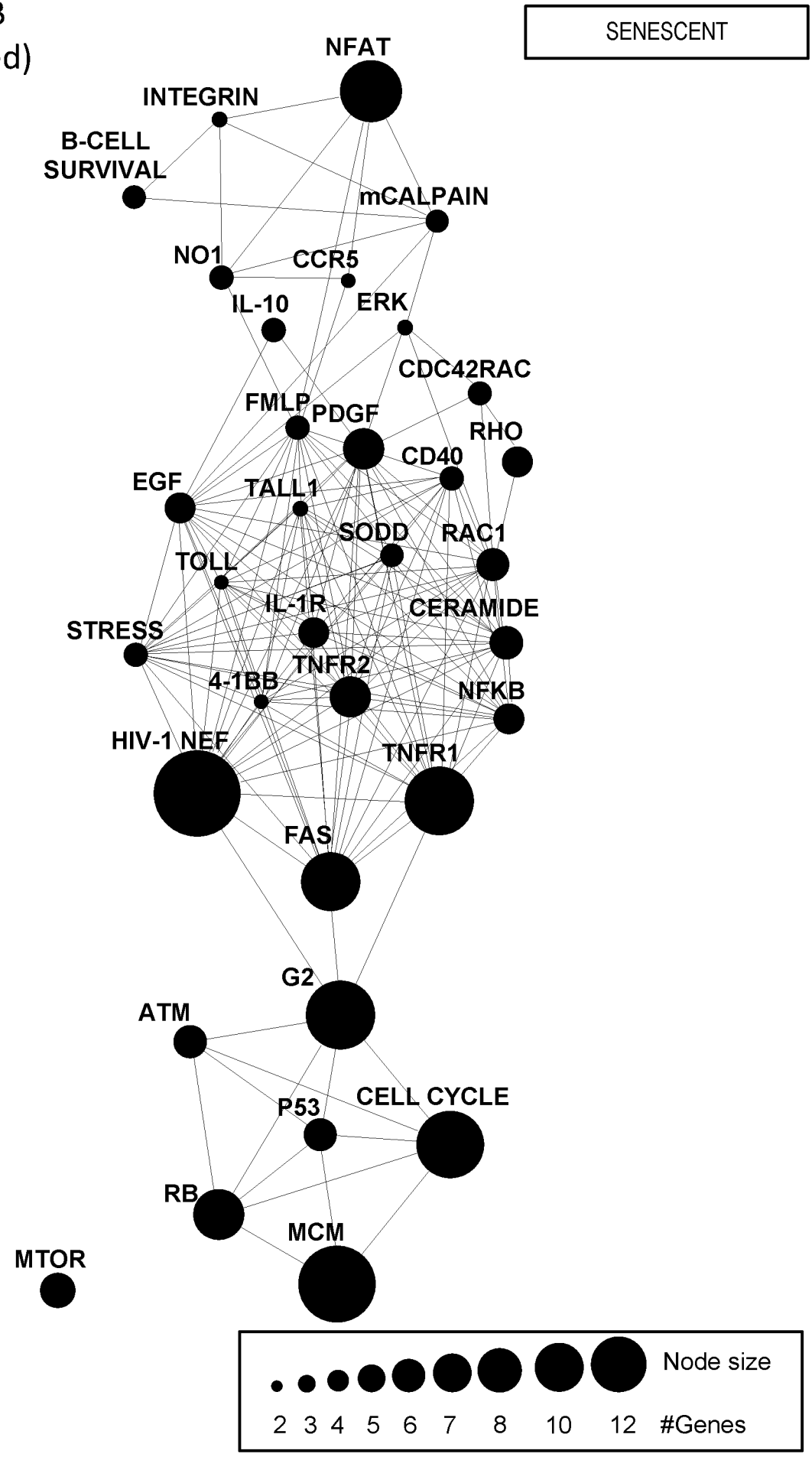
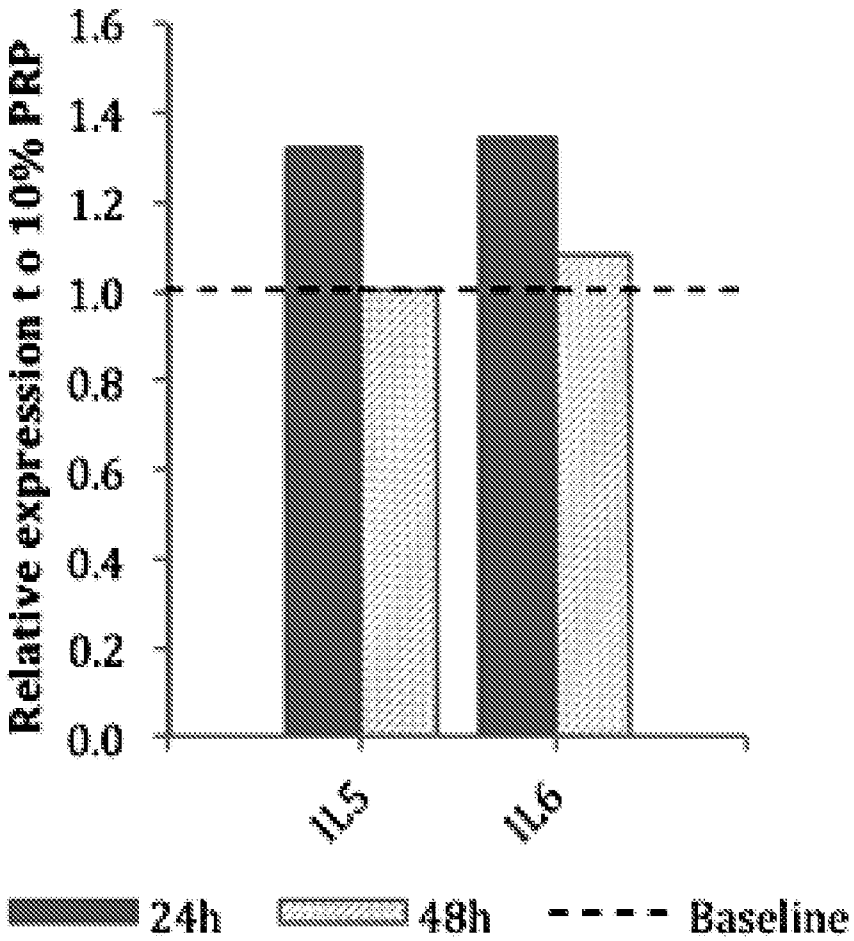


FIG. 10B
(Continued)

PATHWAY	SENESCENT	FDR q-value
G2	PRKDC, CDK1, CDKN1A, CCNB1, CHEK1, CDC25C, CDC25B, PLK1	3.06 e-5
P53	CDK2, CDKN1A, CDK4, PCNA	1.86 e-2
MTOR	EIF4A1, PRS6, TSC1	1.59 e-1
MCM	CDK2, KITLG, ORC6, ORC3, MCM2, MCM3, MCM4, MCM5, MCM7, CDT1	1.62 e-8
PROTEA-SOME	PSMA7, PSMA5, PSMA6, PSMB3, PSMB5, PSMB6, PSMB7, PSMC2, PSMC3	2.17 e-5
HIV-I NEF	PRKDC, CASP8, LMNA, PARP1, LMNB1, LMNB2, MAP3K1, TRAF2, CYCS, MAP3K14, TNFRSF1B, ACTG1	2.52 e-5
CELL CYCLE	CDK2, CDK1, CDKN1A, CCNB1, CDK4, TFDP1, CDKN2C, CCND3	2.52 e-5
RB	CDK2, CDK1, CDK4, CHEK1, CDC25C, CDC25B	6.97 e-5
TNFR1	PRKDC, CASP8, LMNA, PARP1, LMNB1, LMNB2, MAP3K1, TRAF2	1.02 e-4
FAS	PRKDC, CASP8, LMNA, PARP1, LMNB1, LMNB2, MAP3K1, TRAF2	1.1 e-3
TNFR2	MAP3K1, TRAF2, MAP3K14, TNFRSF1B, IKBKAP	4.02 e-3
NFAT	ACTA1, MEF2C, CALM3, CAMK1G, CTF1, FGF2, HAND2	2.9 e-2
SODD	CASP8, TRAF2, TNFRSF1B	3.24 e-2
ATM	CDKN1A, CHEK1, MRE11A, RAD51	3.28 e-2

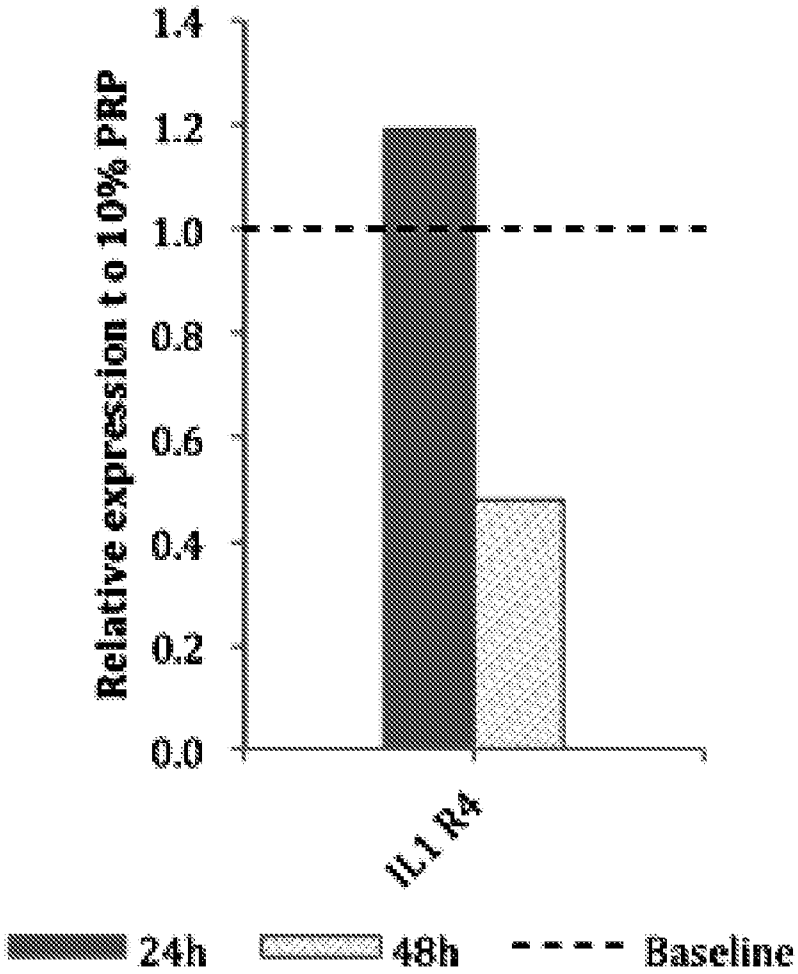
PATHWAY	SENESCENT	FDR q-value
PDGF	MAP3K1, STAT1, SRF, PDGFRA, PDGFA	3.28 e-2
CERAMIDE	CASP8, MAP3K1, TRAF2, CYCS	3.92 e-2
NFKB	MAP3K1, MAP3K14, TNFRSF1B, IL1R1	4.25 e-2
RAC1	MAP3K1, PDGFRA, CFL1, CHN1	4.25 e-2
CD40	IKBKAP, MAP3K1, MAP3K14	6.79 e-2
B-CELL SURVIVAL	BIRC5, CCT4, ITGA1	7.61 e-2
CDC42RAC	ARPC4, CDC42, PDGFRA	7.61 e-2
IL-10	BLVRA, BLVRB, STAT1	8.64 e-2
EGF	EGFR, MAP3K1, SRF, STAT1	9.19 e-2
RHO	ARHGAP1, ARPC4, CFL1, PIP5K1A	1 e-1
IL-1R	IL1R1,IRAK3, MAP3K1, MAP3K14	1.09 e-1
mCALPAIN	ACTA1, EGFR, ITGA1	1.79 e-1
STRESS	MAP3K1, MAP3K14, TRAF2	1.79 e-1
TALL1	MAP3K14, TRAF2	2.81 e-1
NO1	ACTA1, CALM3, FLT1	2.97 e-1
4-1BB	MAP3K1, TRAF2	3.21 e-1
LAIR	C5, ITGA4	3.21 e-1
ETS	E2F4, ETS1	3.4 e-1
FMLP	CALM3, CAMK1G, MAP3K1	3.8 e-1
CCR5	CALM3, CCL2	3.8 e-1
ERK	EGFR, PDGFRA	5.82 e-1
TOLL	MAP3K1, MAP3K14	8.06 e-1
INTEGRIN	ACTA1, ITGA1	8.25 e-1

FIG. 11



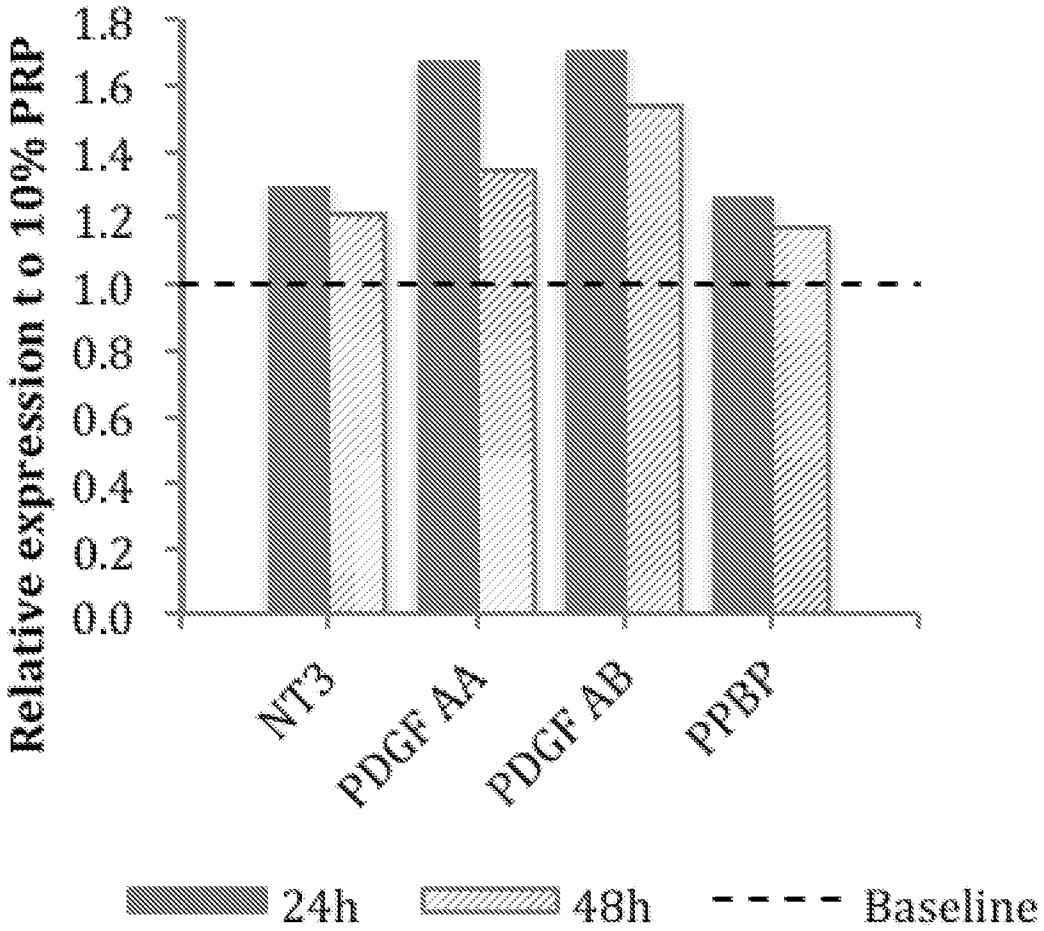
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 12



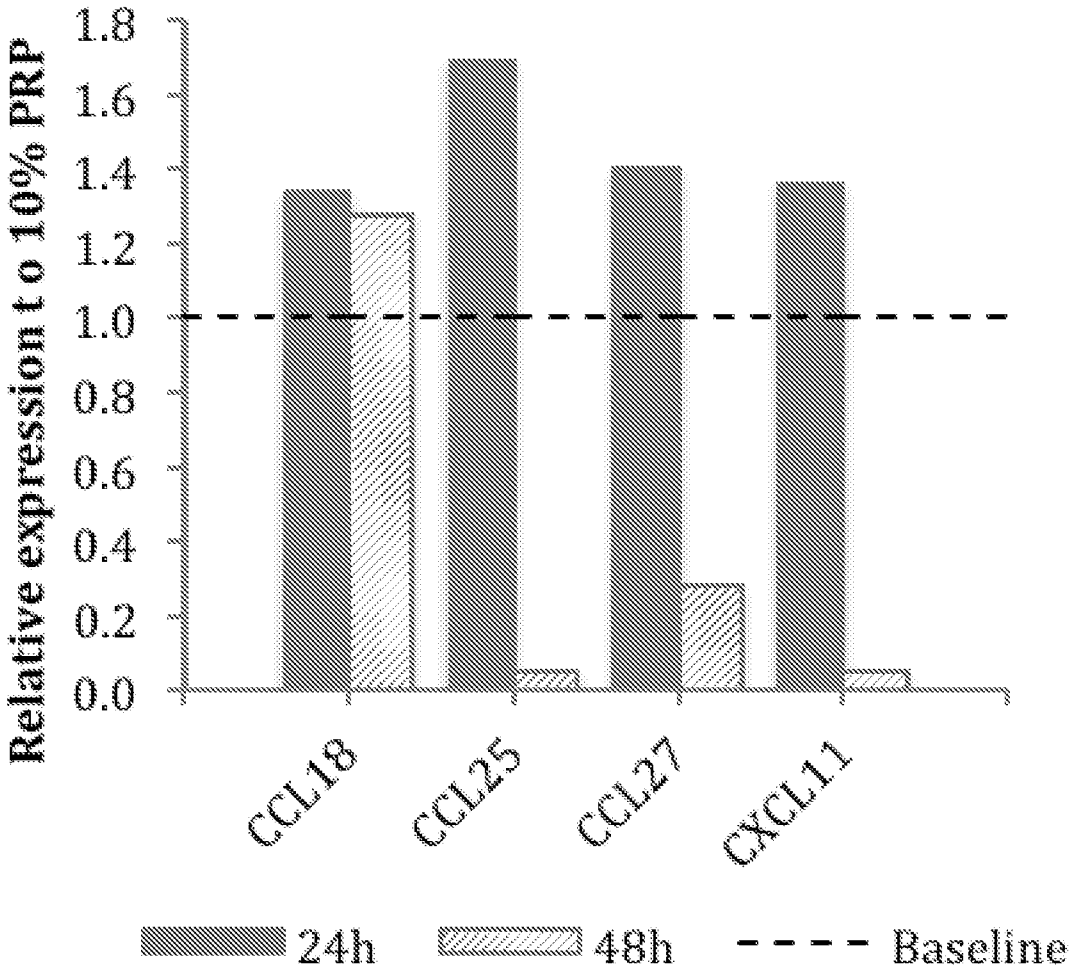
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 13



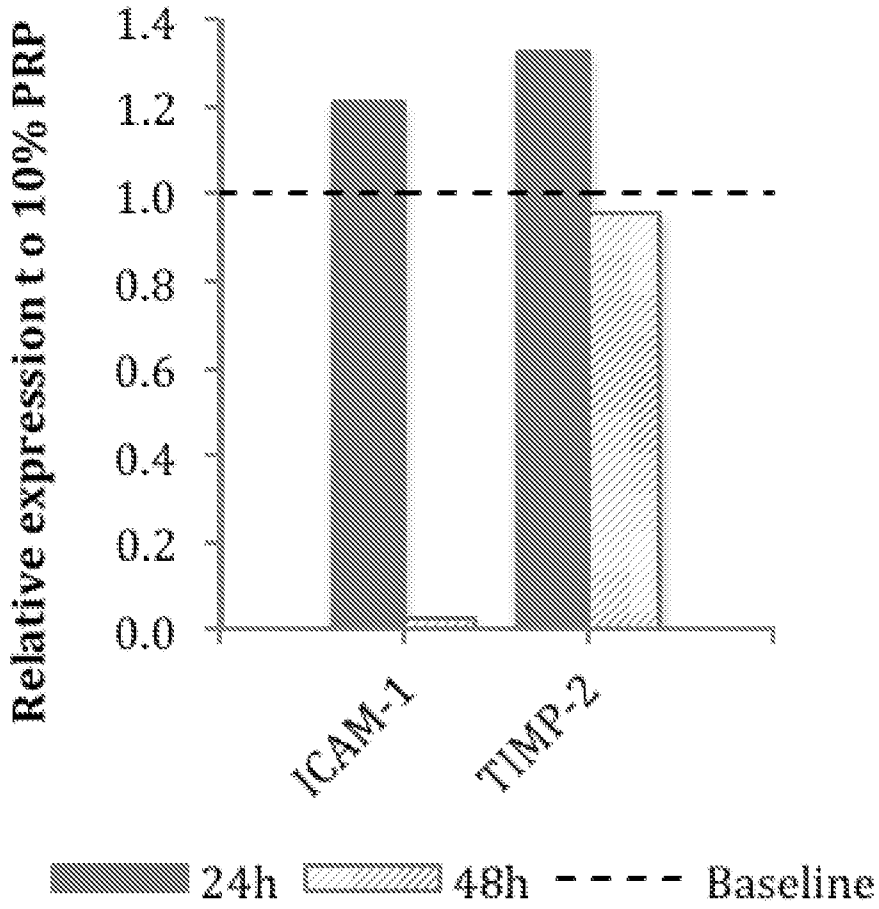
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 14



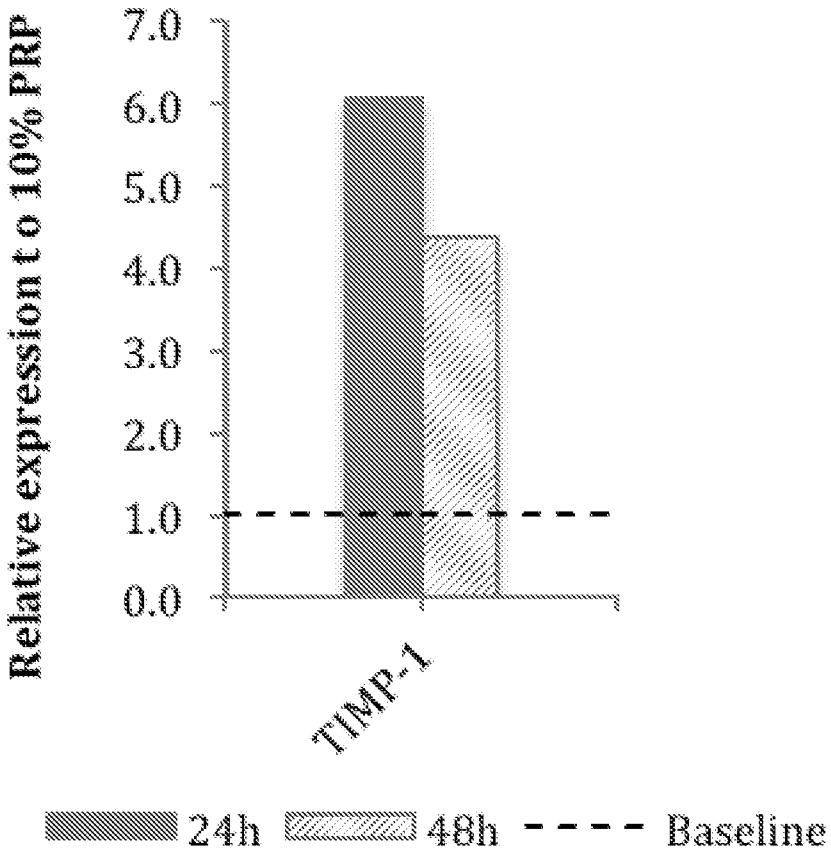
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 15



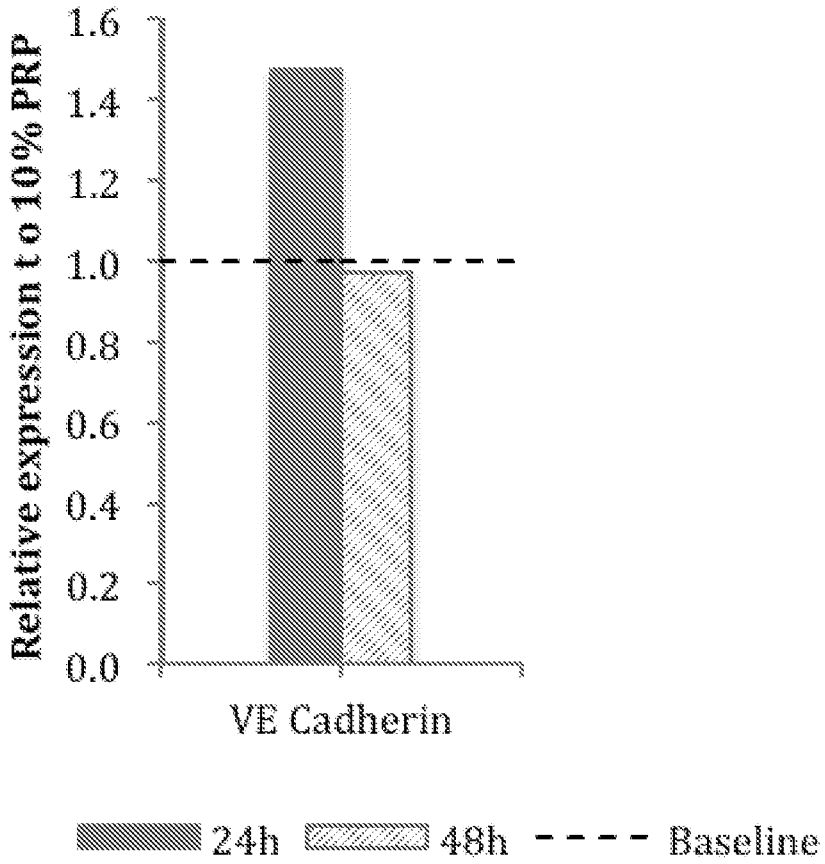
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 16



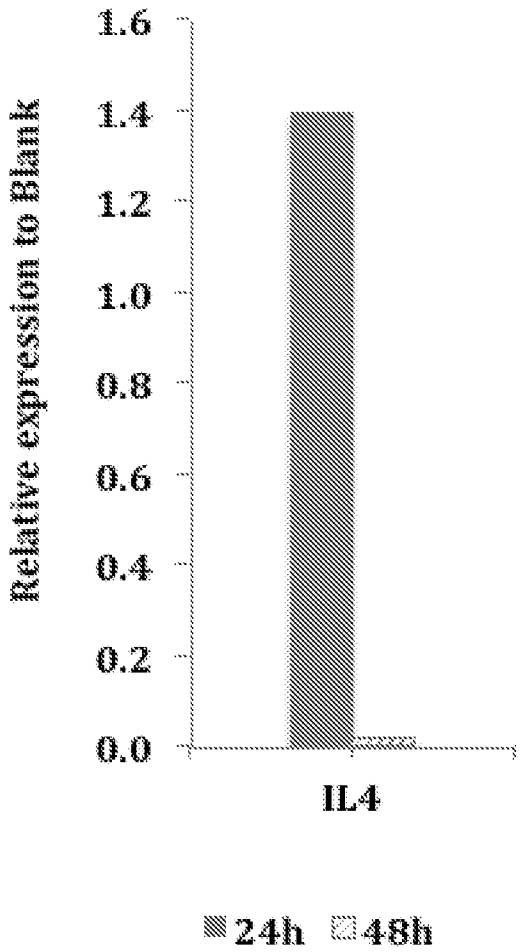
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 17



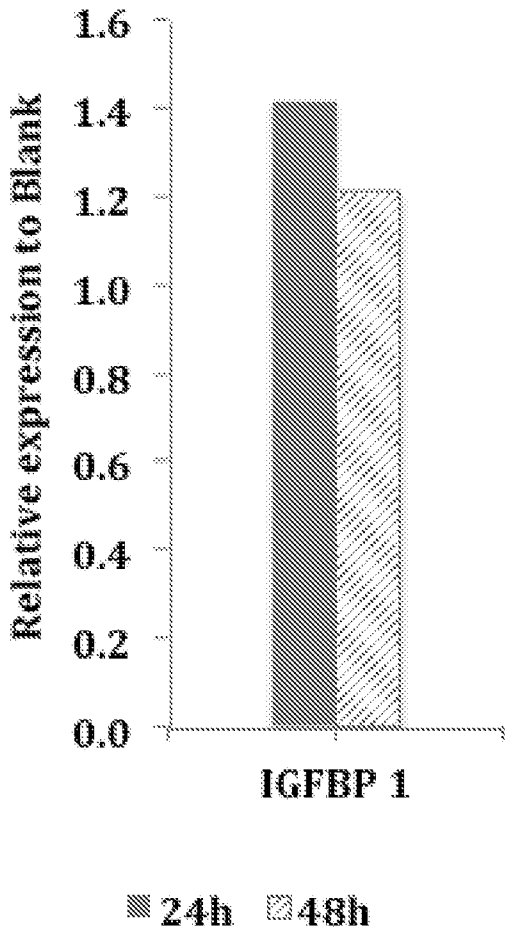
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 18



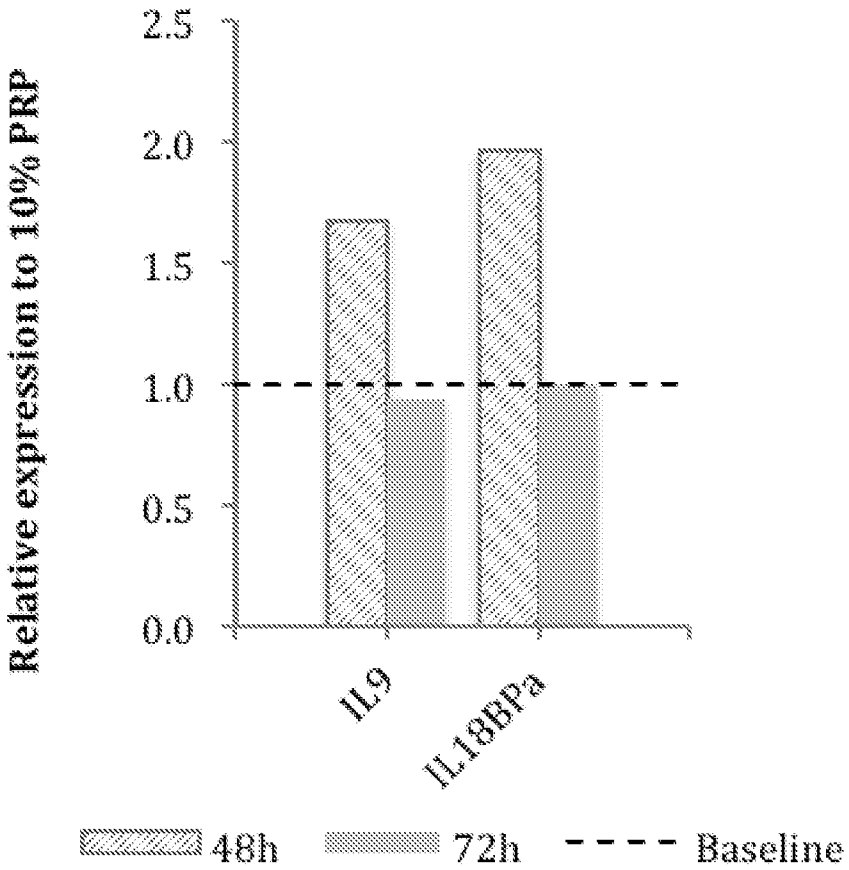
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 19



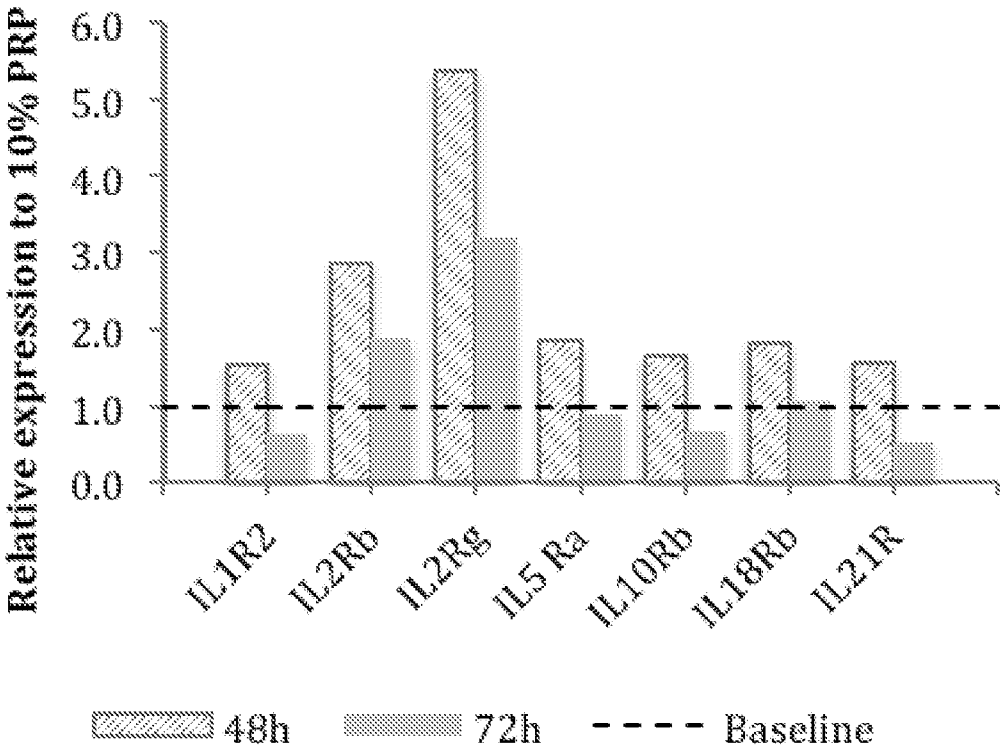
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 20



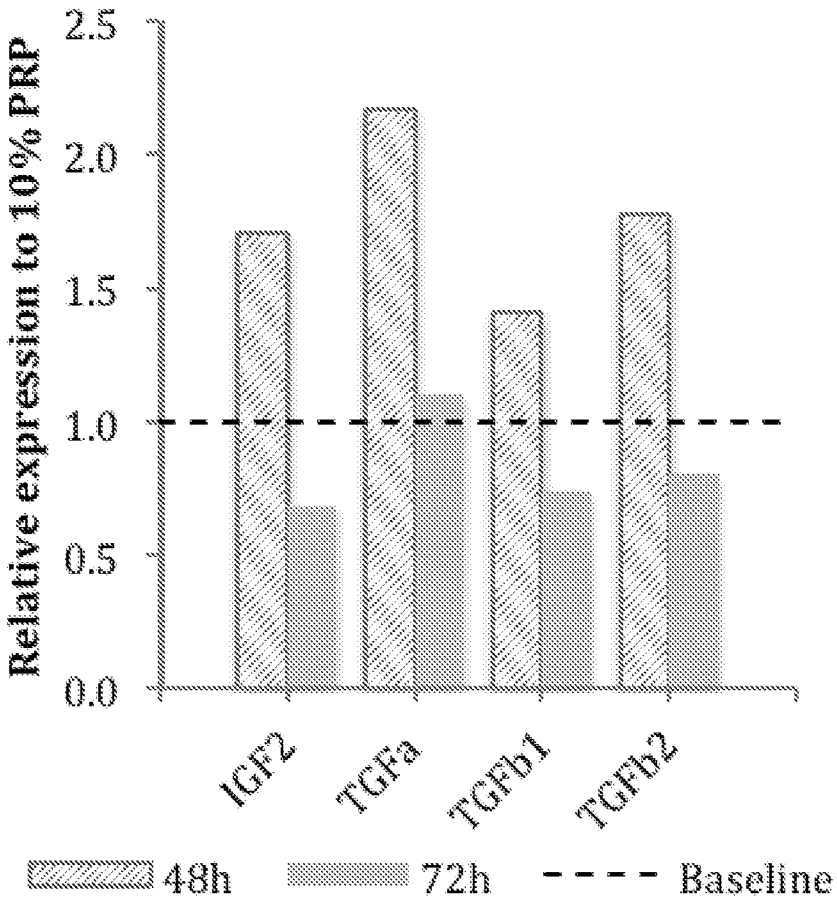
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 21



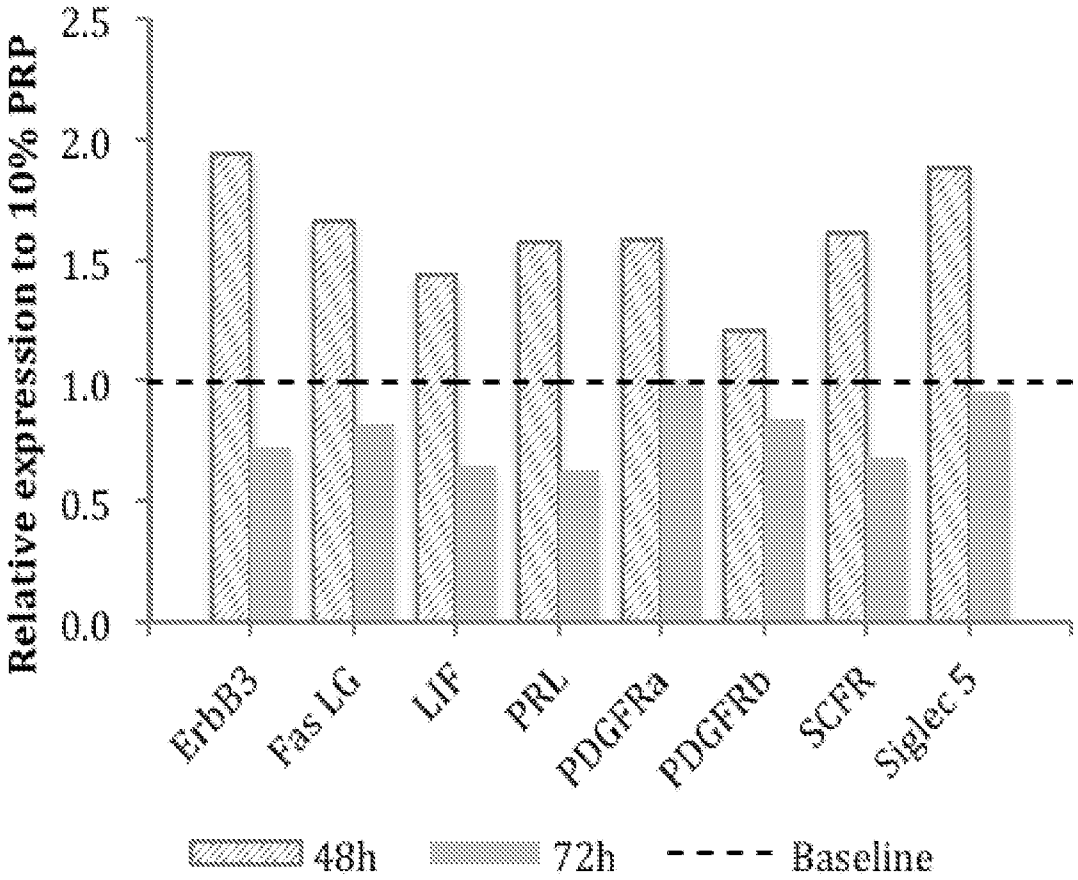
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 22



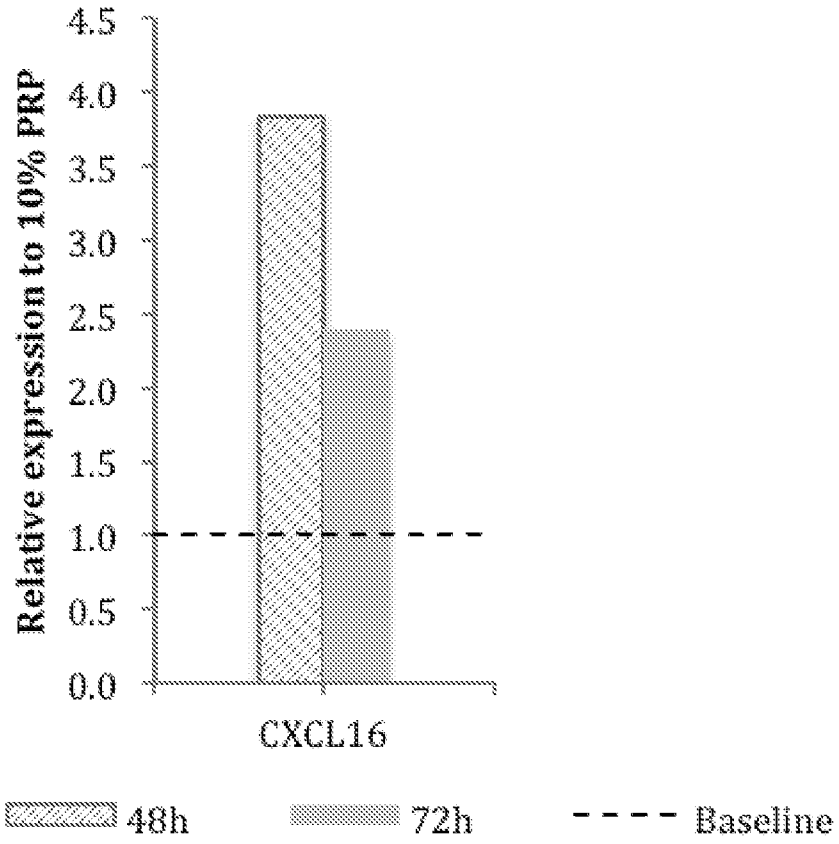
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 23



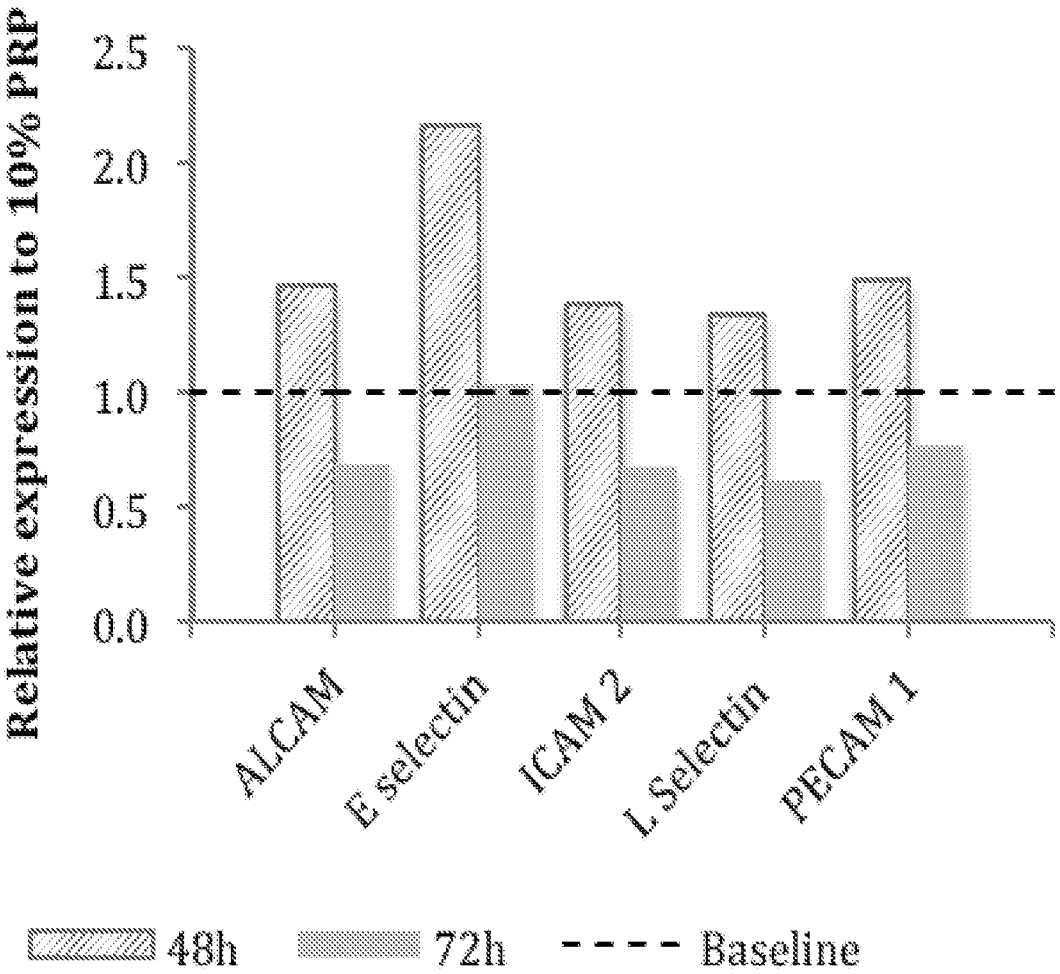
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 24



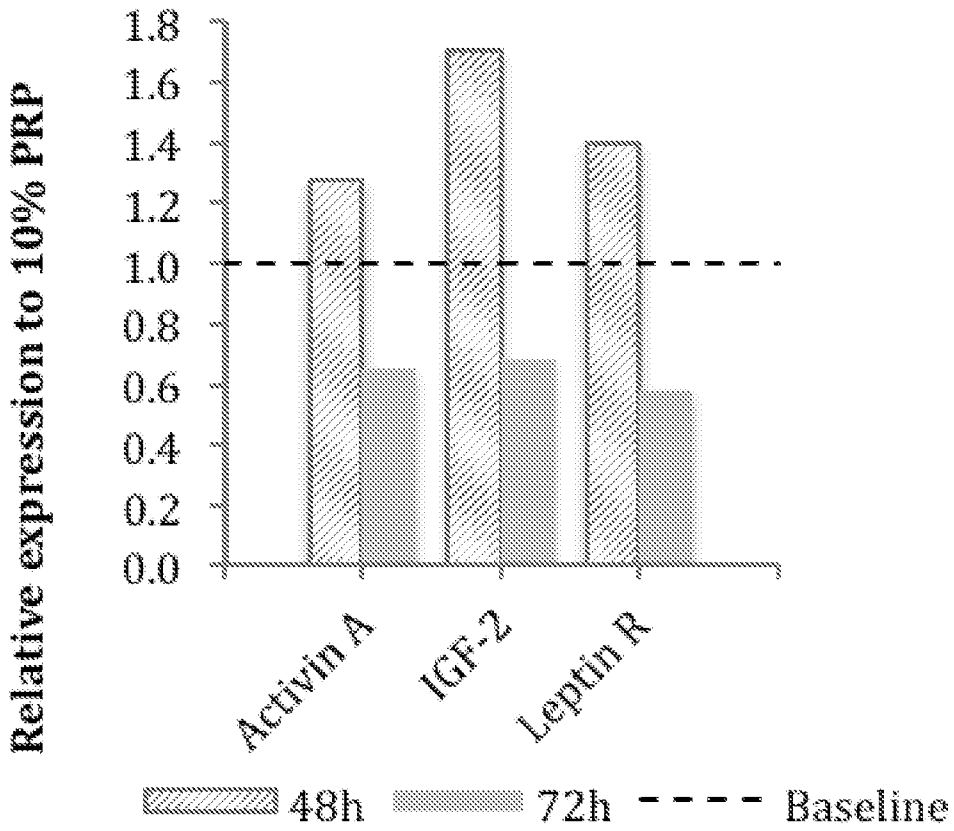
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 25



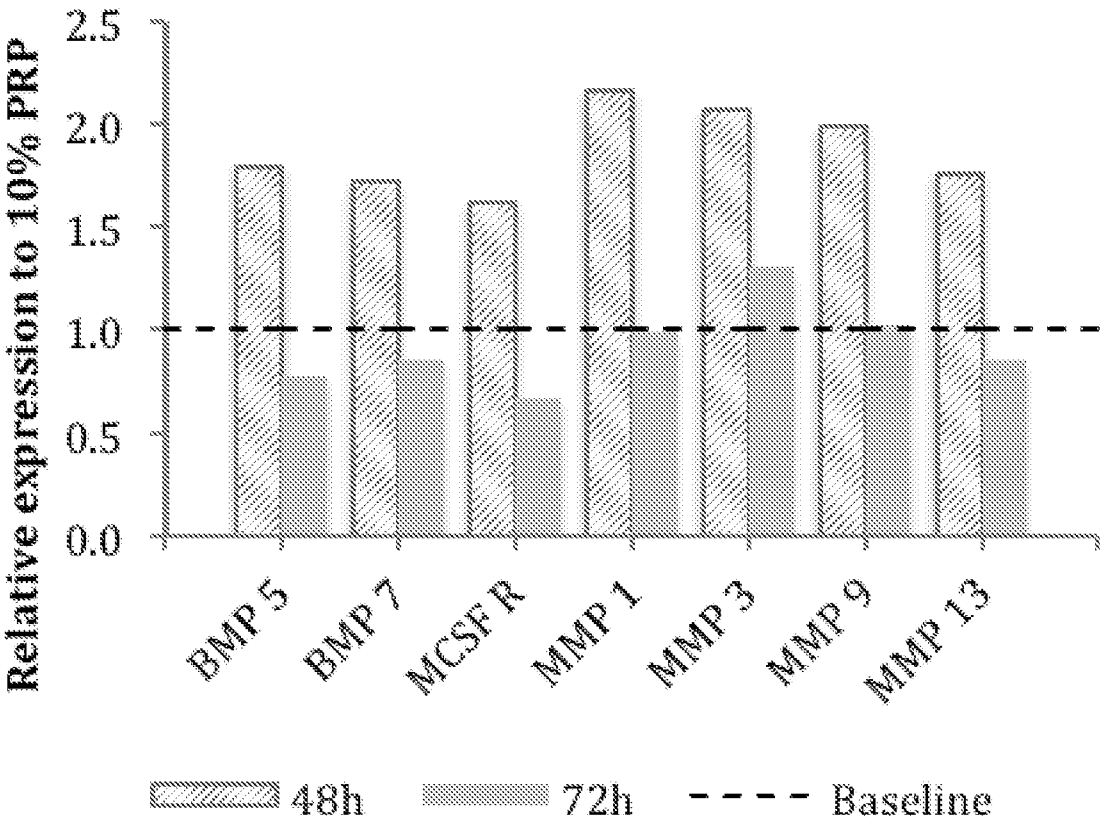
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 26



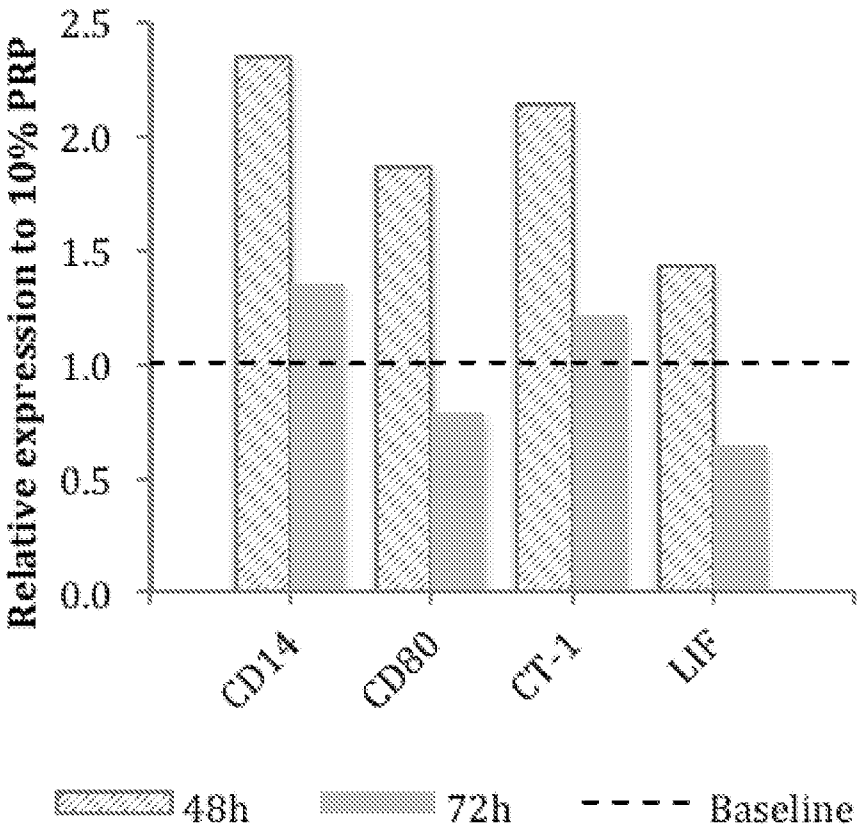
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 27



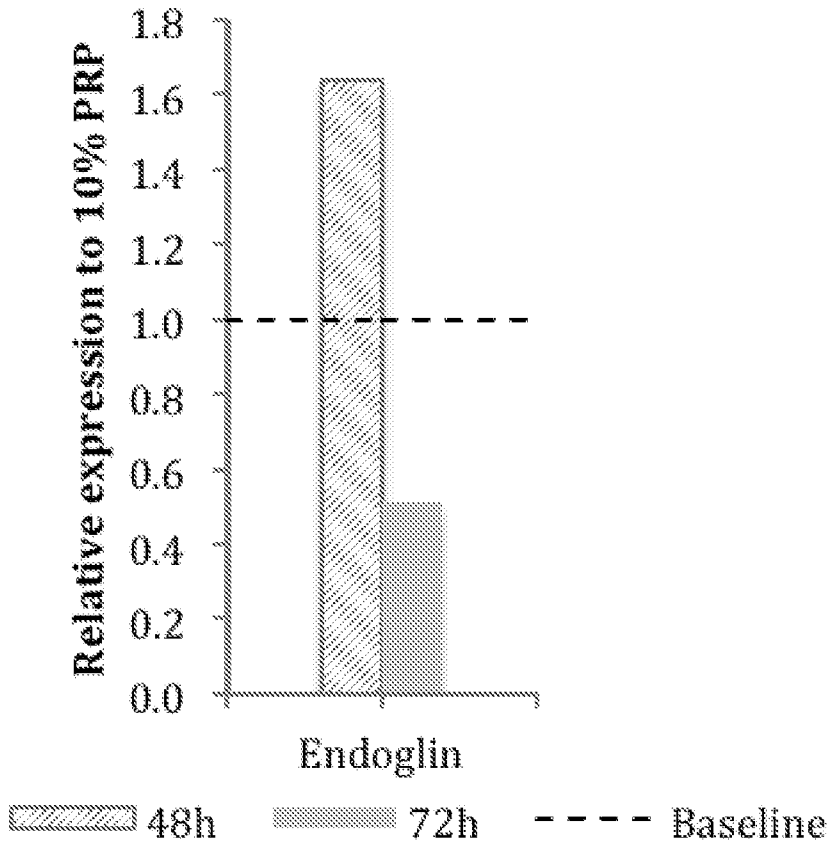
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 28



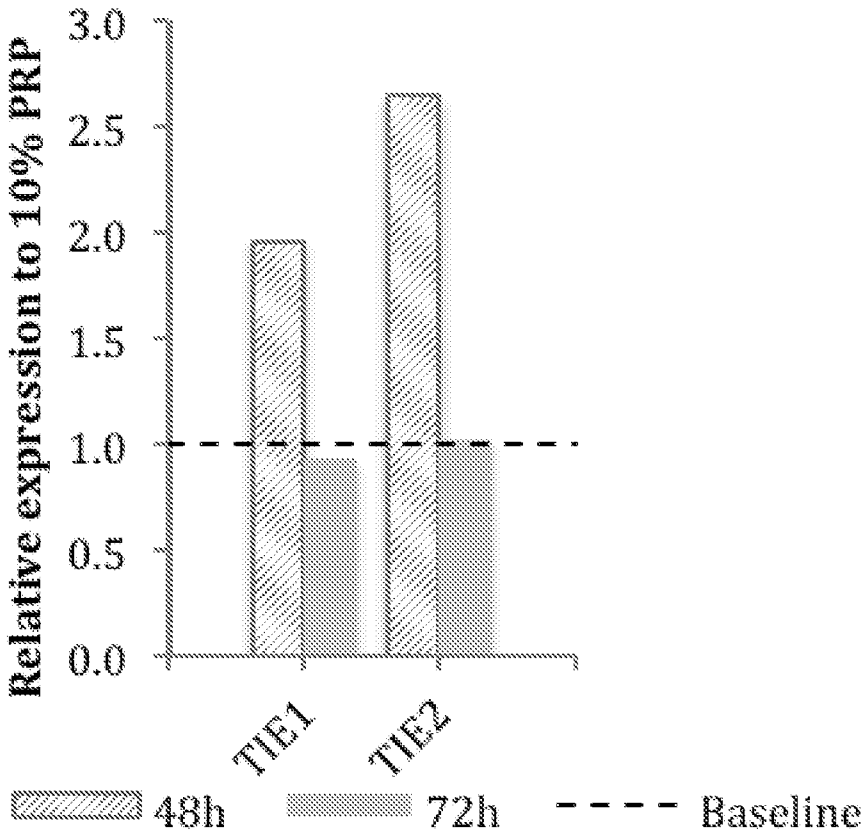
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 29



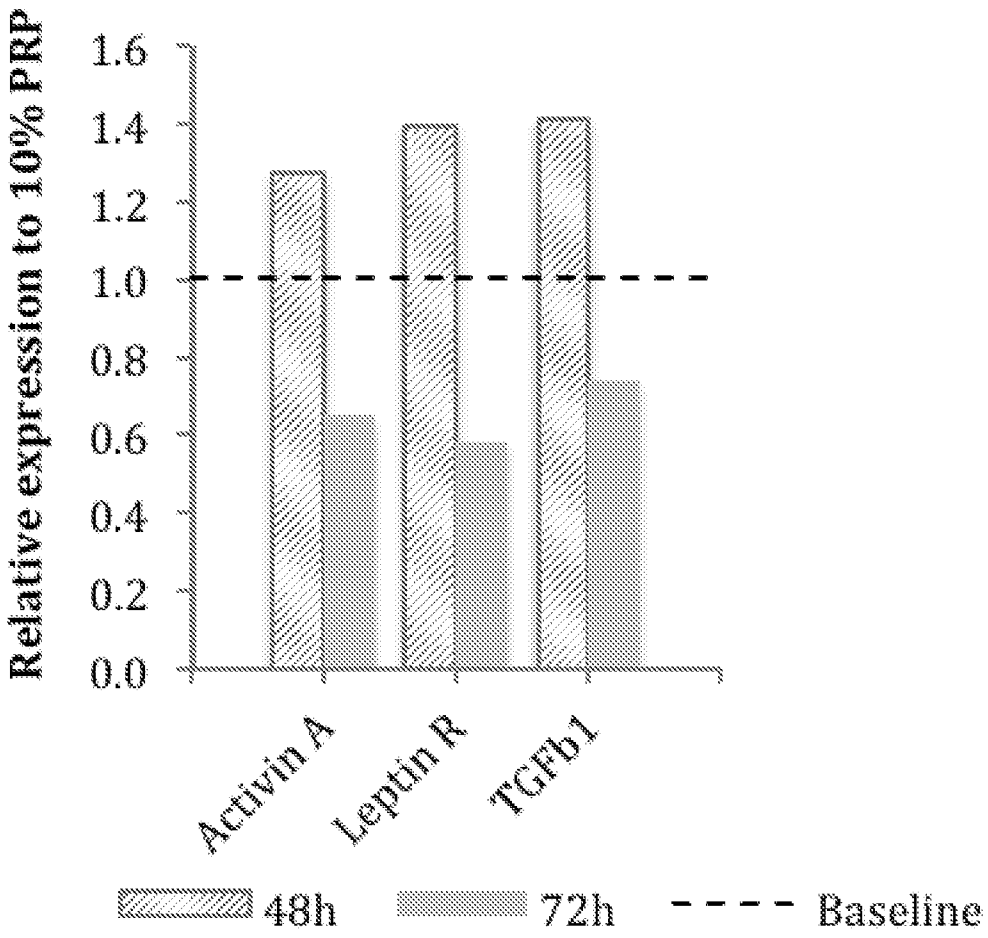
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 30



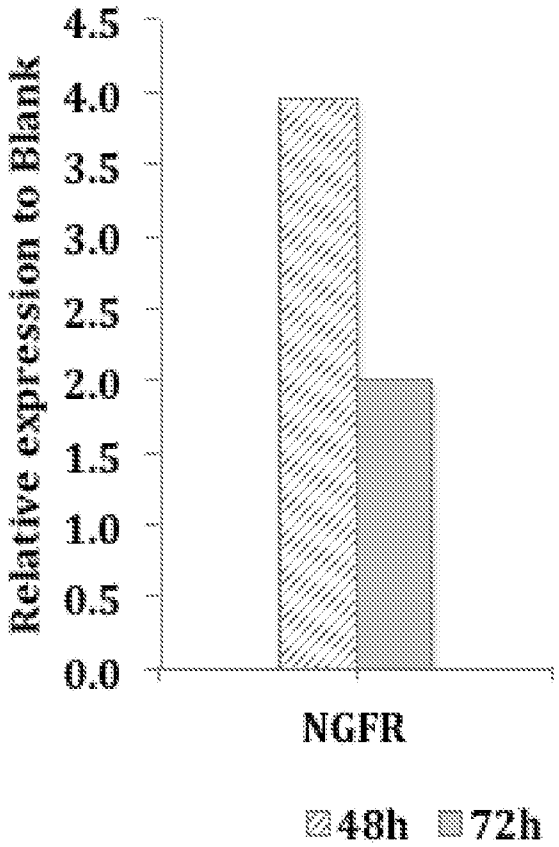
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 31



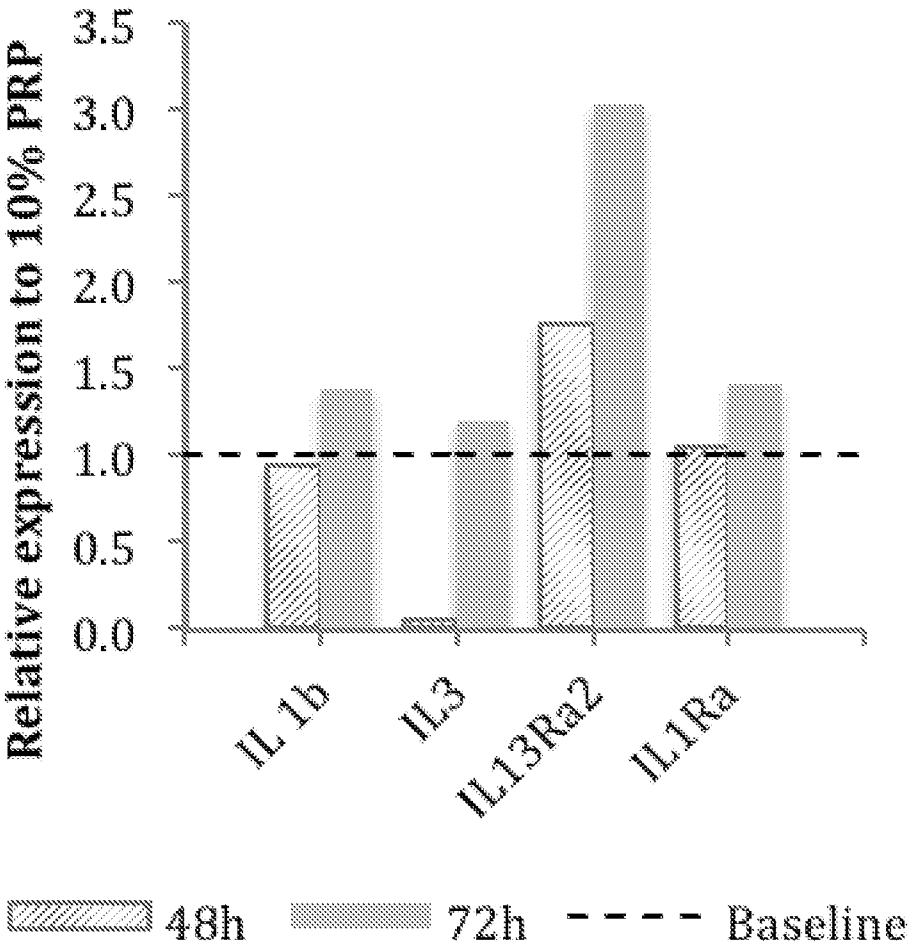
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 32



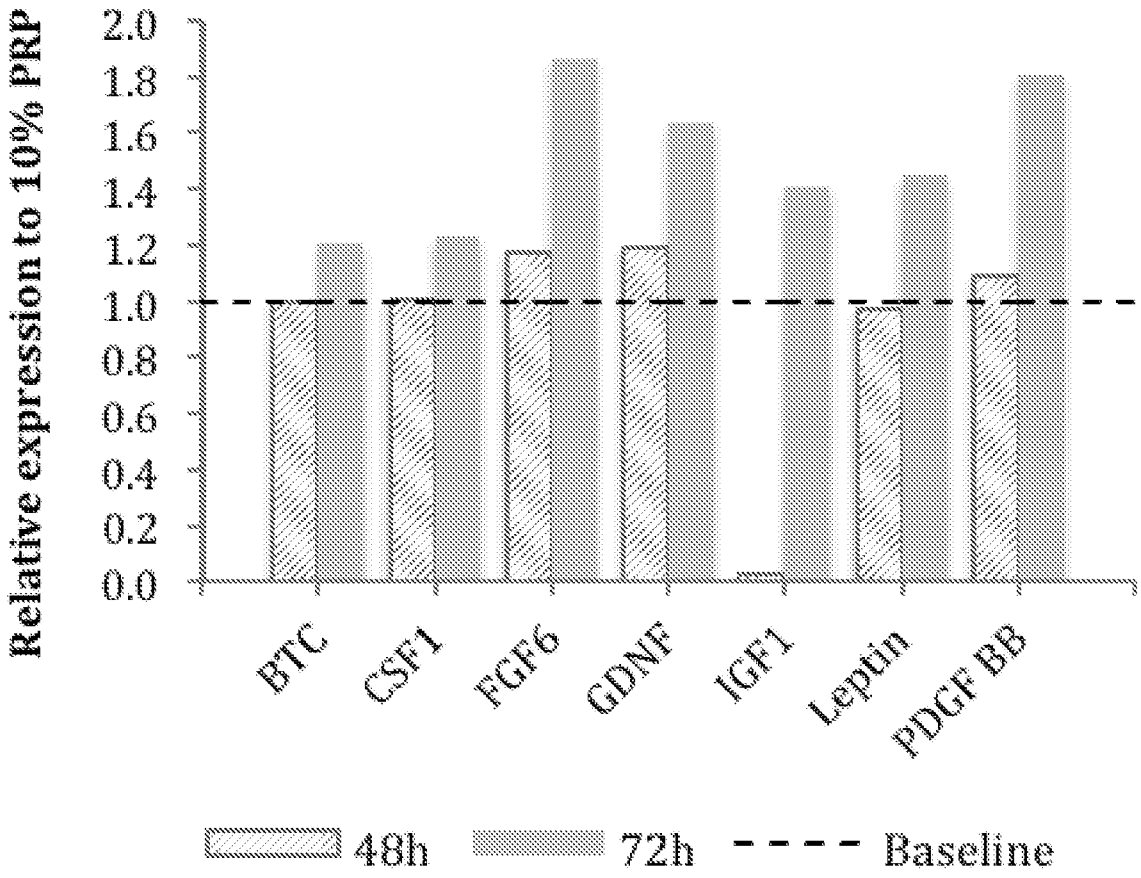
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 33



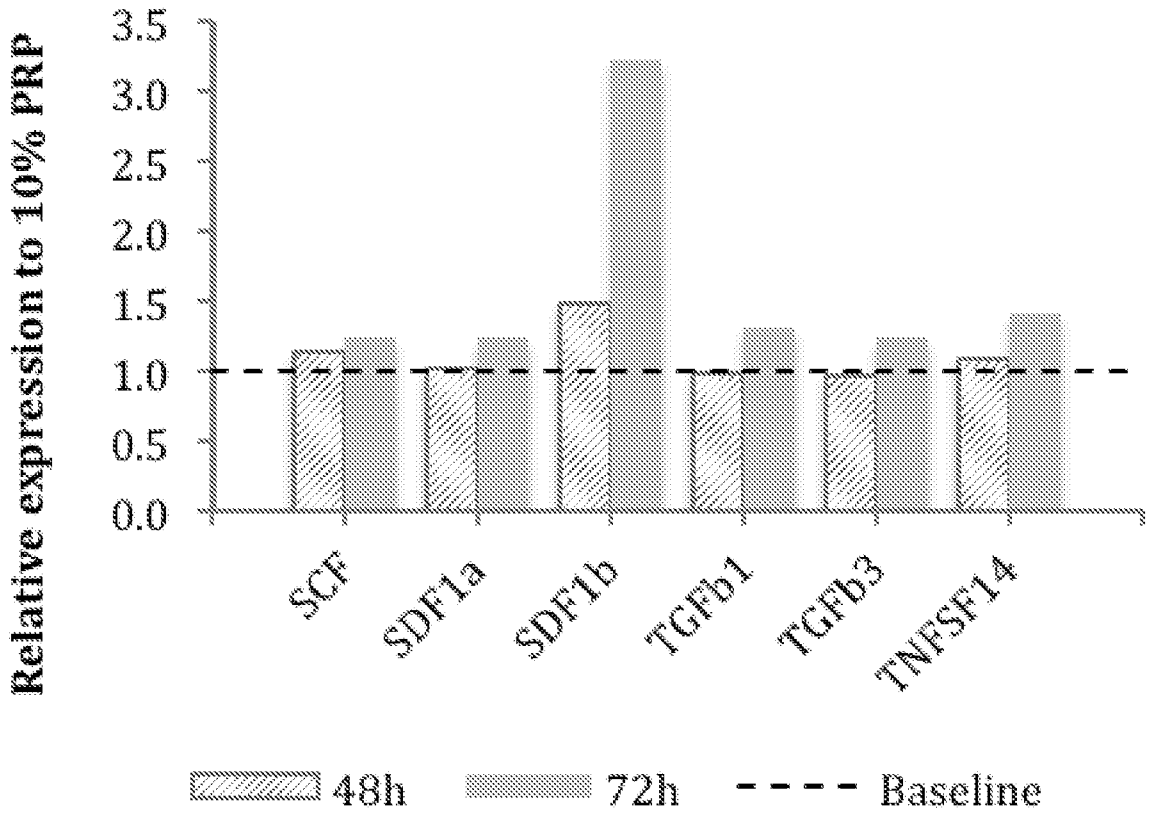
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 34



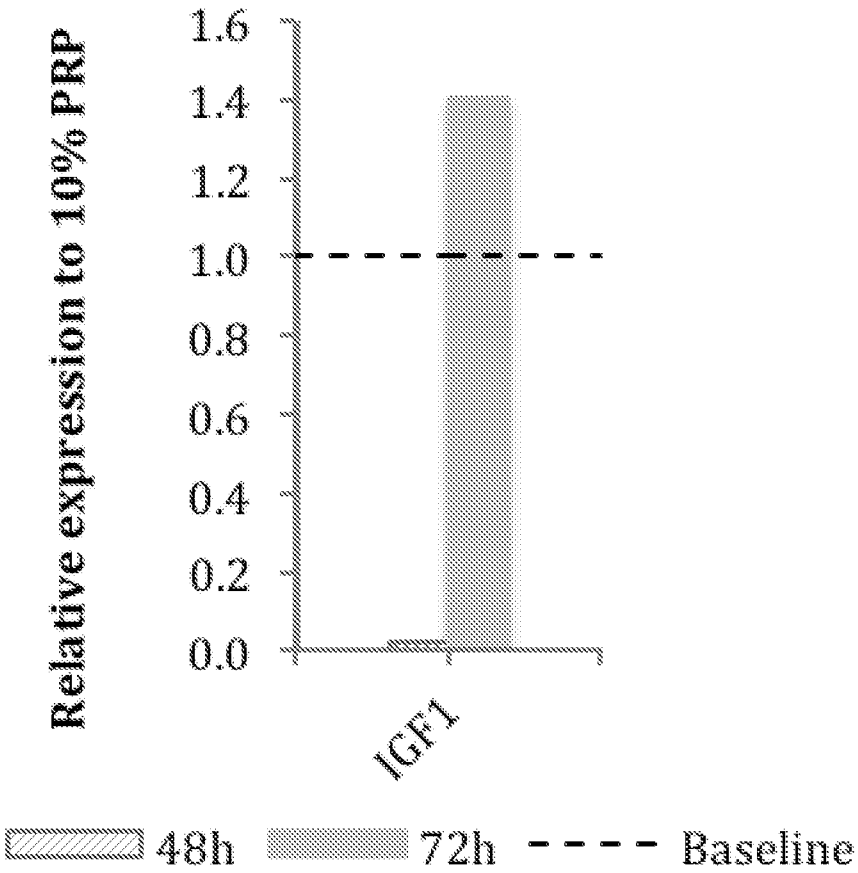
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 35



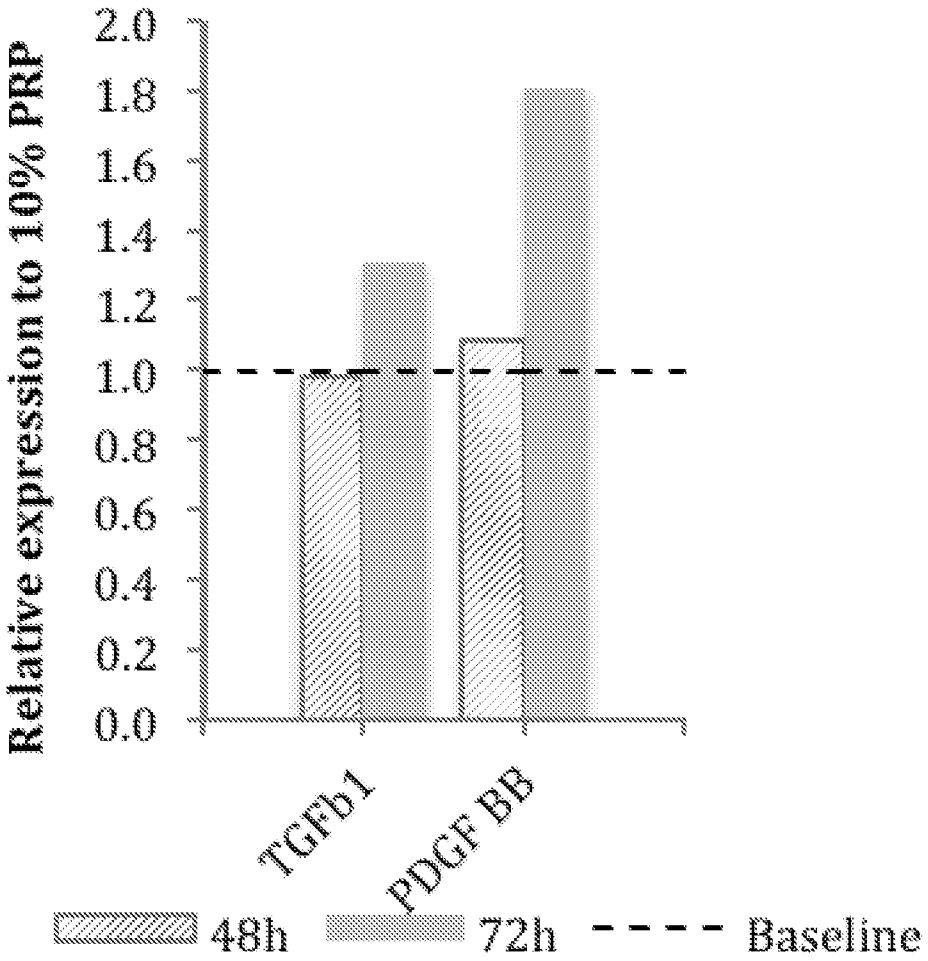
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 36



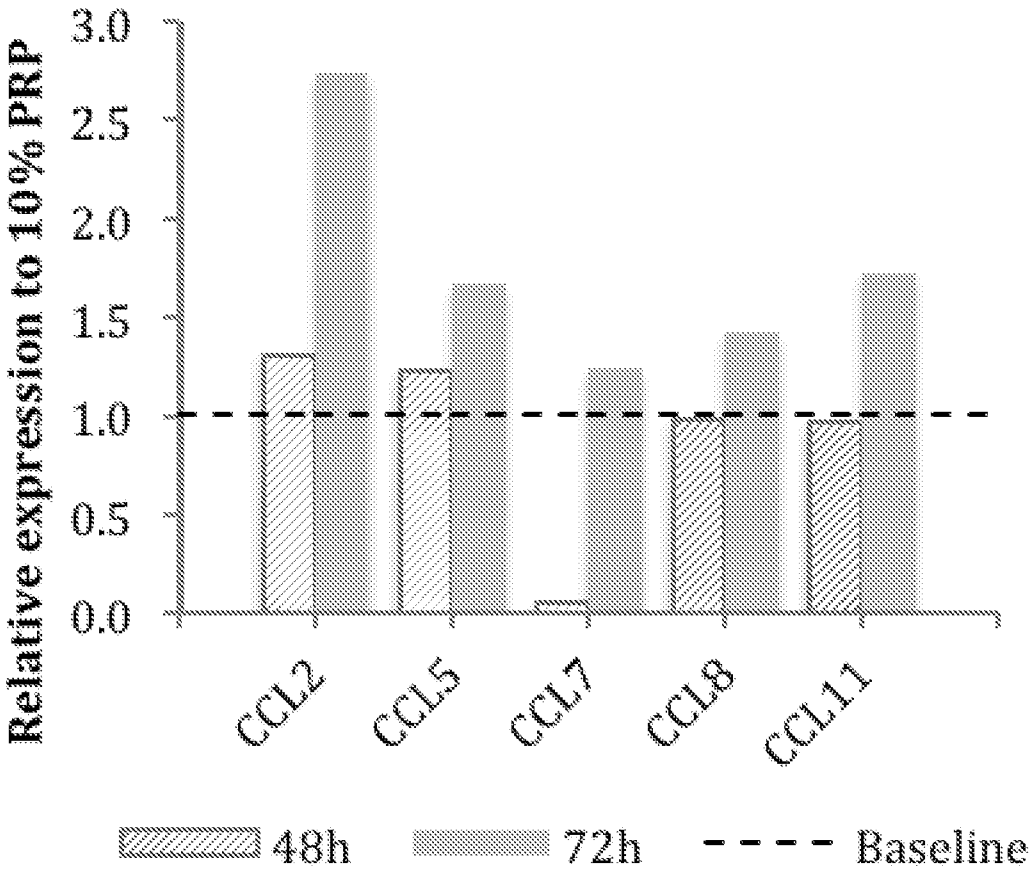
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 37



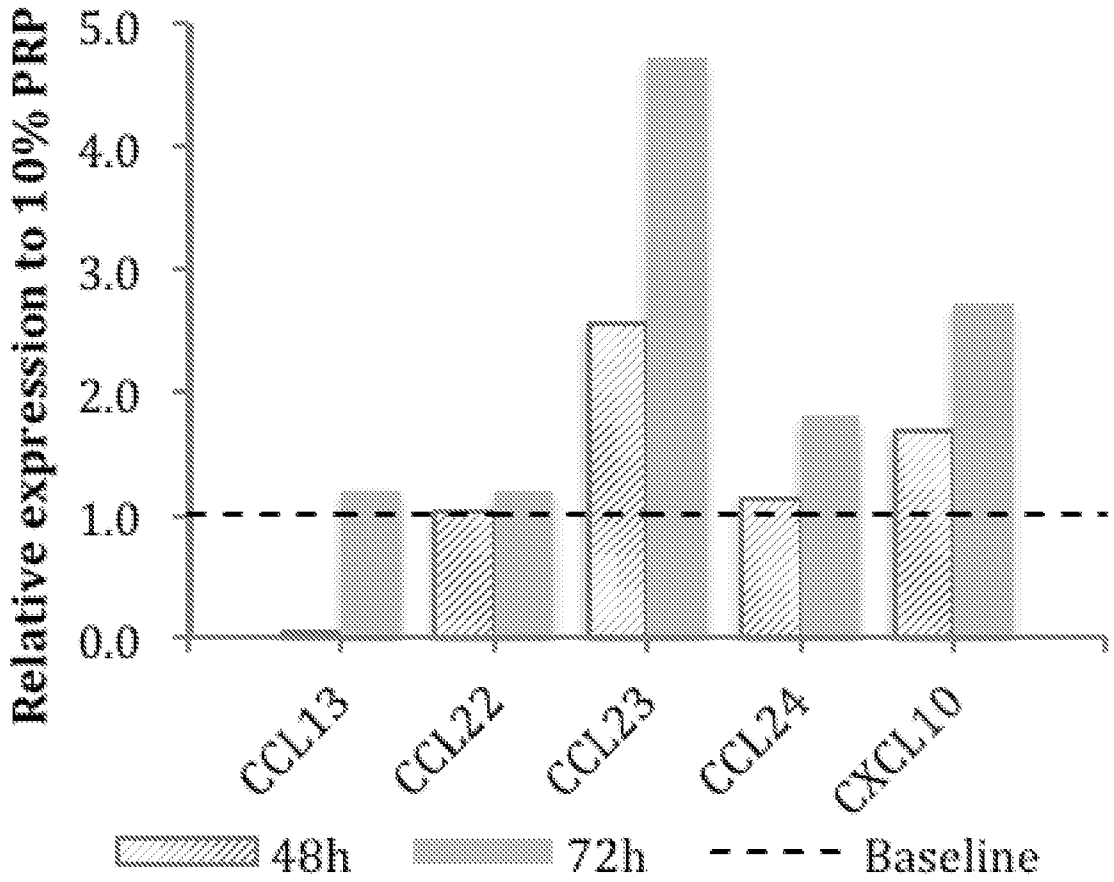
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 38



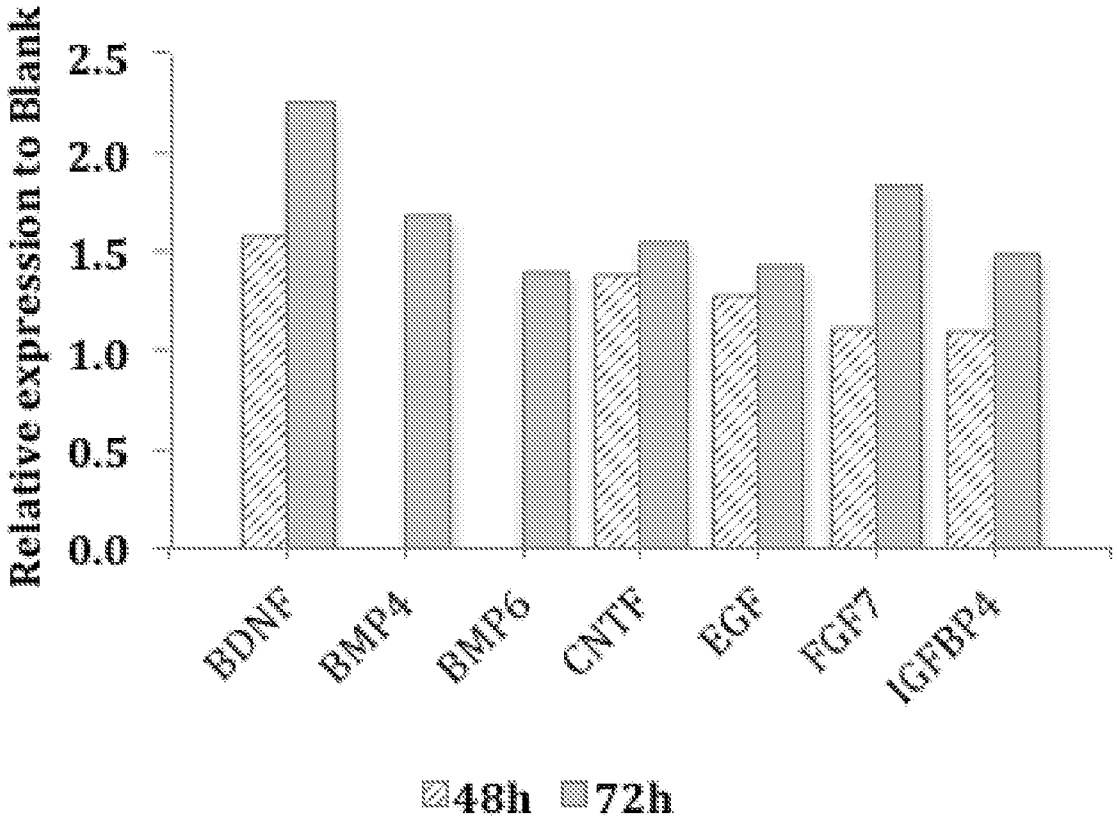
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 39



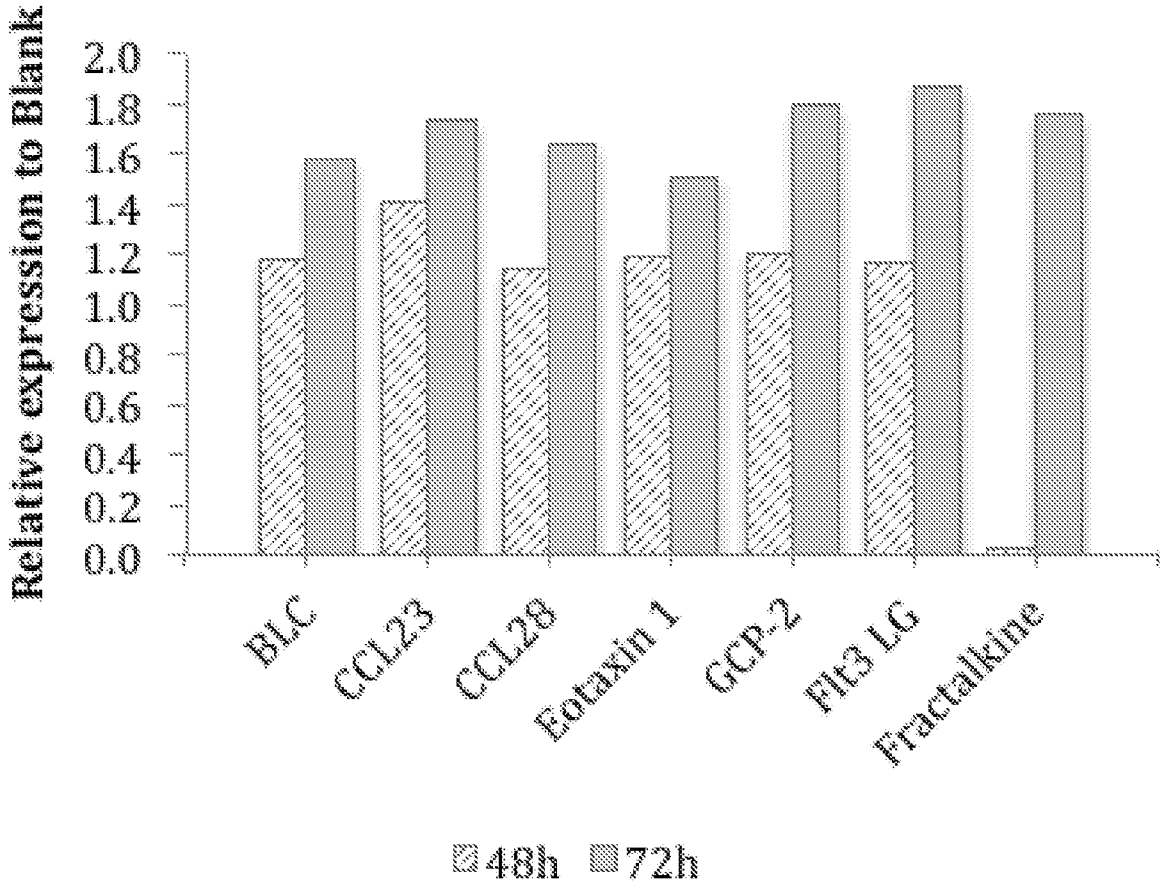
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 40



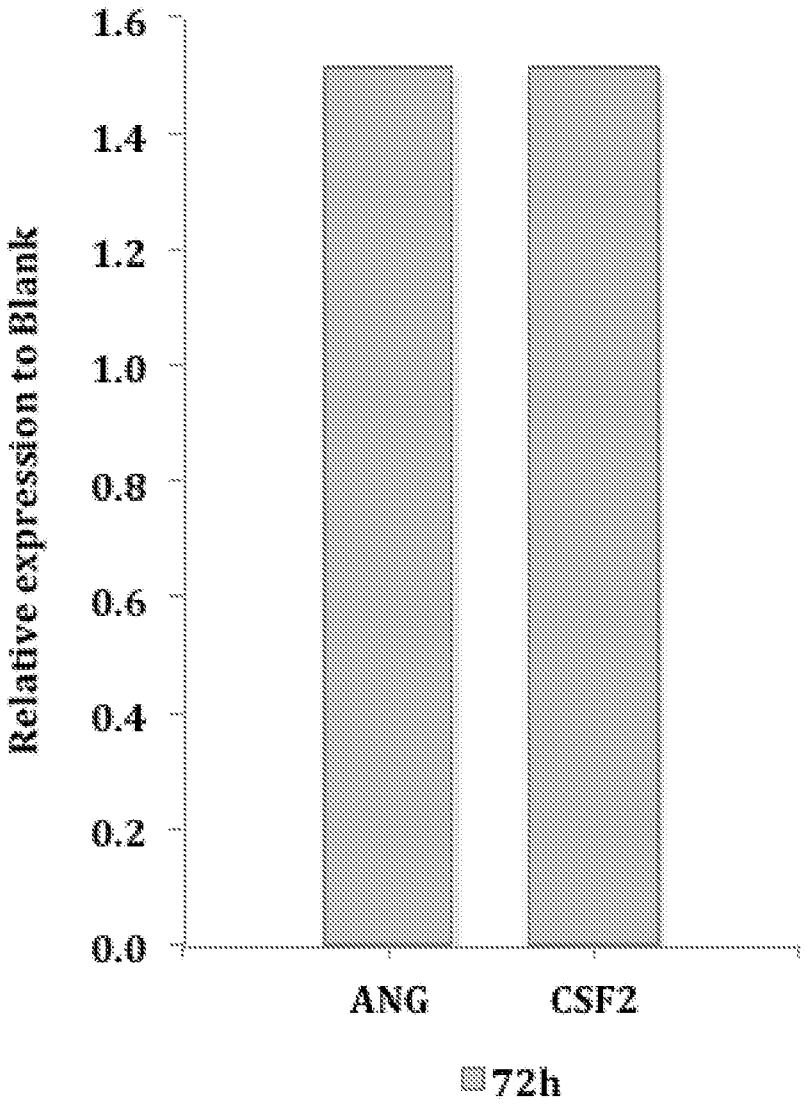
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 41



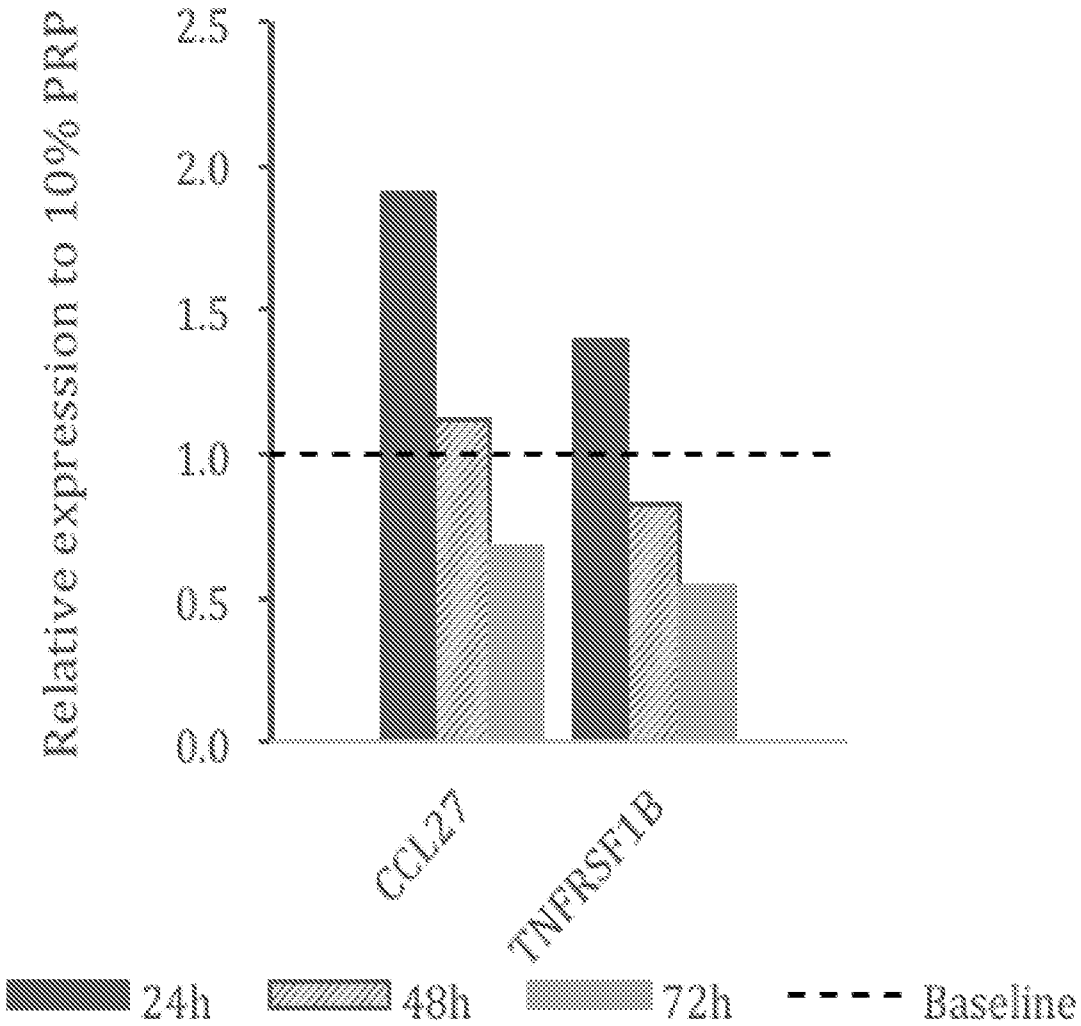
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 42



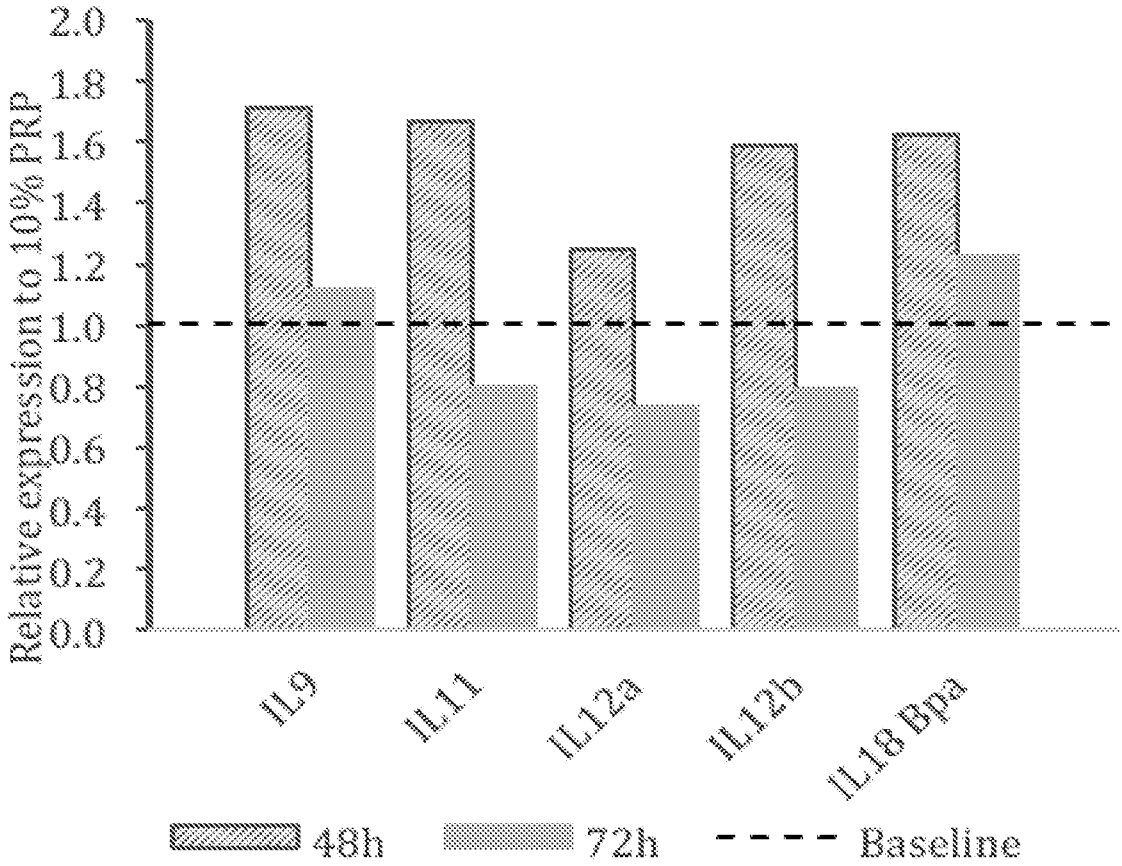
SR-MSCs in a FPU
No IL-2 Stimulation

FIG. 43



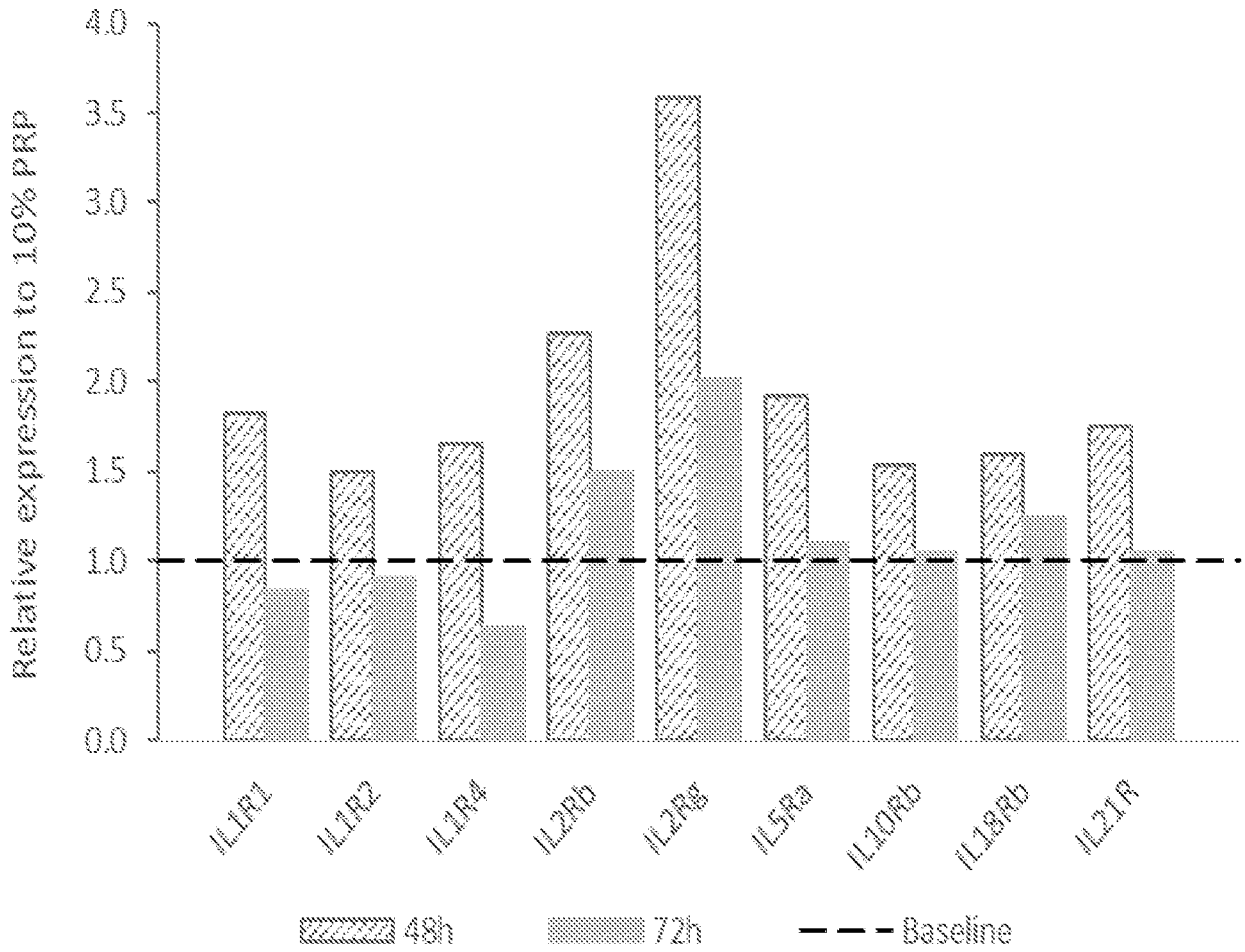
SR-MSCs in a FPU
+ IL-2 Stimulation

FIG. 44



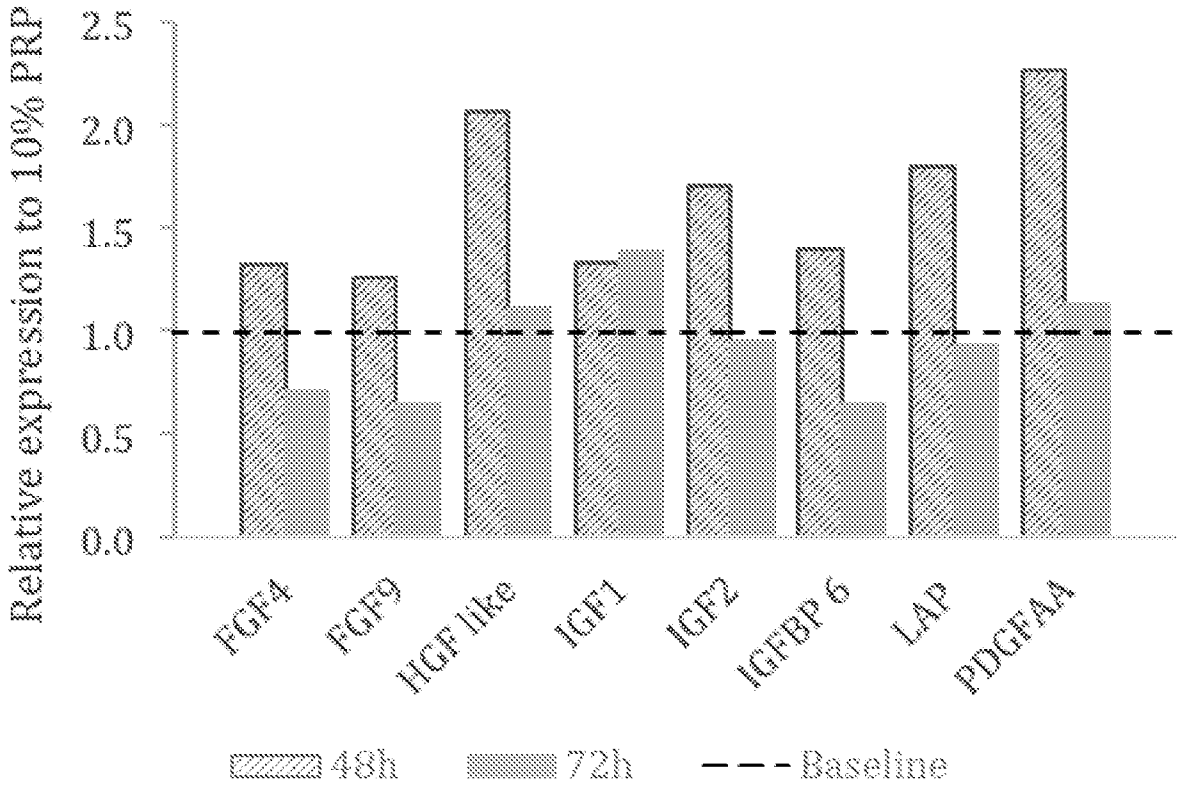
SR-MSCs in a FPU
+ IL-2 Stimulation

FIG. 45



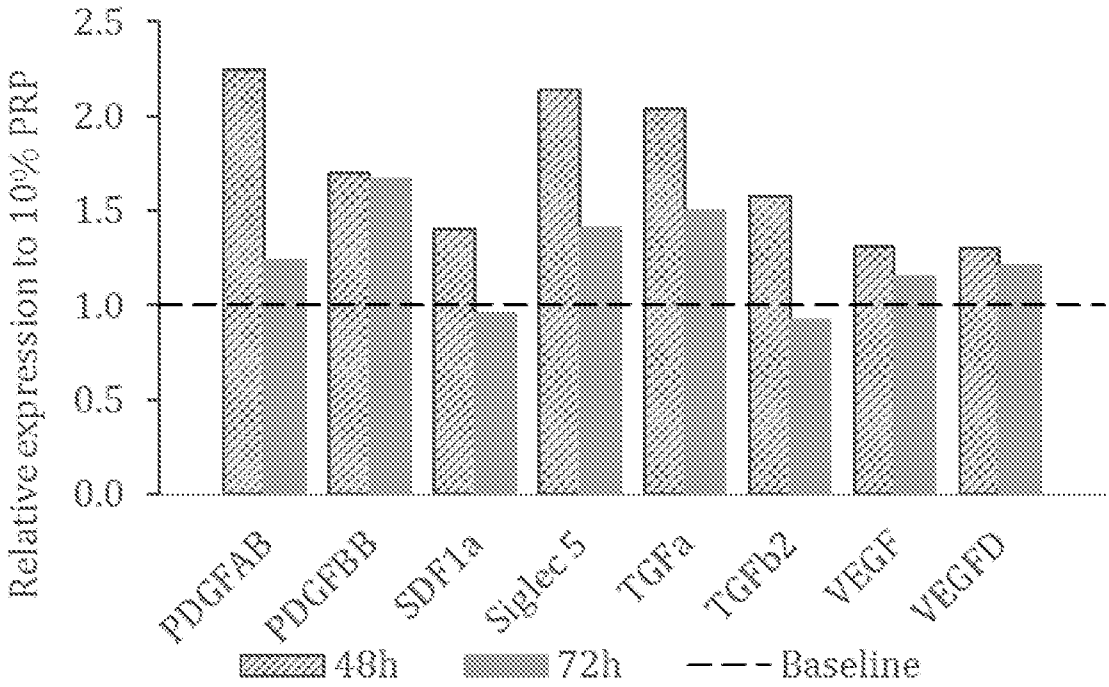
SR-MSCs in a FPU
+ IL-2 Stimulation

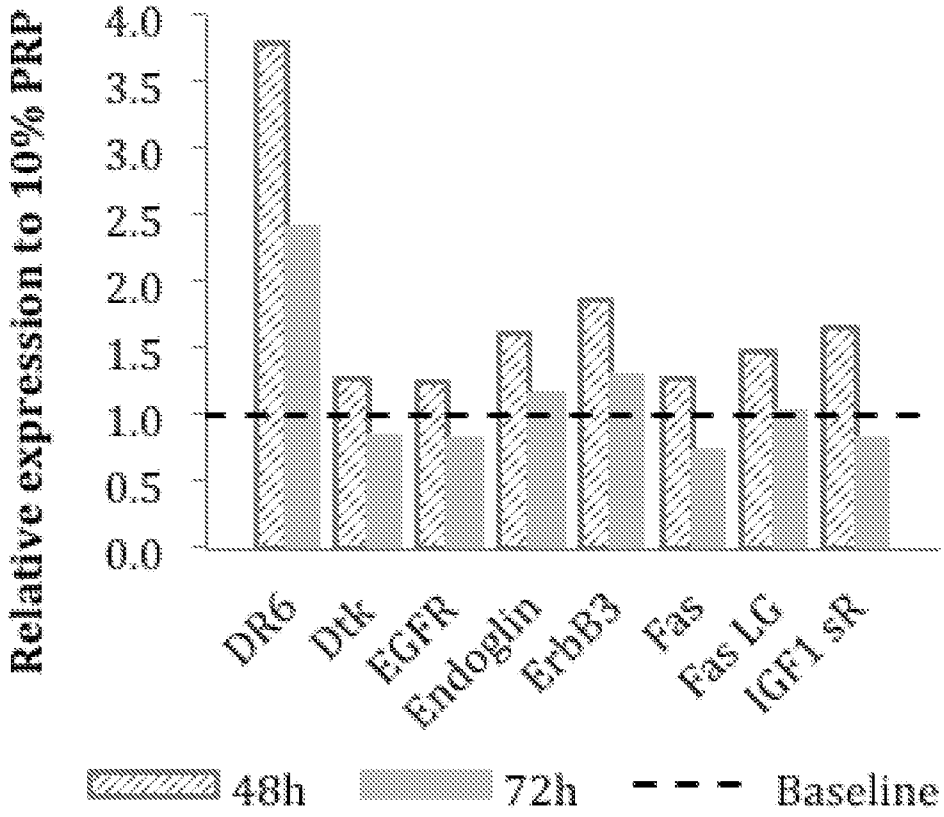
FIG. 46



SR-MSCs in a FPU
+ IL-2 Stimulation

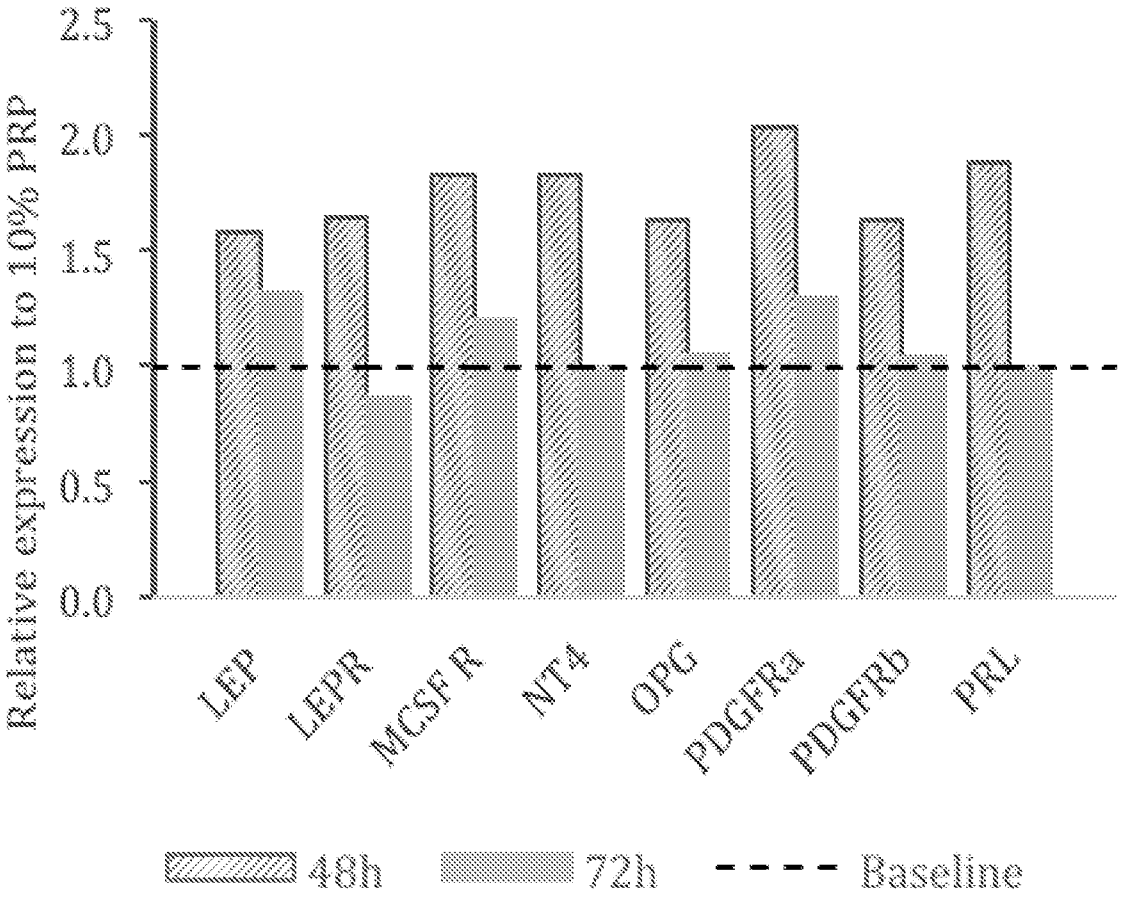
FIG. 47





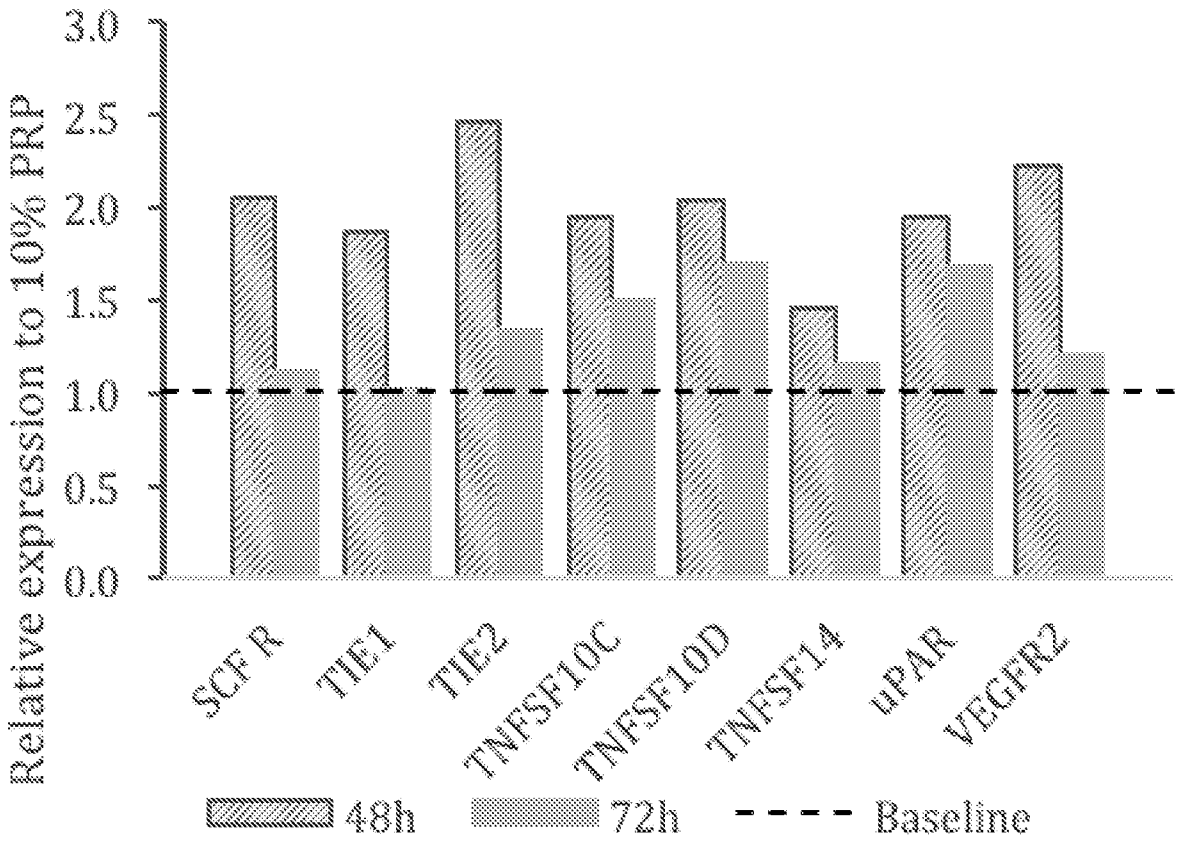
SR-MSCs in a FPU
+ IL-2 Stimulation

FIG. 48



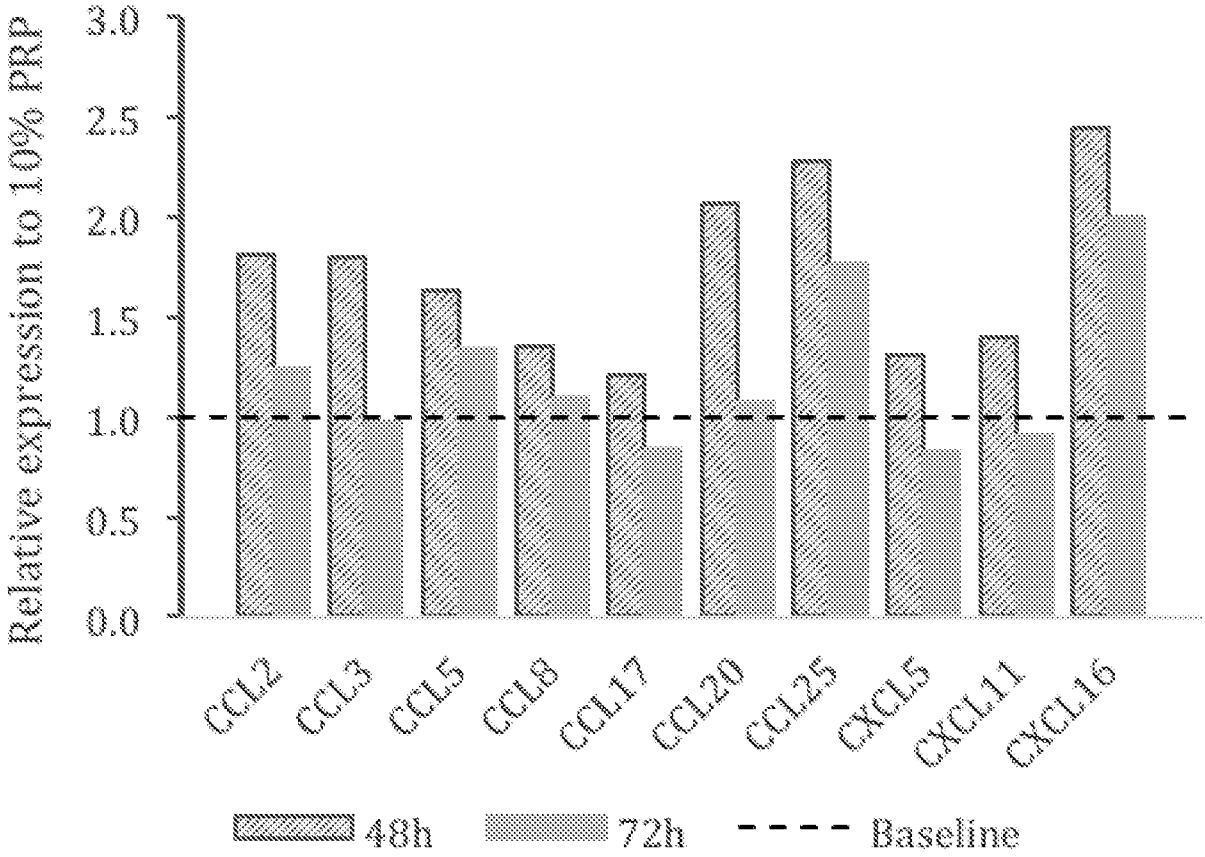
SR-MSCs in a FPU
+ IL-2 Stimulation

FIG. 49



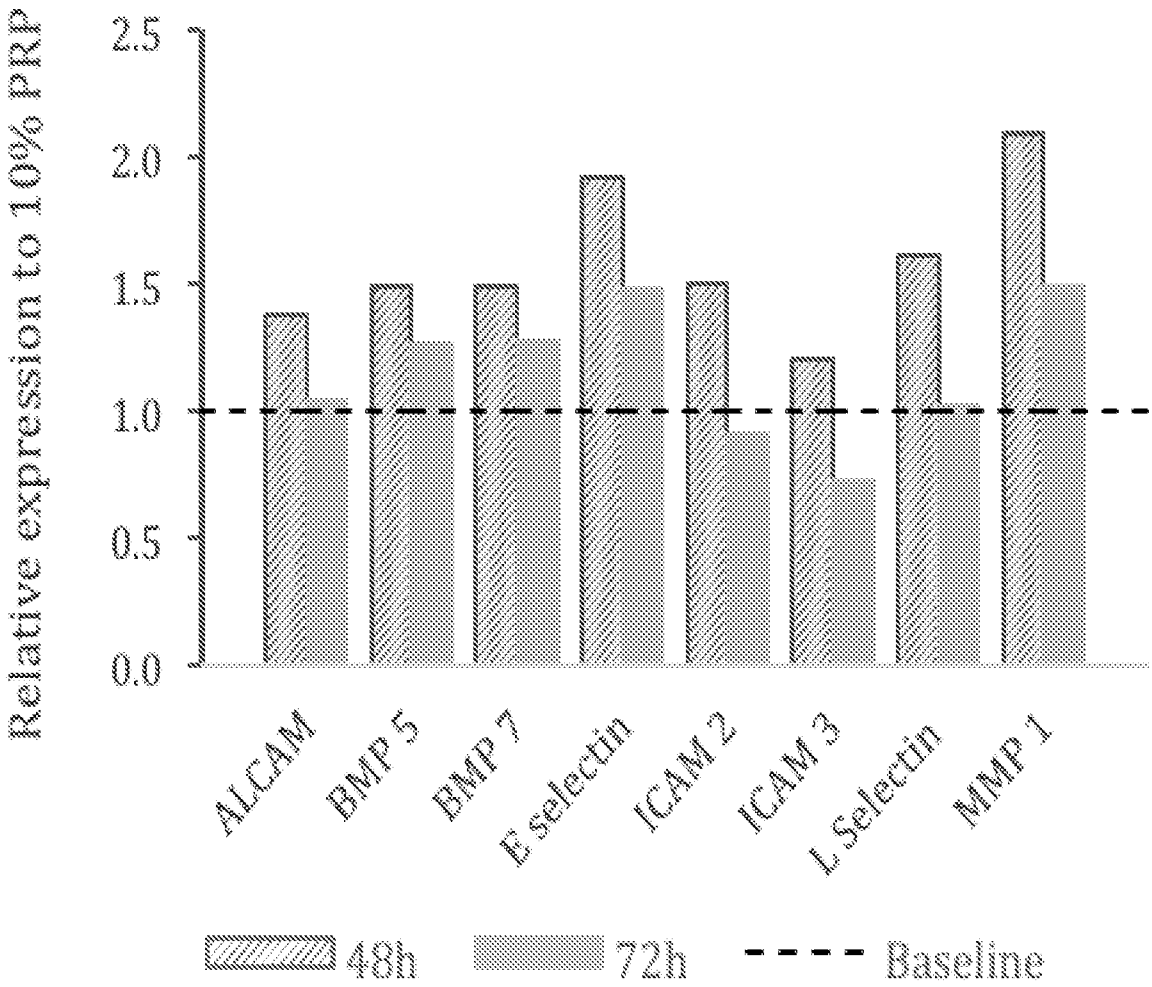
SR-MSCs in a FPU
+ IL-2 Stimulation

FIG. 50



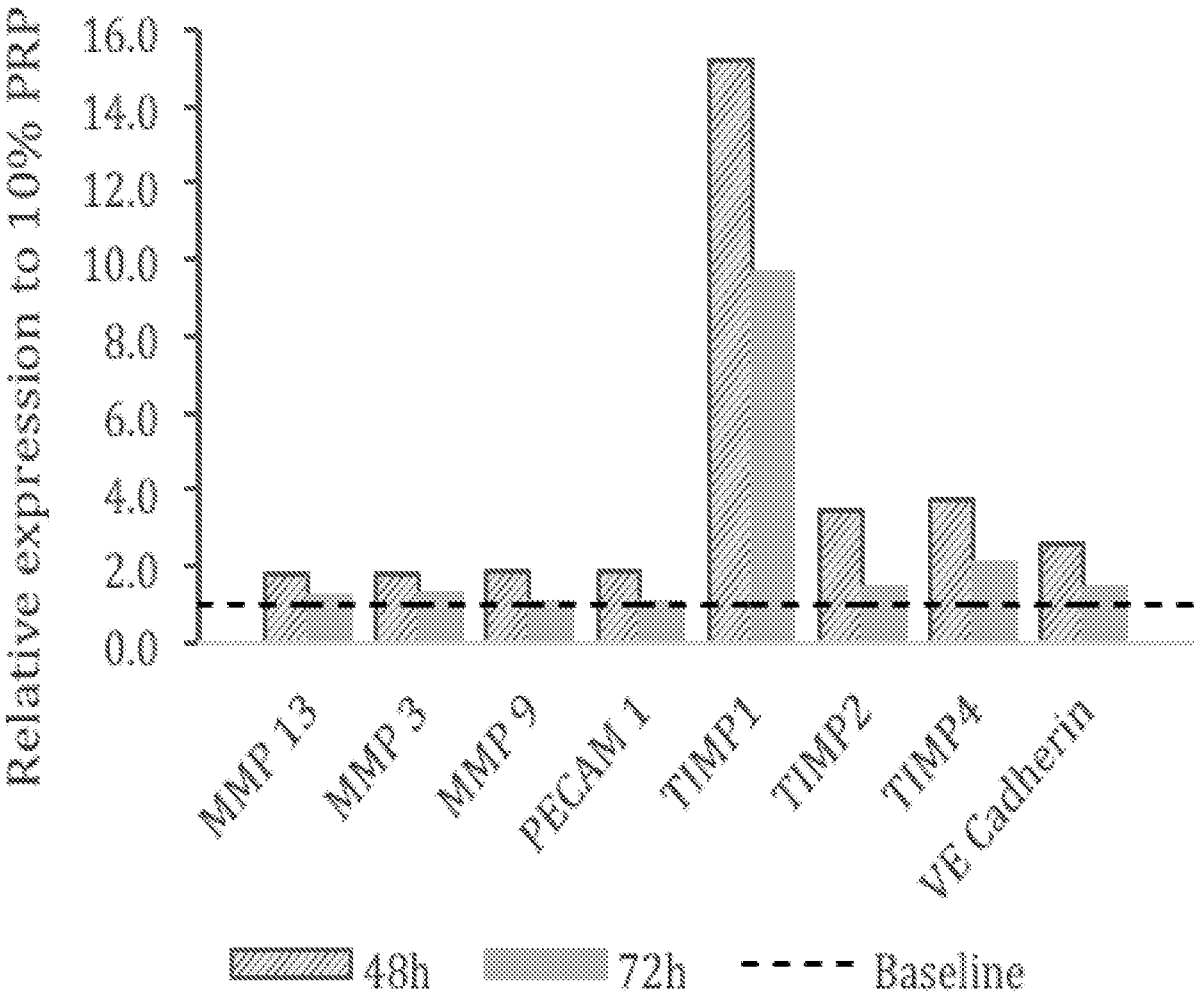
SR-MSCs in a FPU
+ IL-2 Stimulation

FIG. 51



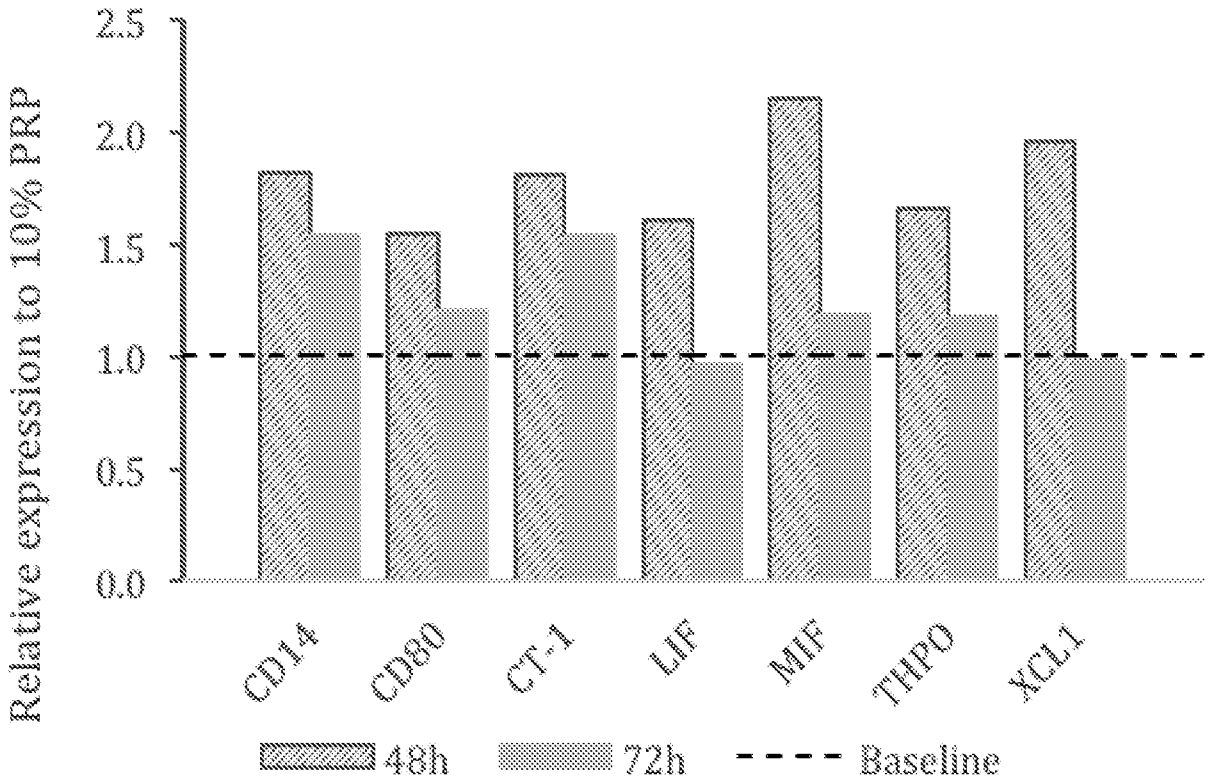
SR-MSCs in a FPU
+ IL-2 Stimulation

FIG. 52



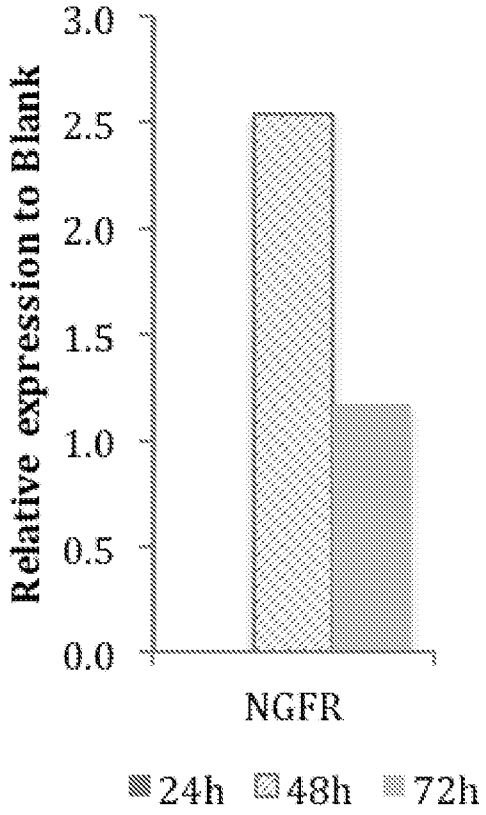
SR-MSCs in a FPU
+ IL-2 Stimulation

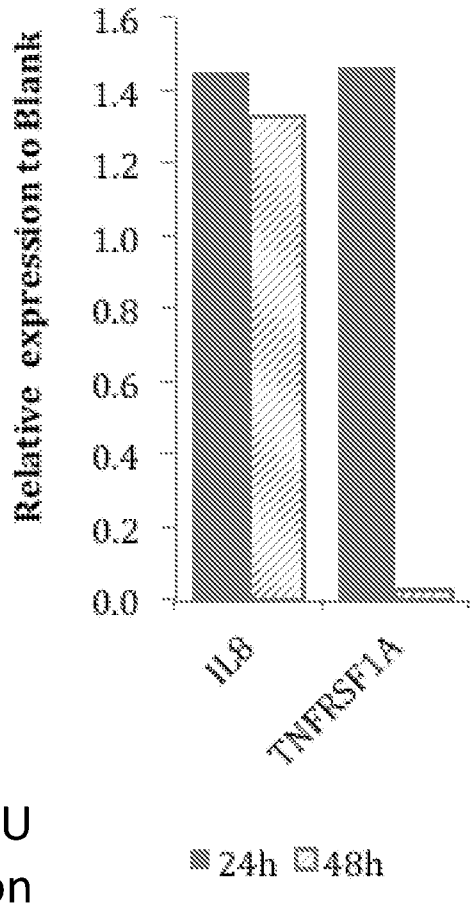
FIG. 53



SR-MSCs in a FPU
+ IL-2 Stimulation

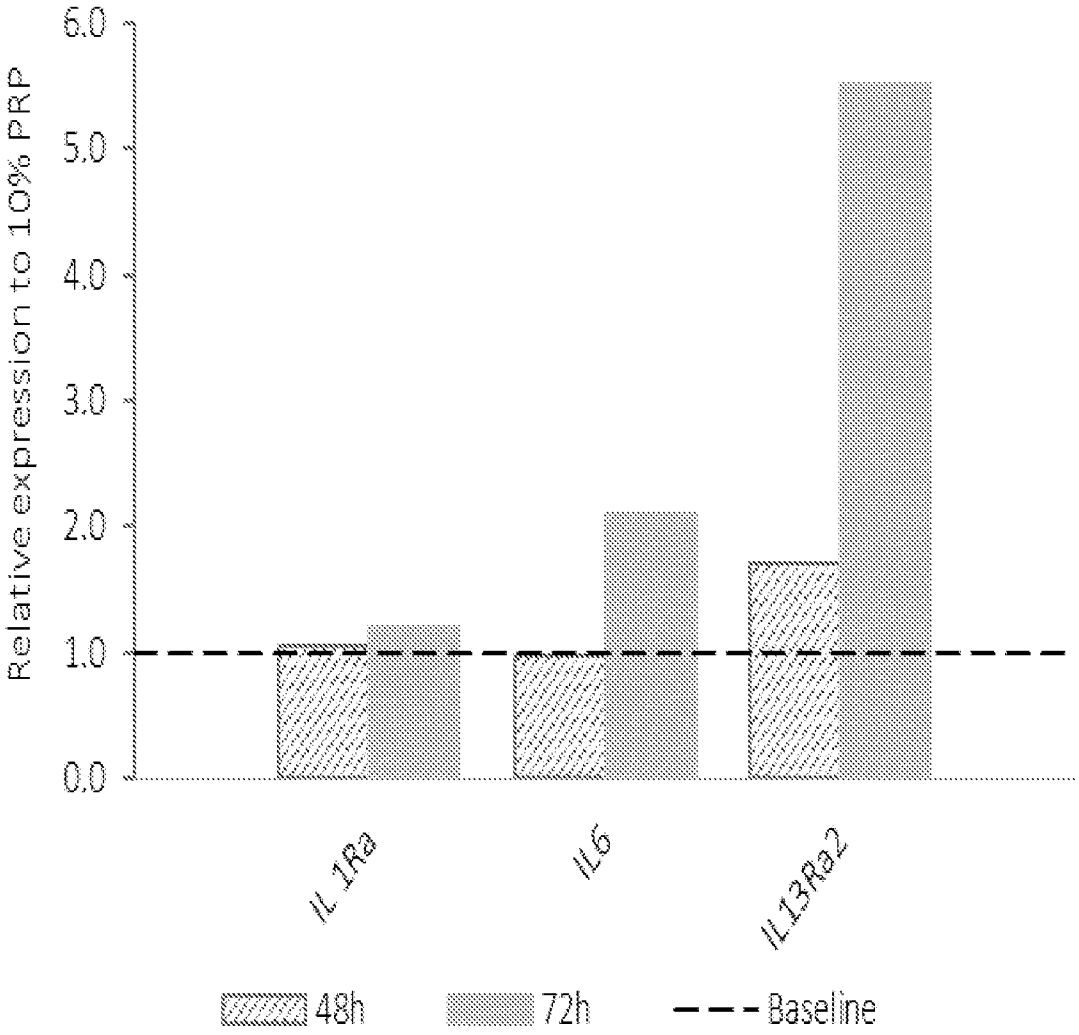
FIG. 54





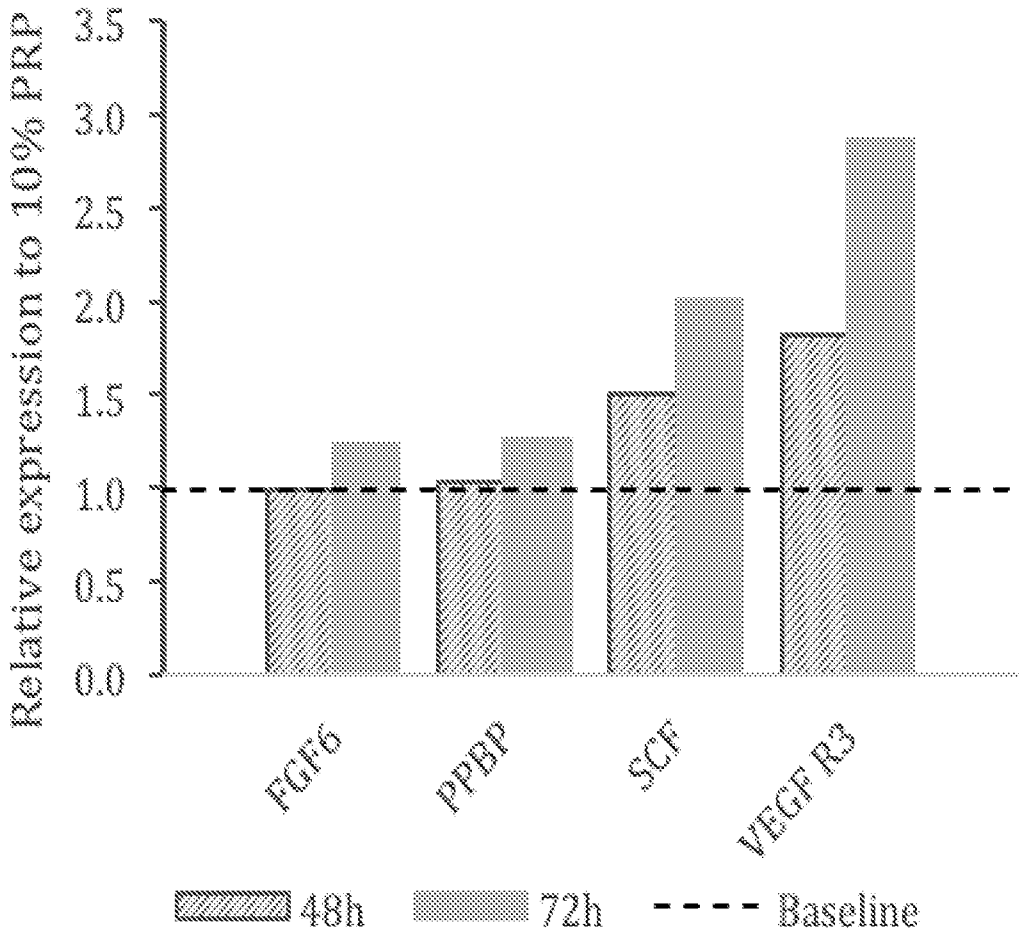
SR-MSCs in a FPU
+ IL-2 Stimulation

FIG. 55



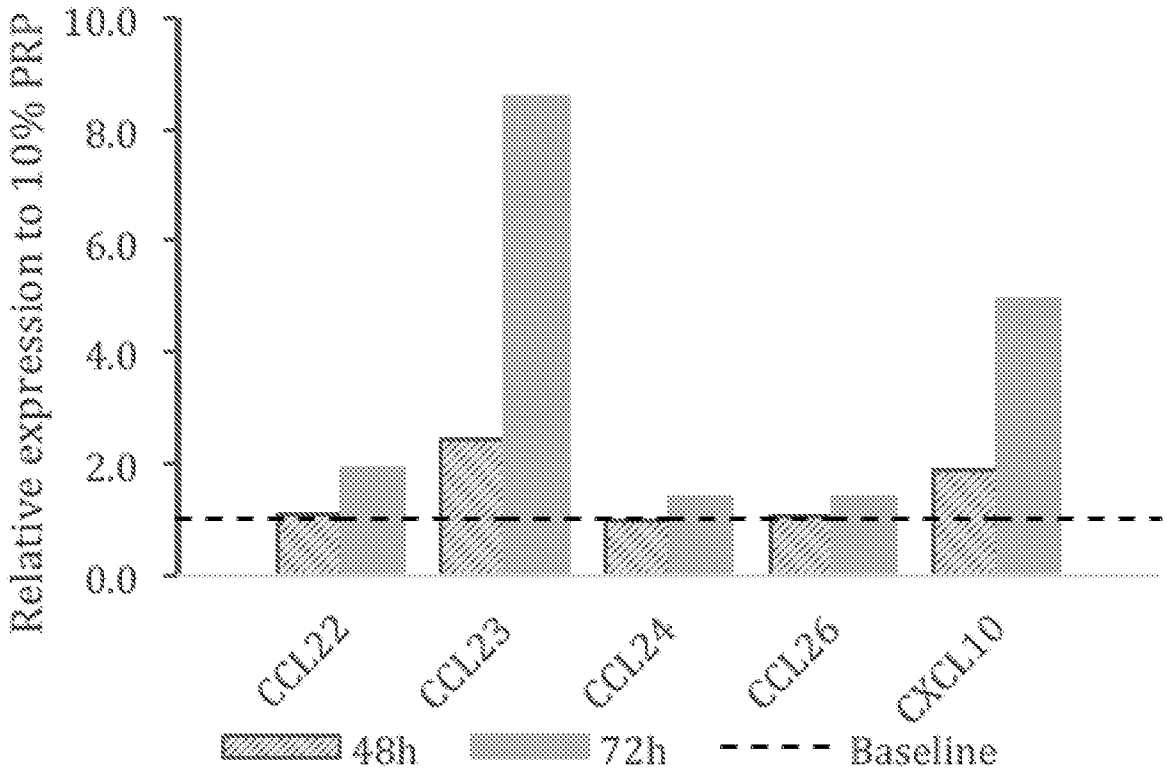
SR-MSCs in a FPU
+ IL-2 Stimulation

FIG. 56



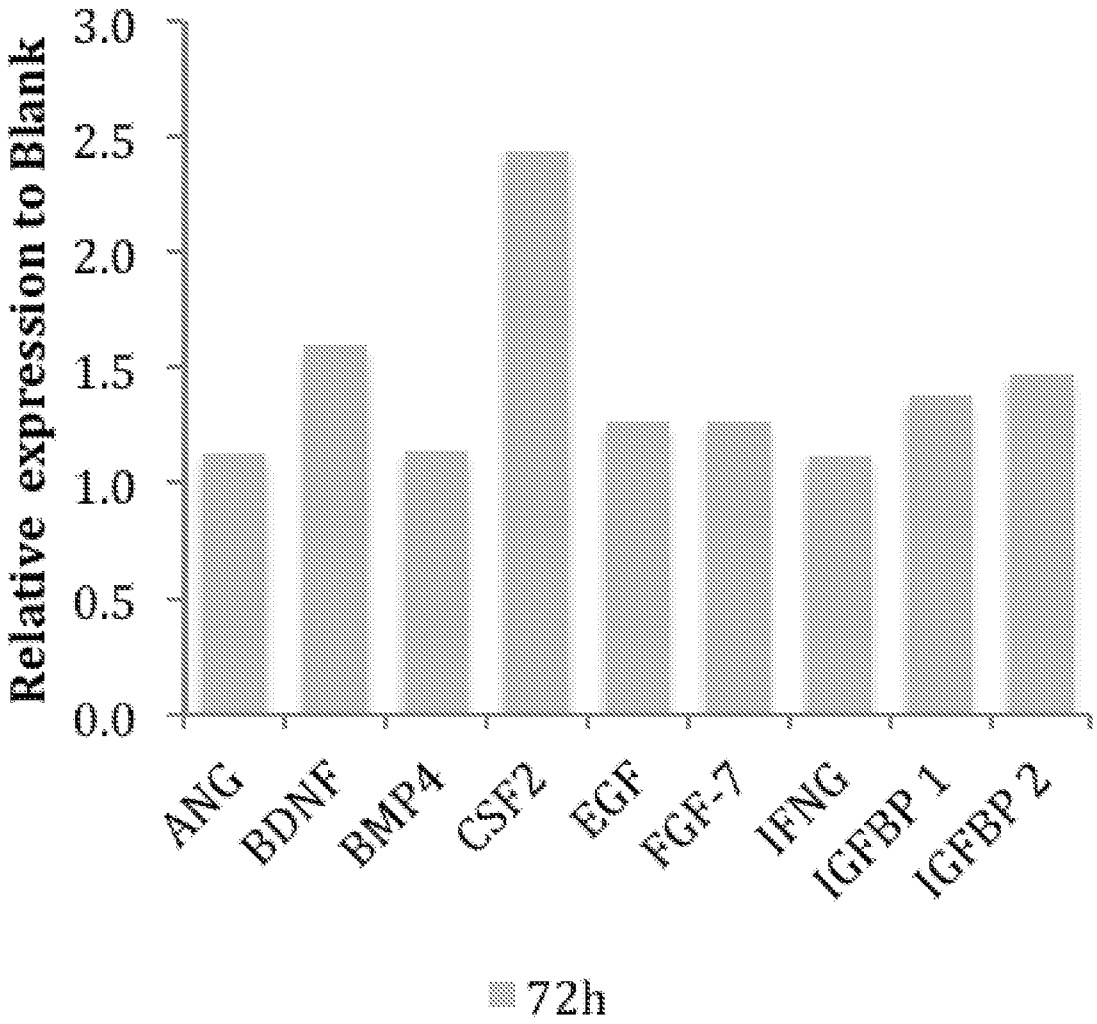
SR-MSCs in a FPU
+ IL-2 Stimulation

FIG. 57



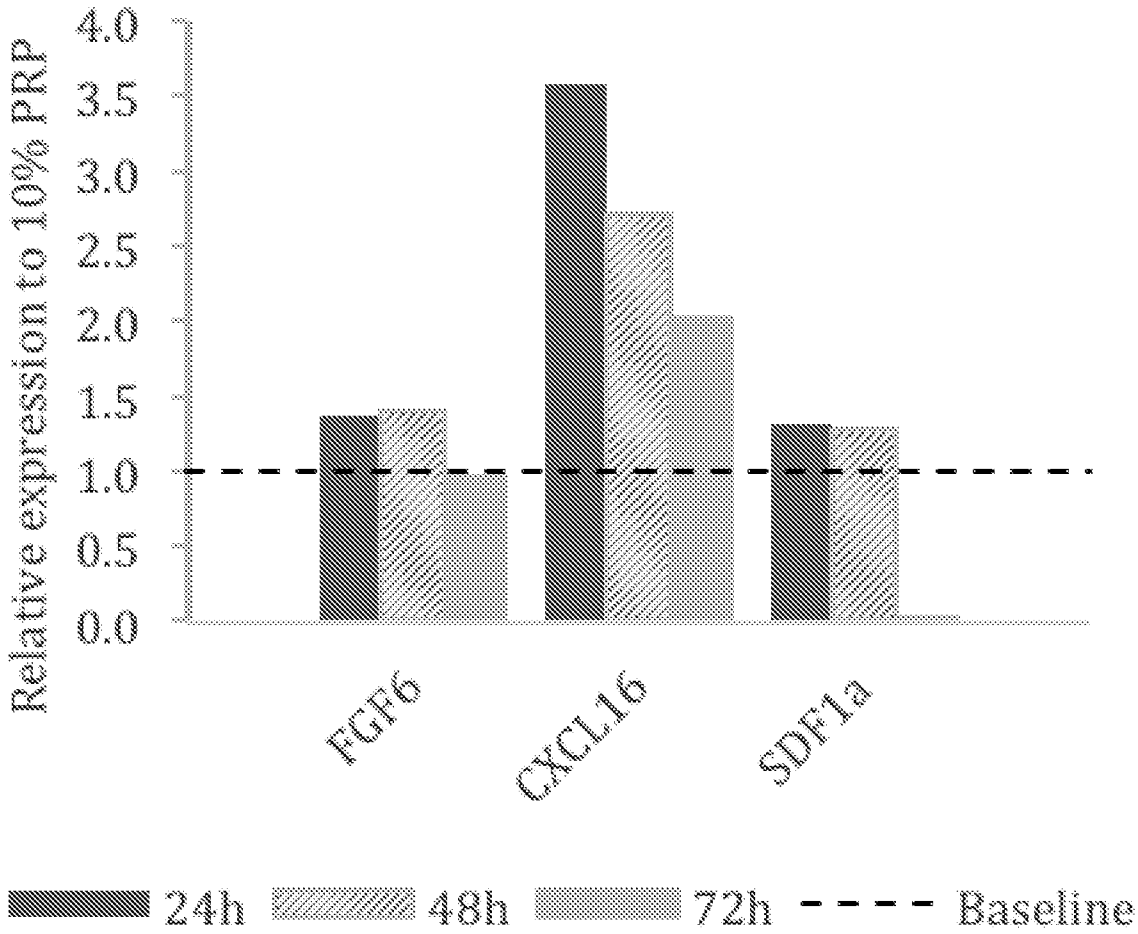
SR-MSCs in a FPU
+ IL-2 Stimulation

FIG. 58



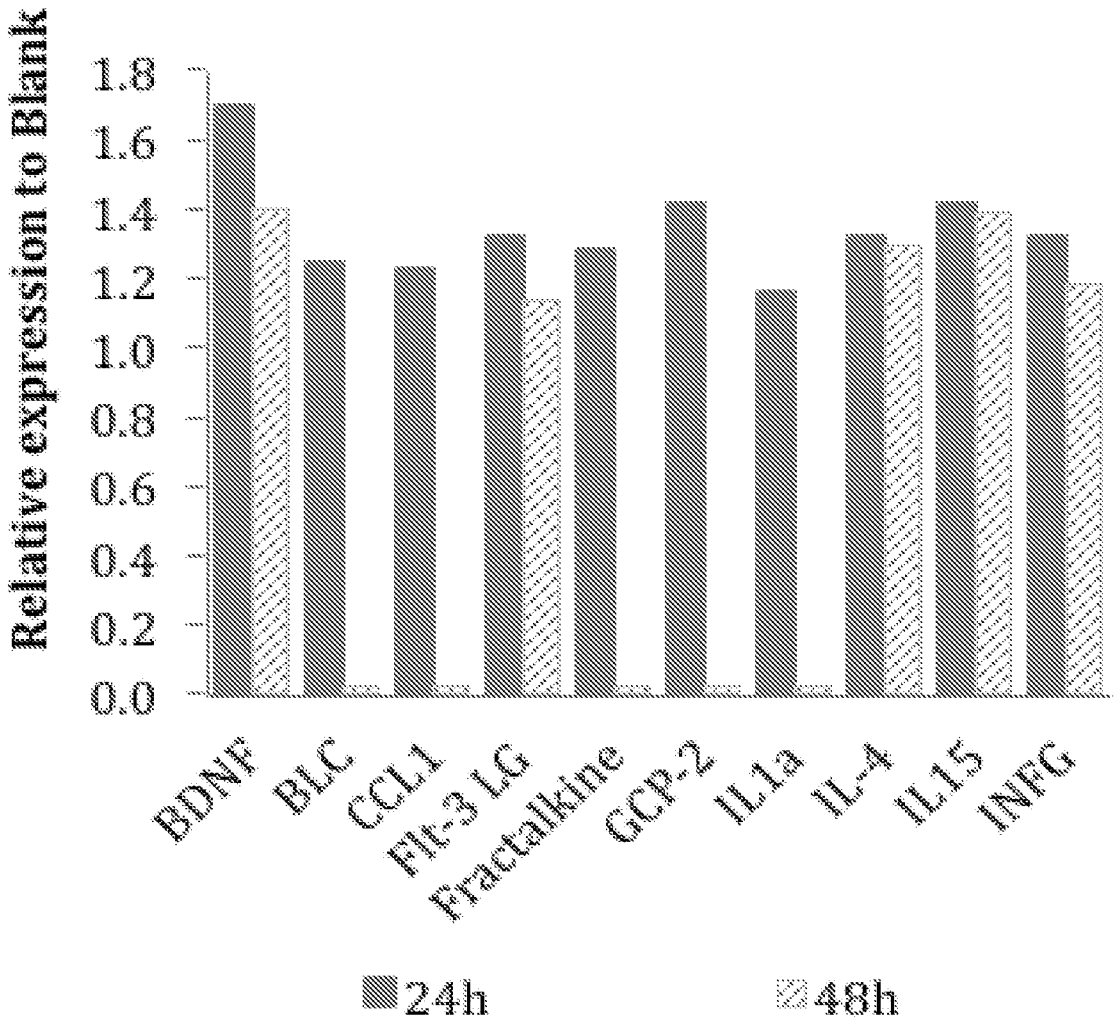
SR-MSCs in a FPU
+ IL-2 Stimulation

FIG. 59



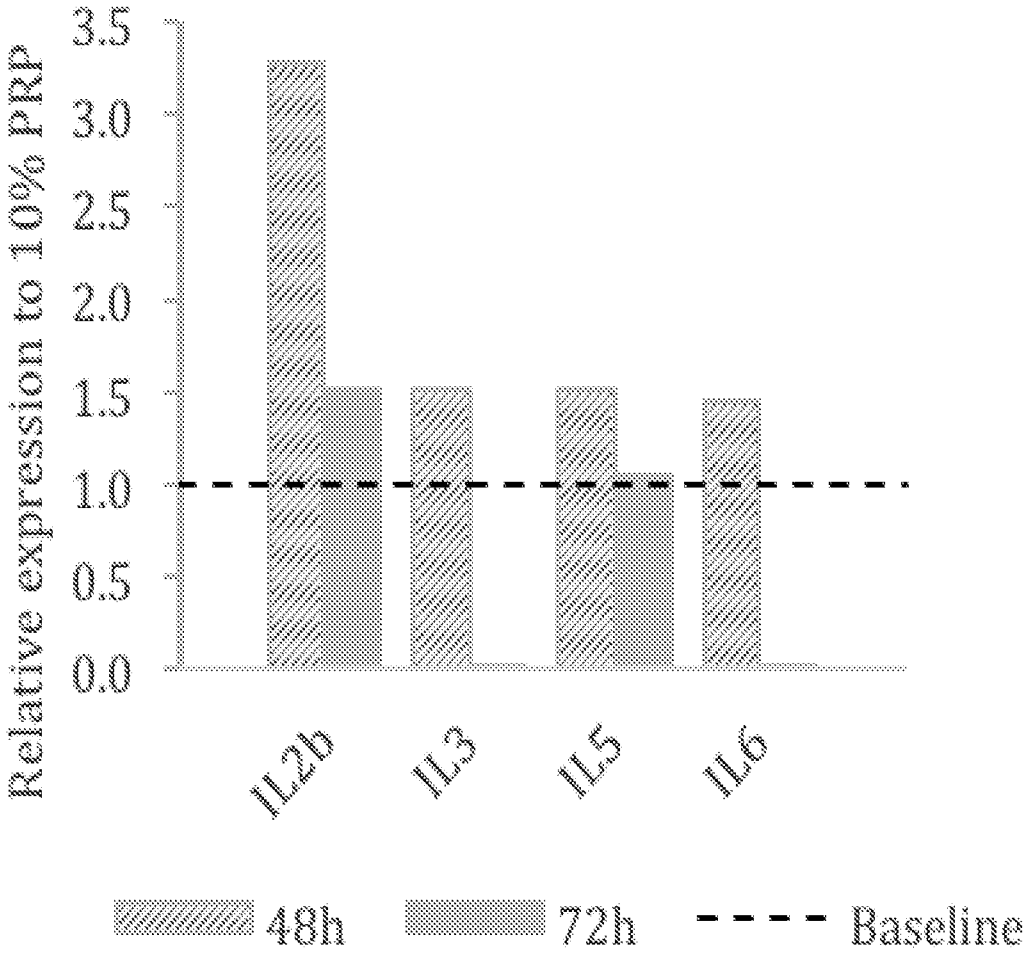
SEN-MSCs in a FPU
No IL-2 Stimulation

FIG. 60



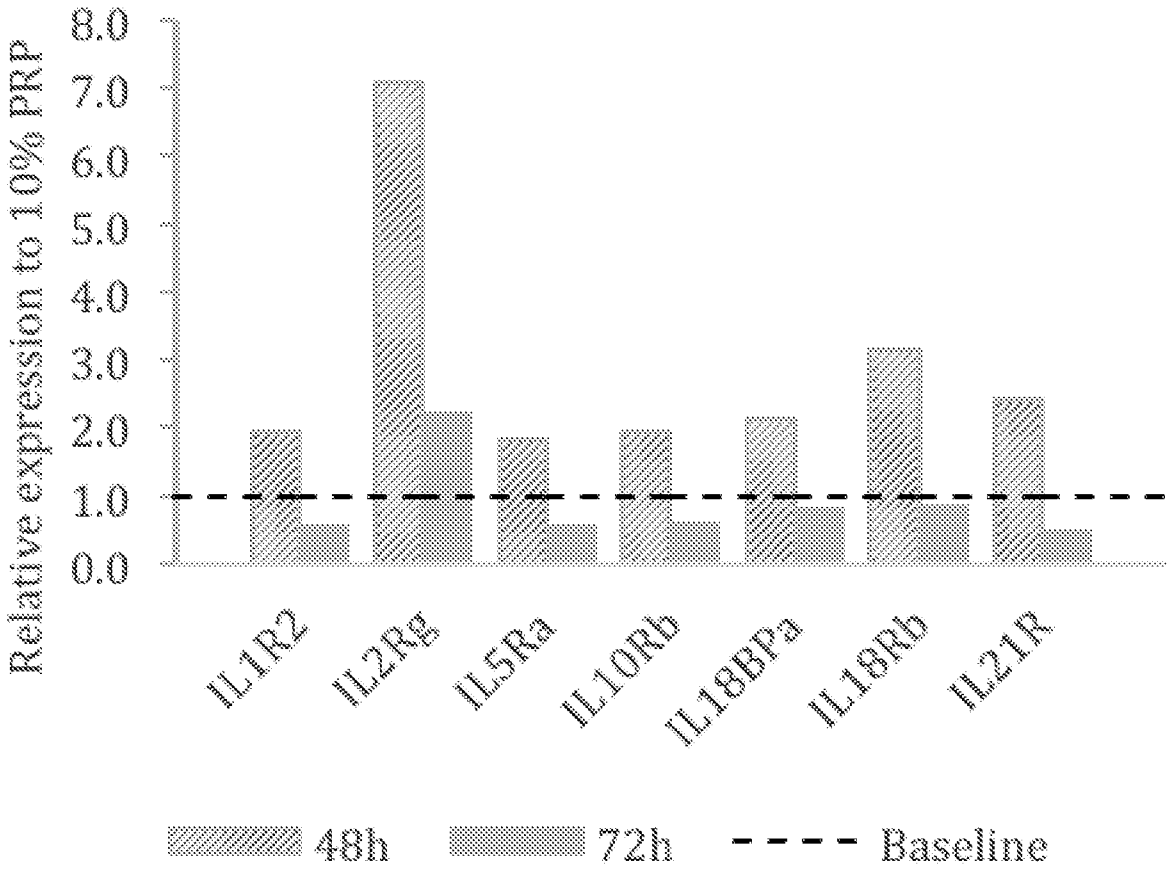
SEN-MSCs in a FPU
No IL-2 Stimulation

FIG. 61



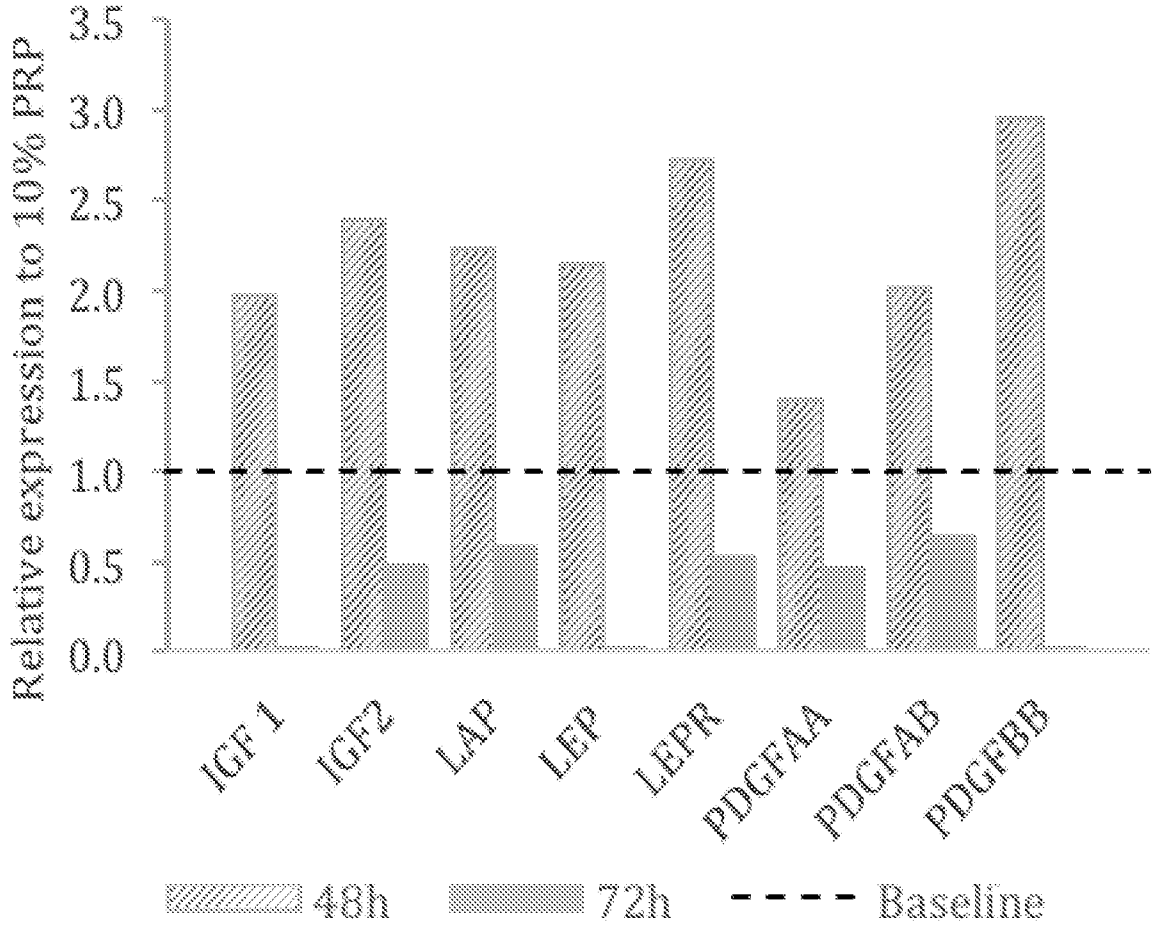
SEN-MSCs in a FPU
No IL-2 Stimulation

FIG. 62



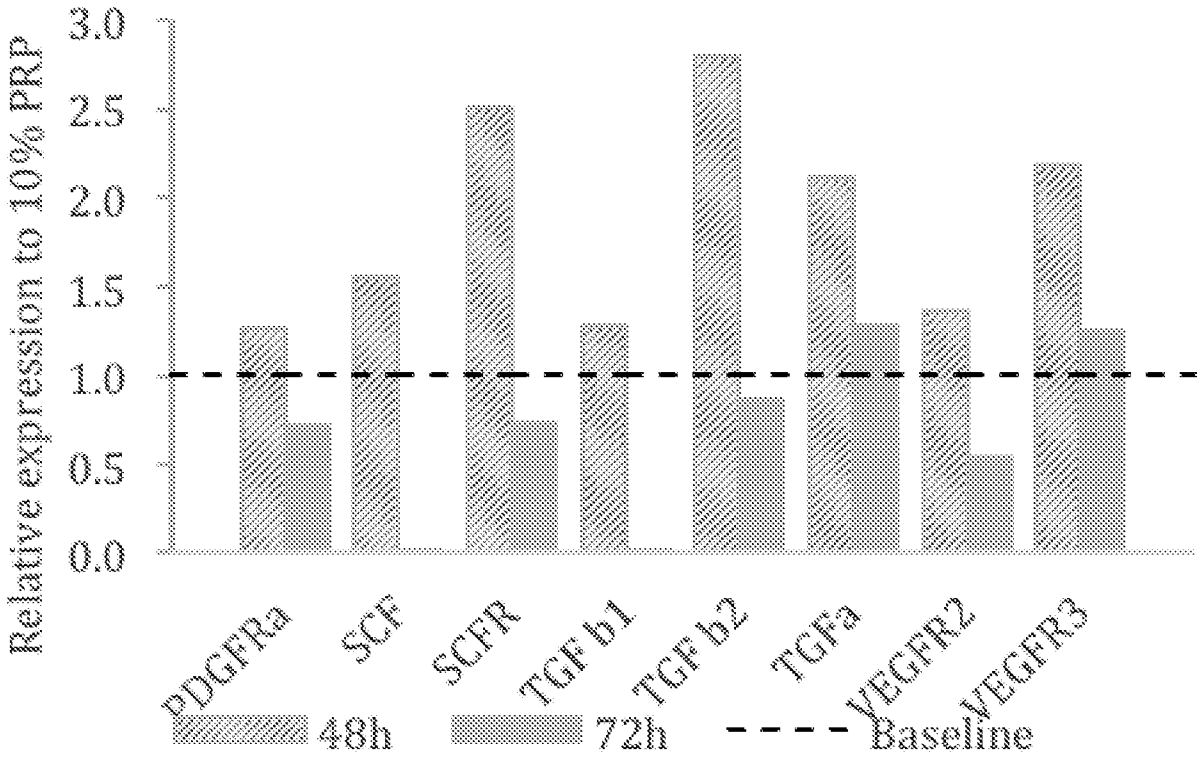
SEN-MSCs in a FPU
No IL-2 Stimulation

FIG. 63



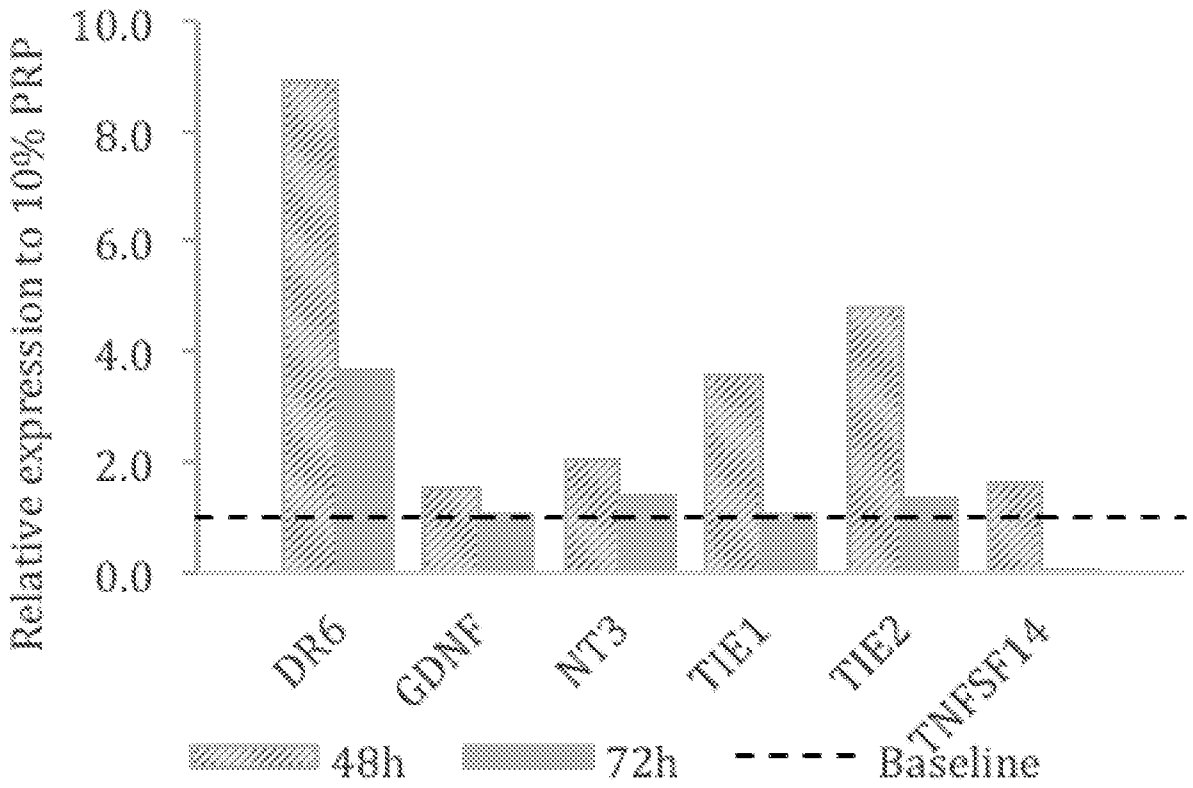
SEN-MSCs in a FPU
No IL-2 Stimulation

FIG. 64



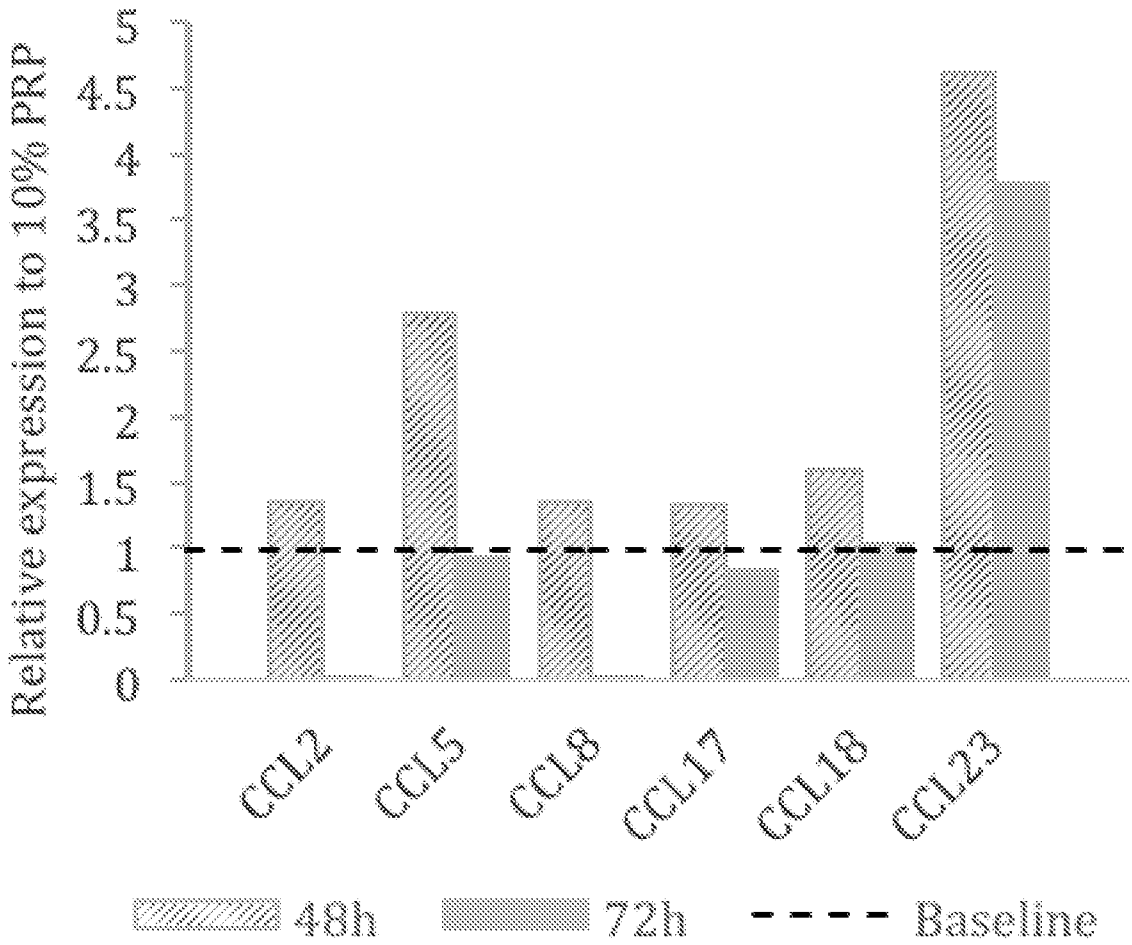
SEN-MSCs in a FPU
No IL-2 Stimulation

FIG. 65



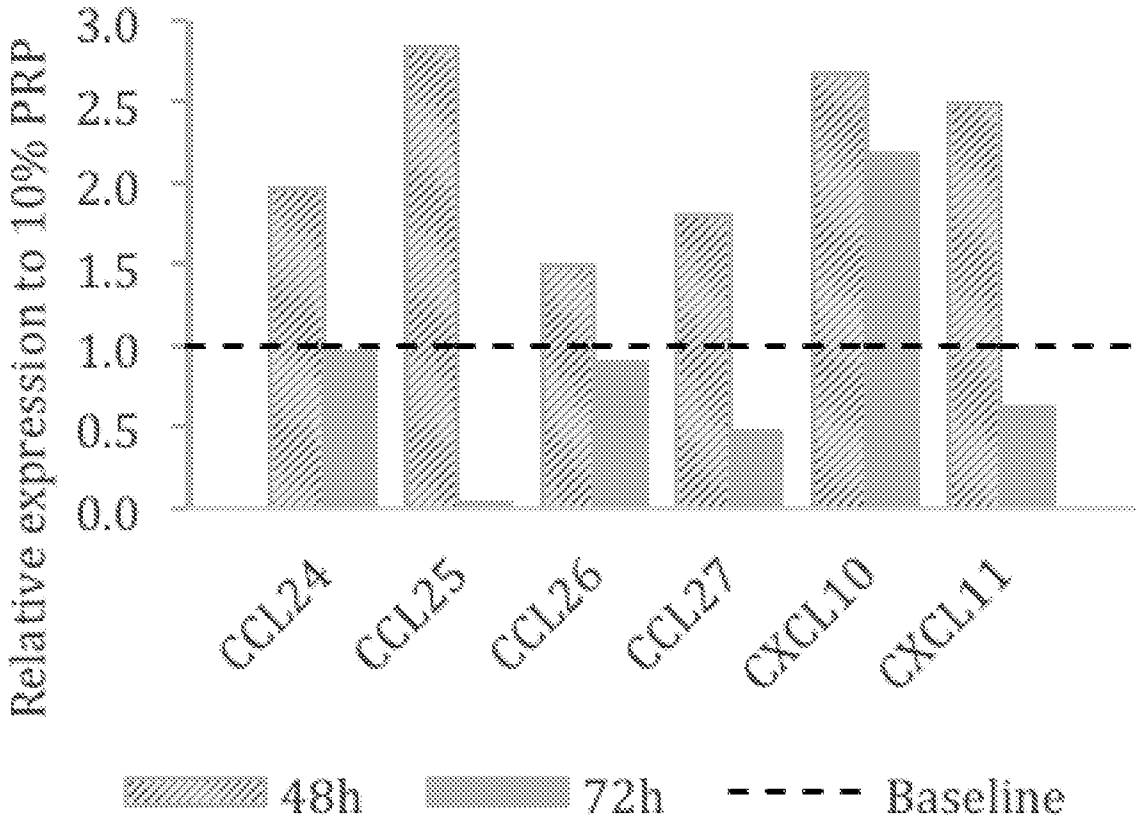
SEN-MSCs in a FPU
No IL-2 Stimulation

FIG. 66



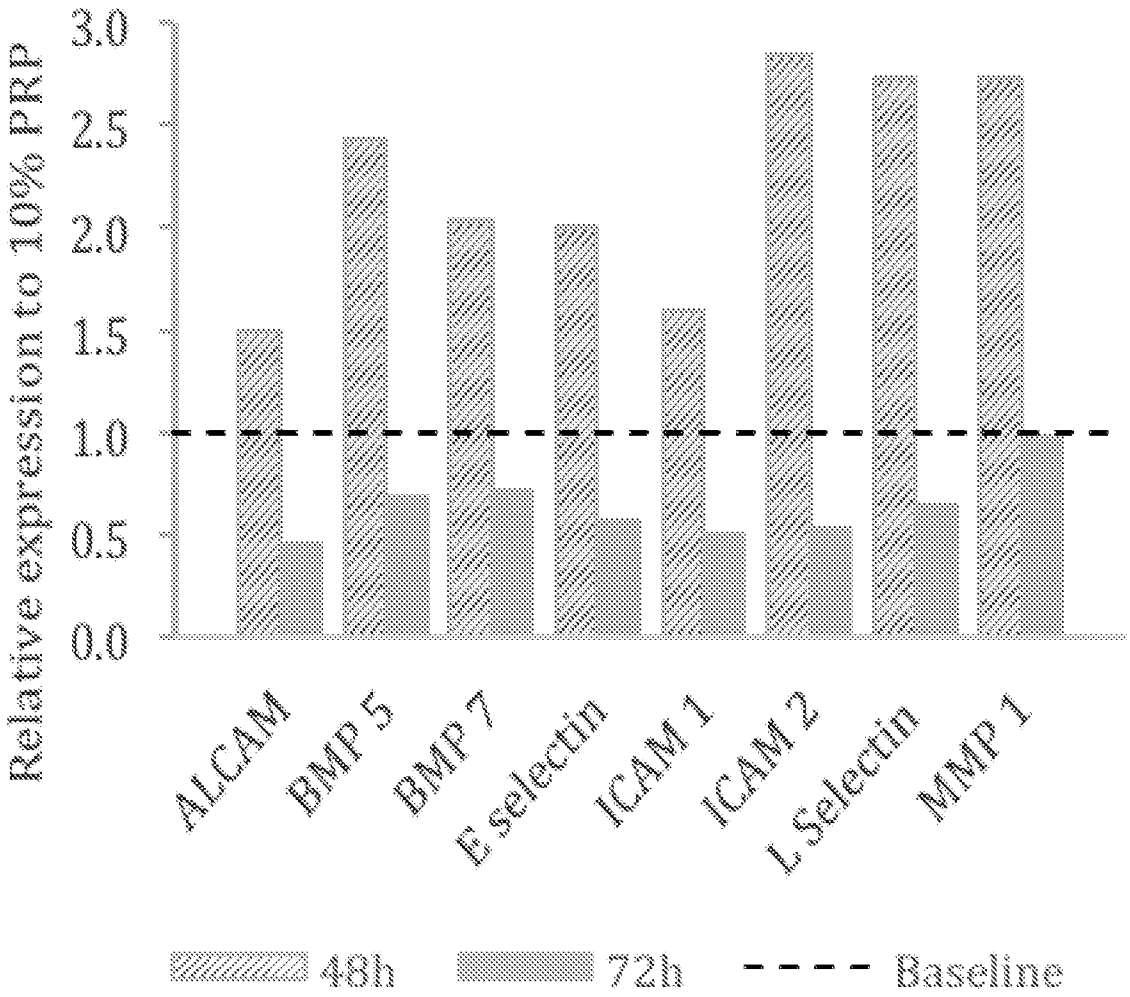
SEN-MSCs in a FPU
No IL-2 Stimulation

FIG. 67



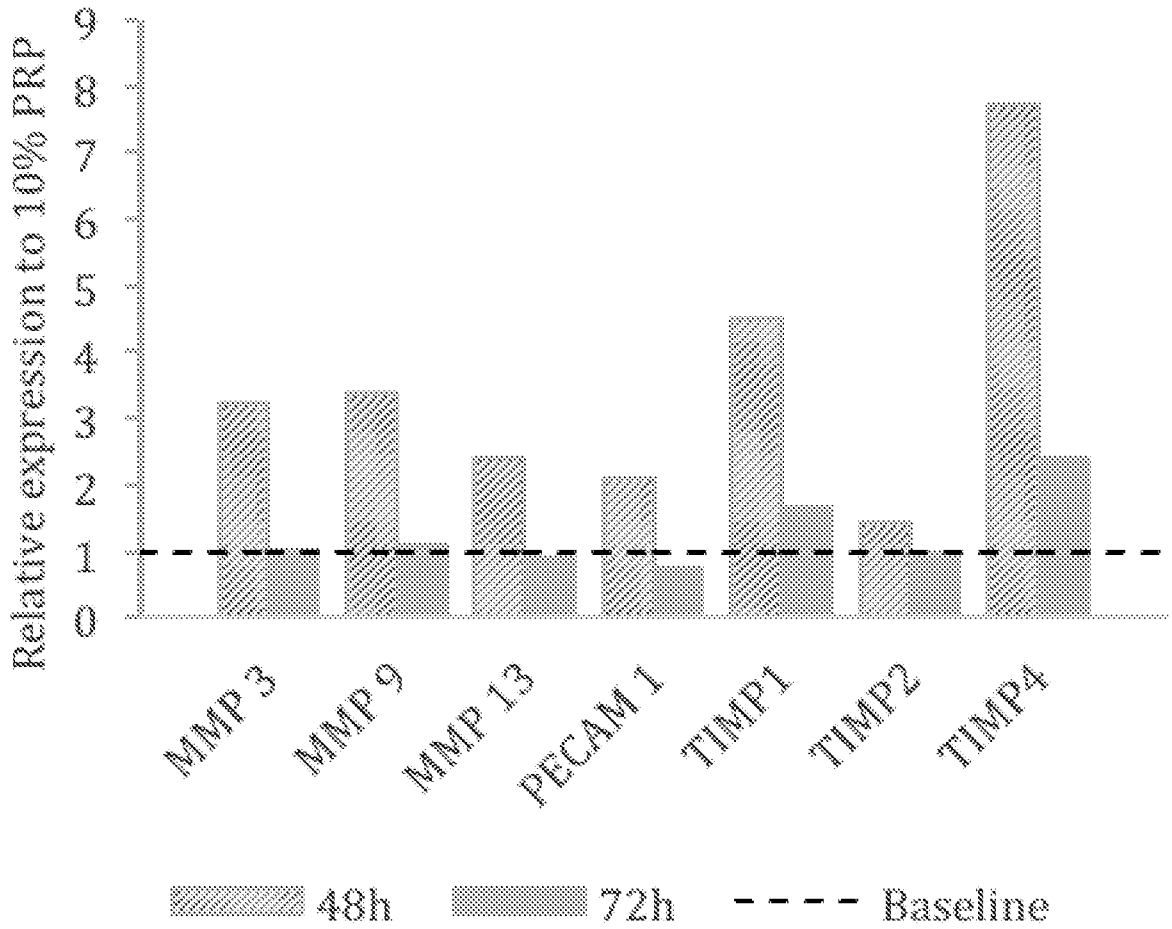
SEN-MSCs in a FPU
No IL-2 Stimulation

FIG. 68



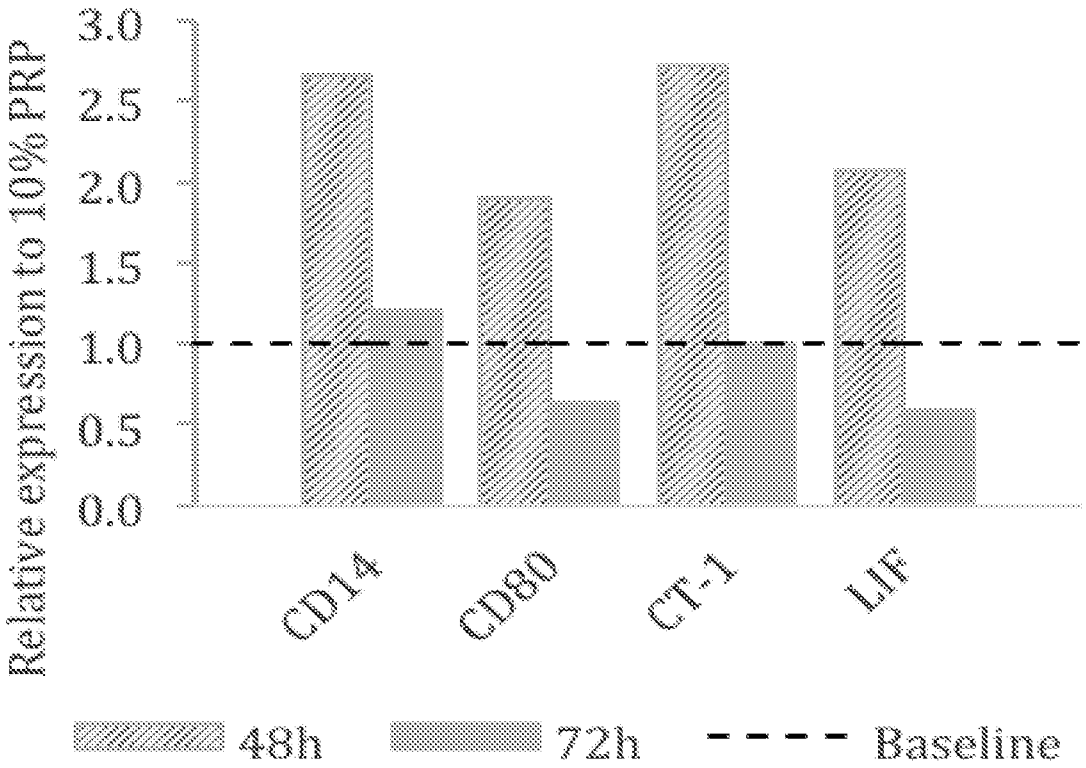
SEN-MSCs in a FPU
No IL-2 Stimulation

FIG. 69



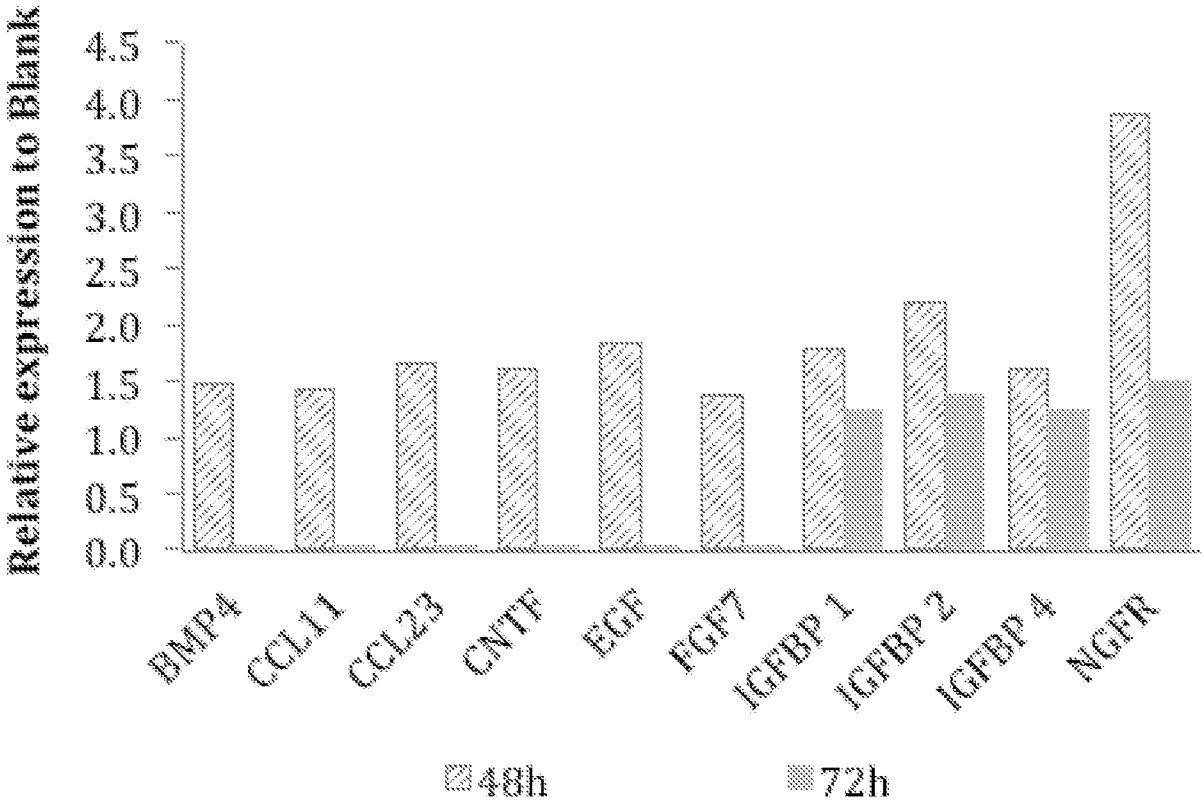
SEN-MSCs in a FPU
No IL-2 Stimulation

FIG. 70



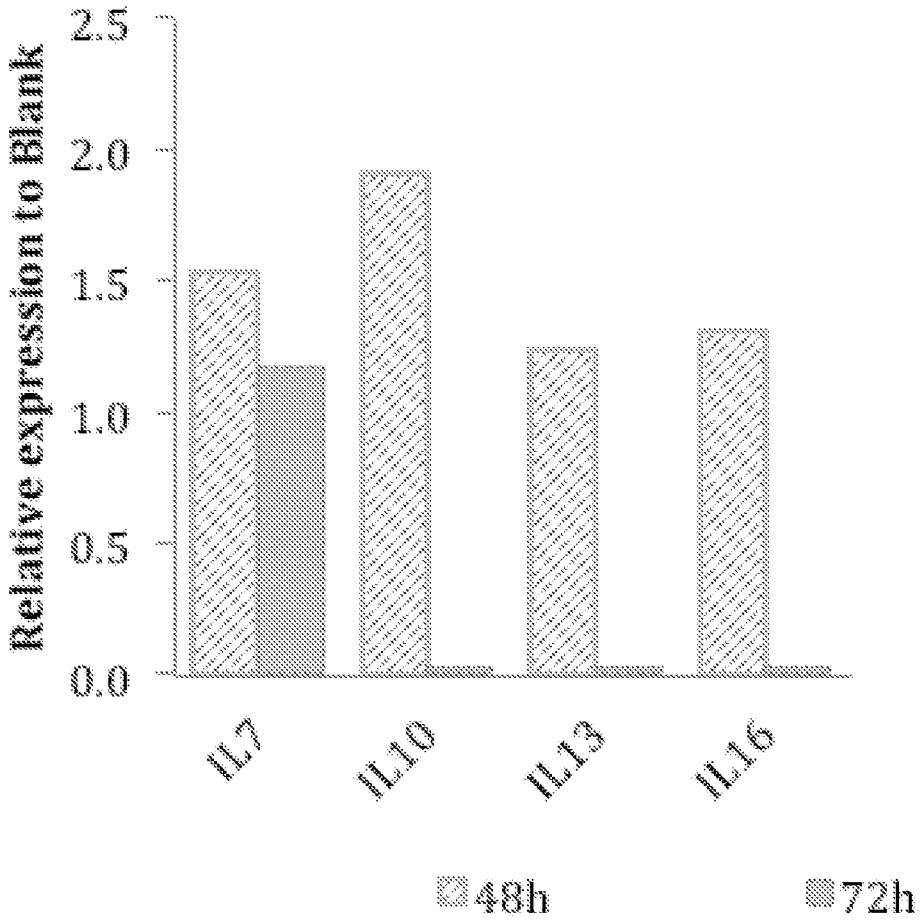
SEN-MSCs in a FPU
No IL-2 Stimulation

FIG. 71



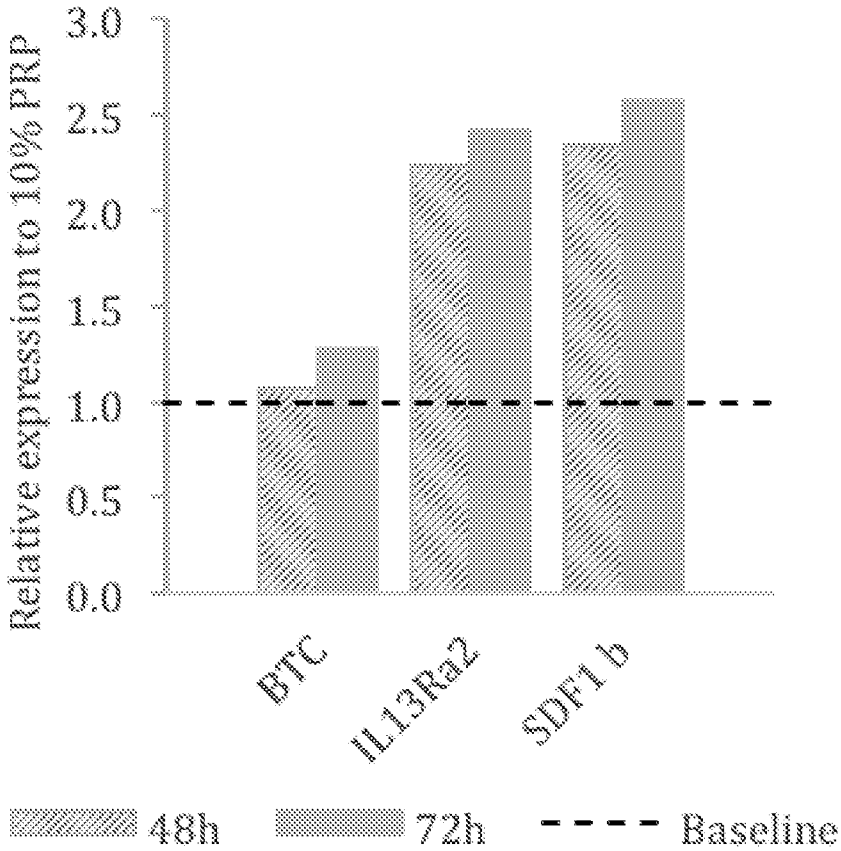
SEN-MSCs in a FPU
No IL-2 Stimulation

FIG. 72



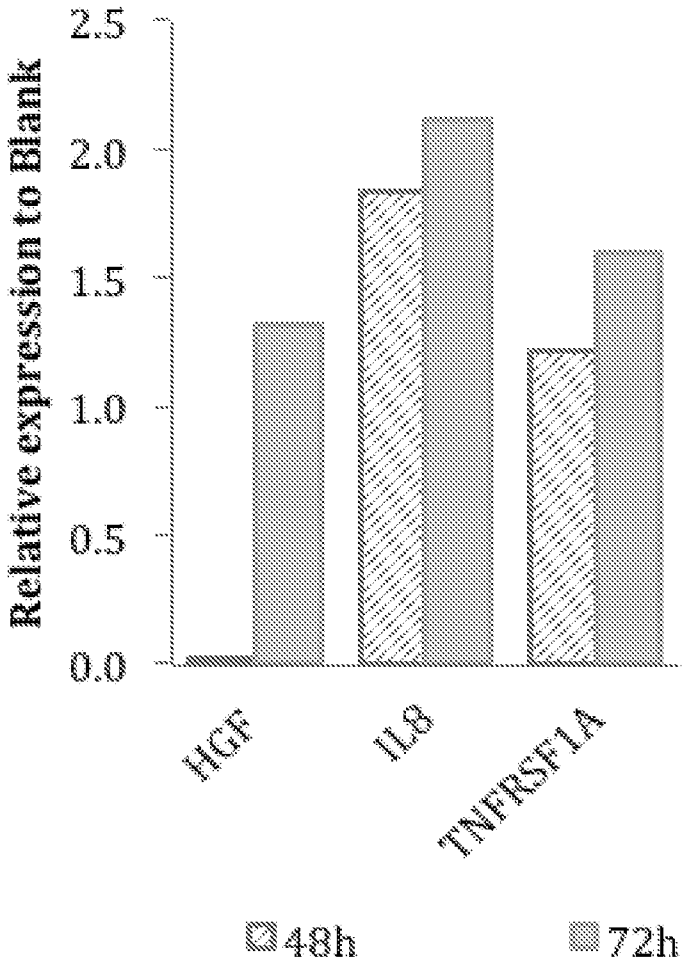
SEN-MSCs in a FPU
No IL-2 Stimulation

FIG. 73



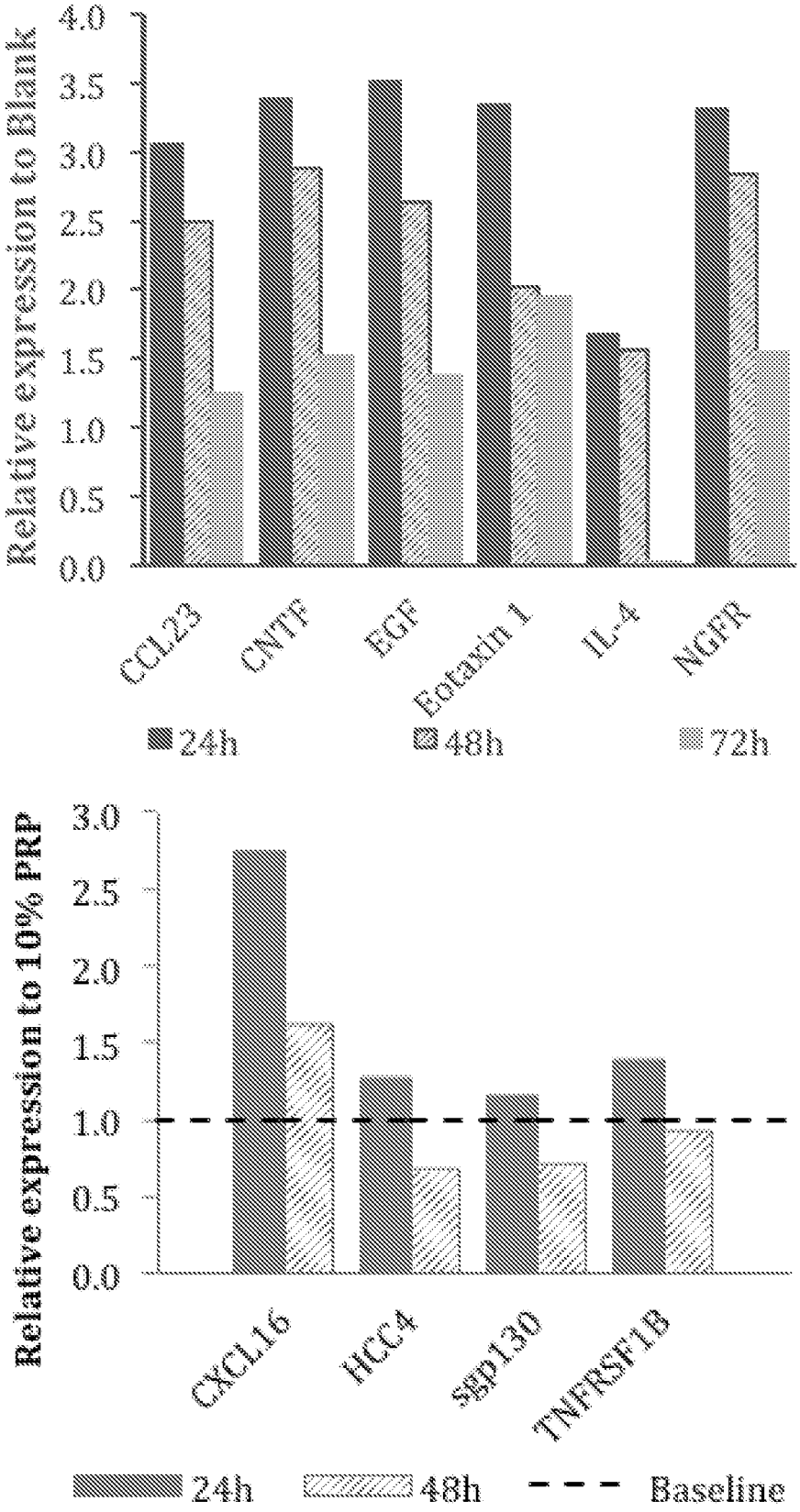
SEN-MSCs in a FPU
No IL-2 Stimulation

FIG. 74



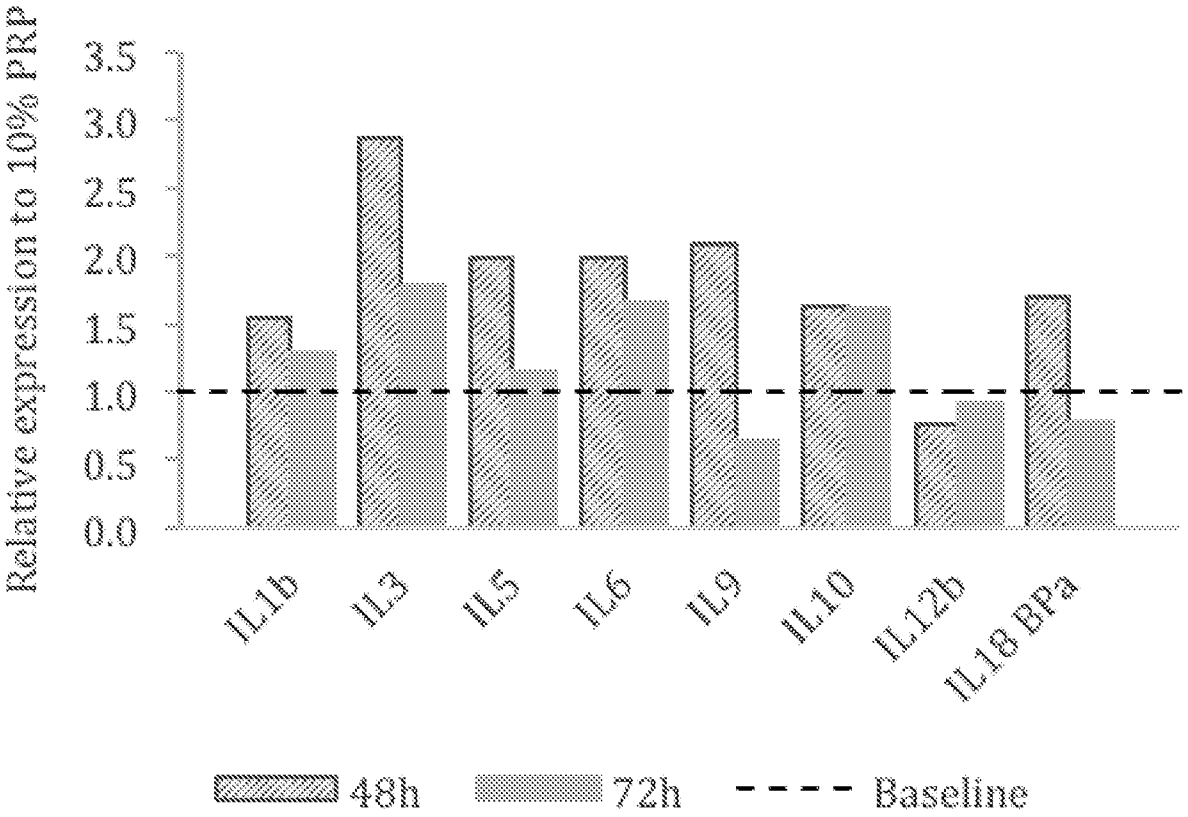
SEN-MSCs in a FPU
No IL-2 Stimulation

FIG. 75



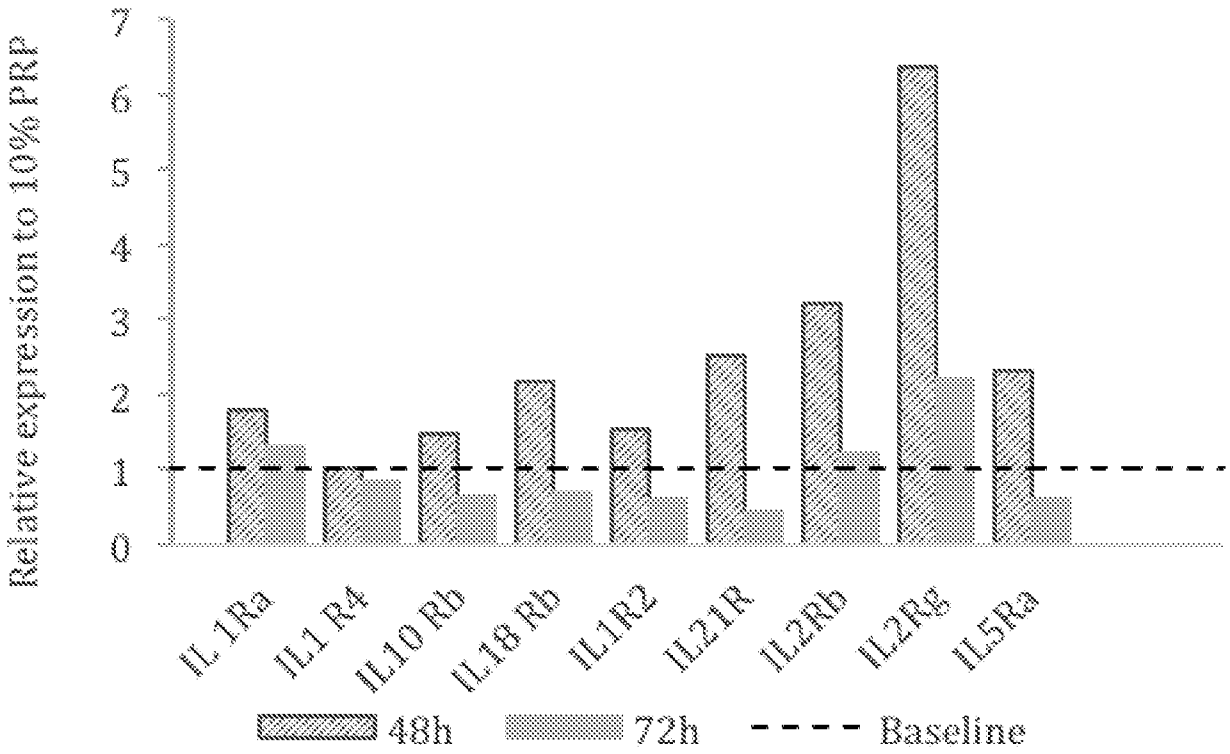
SEN-MSCs in a FPU
+ IL-2 Stimulation

FIG. 76



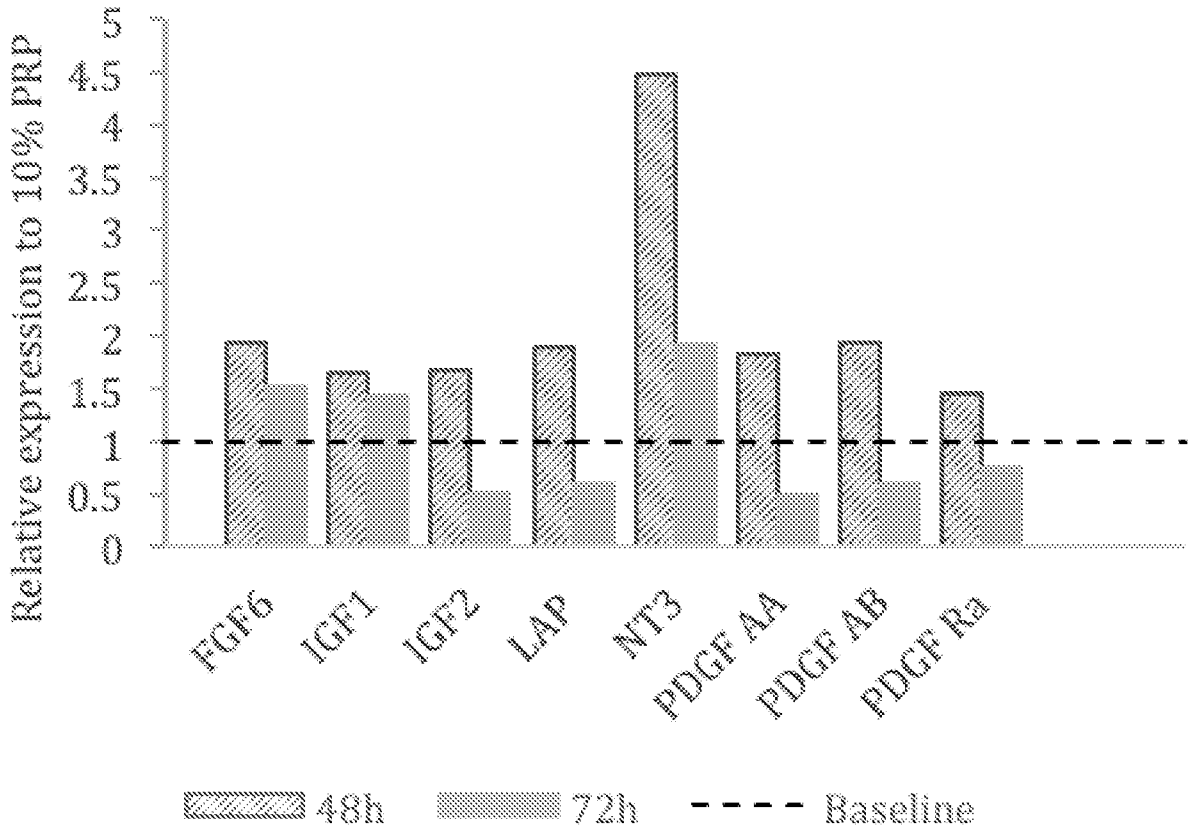
SEN-MSCs in a FPU
+ IL-2 Stimulation

FIG. 77



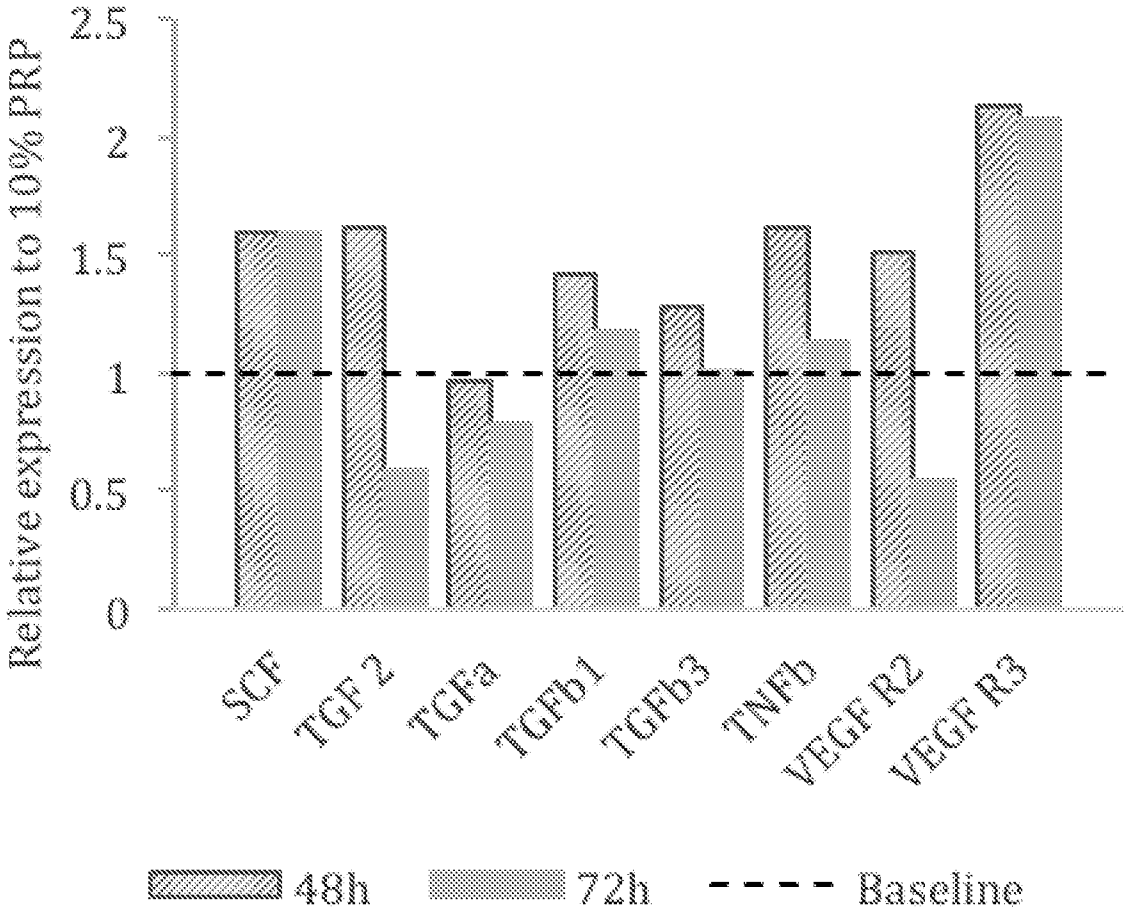
SEN-MSCs in a FPU
+ IL-2 Stimulation

FIG. 78



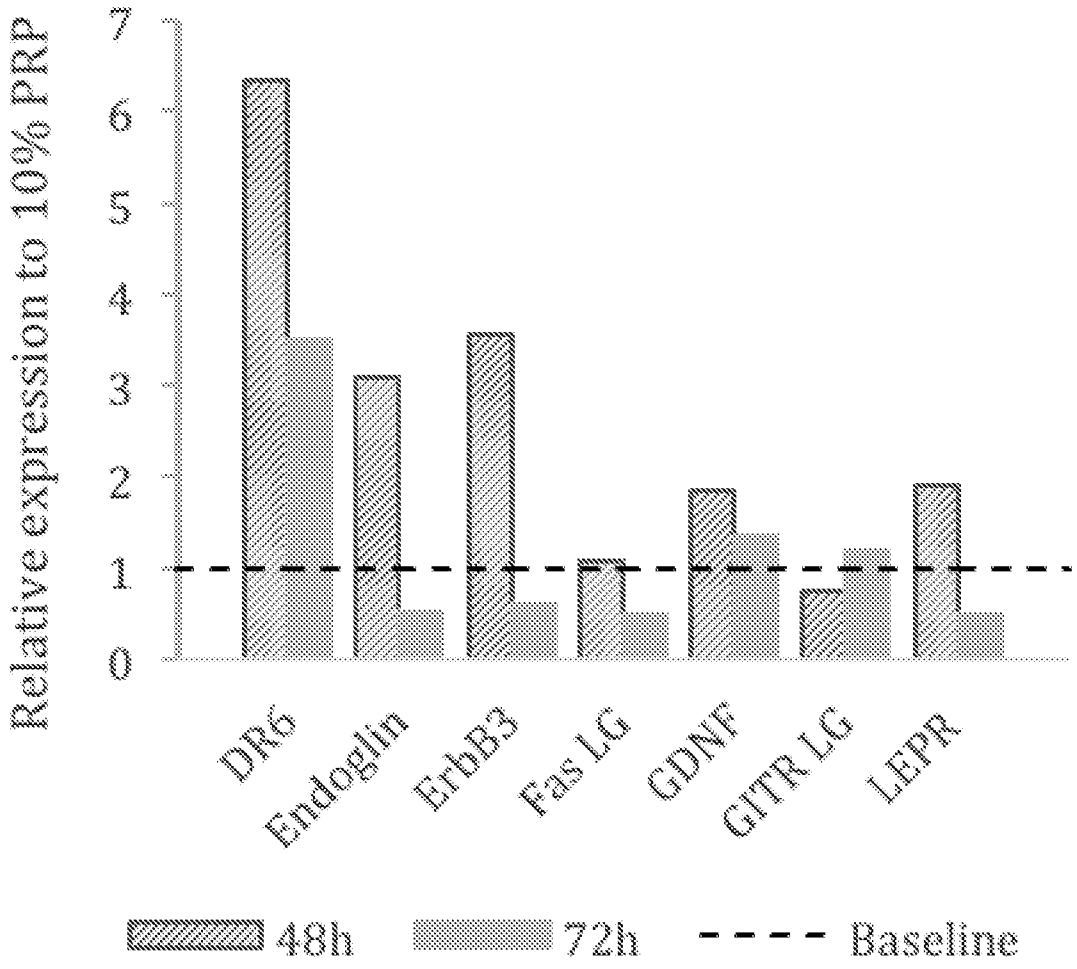
SEN-MSCs in a FPU
+ IL-2 Stimulation

FIG. 79



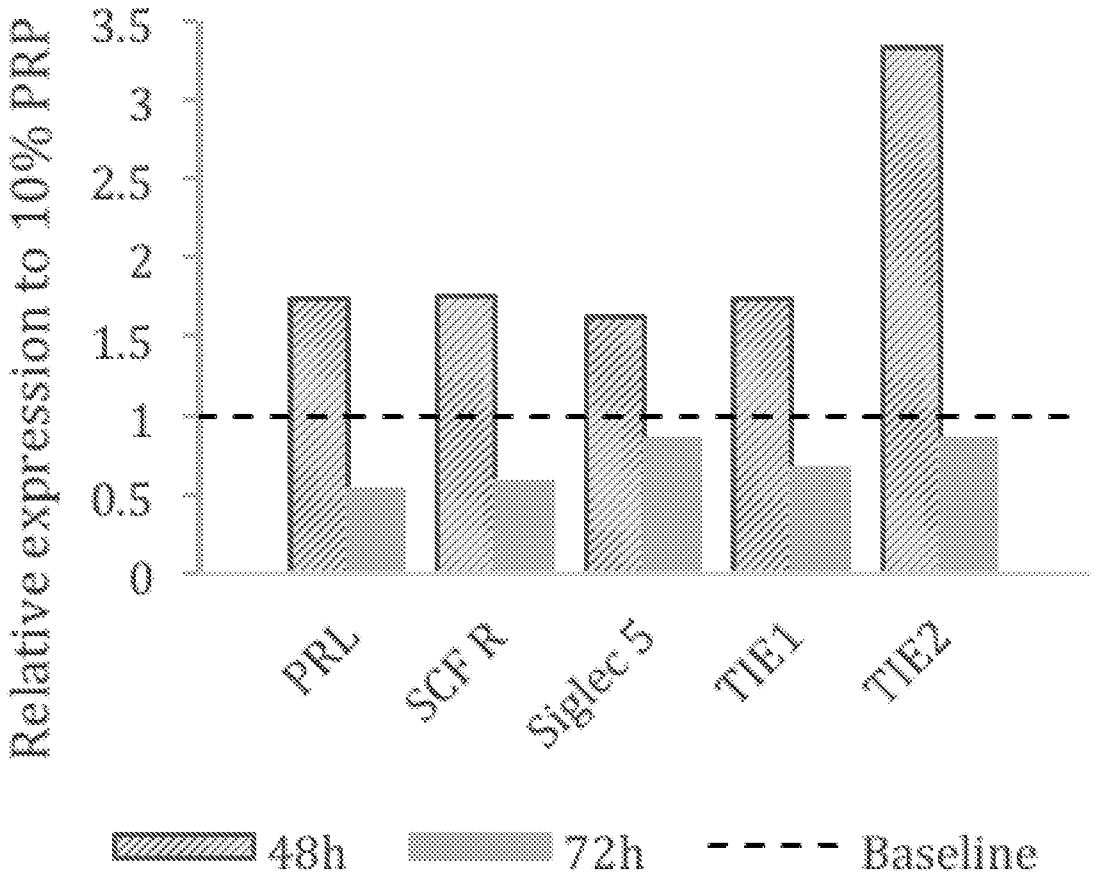
SEN-MSCs in a FPU
+ IL-2 Stimulation

FIG. 80



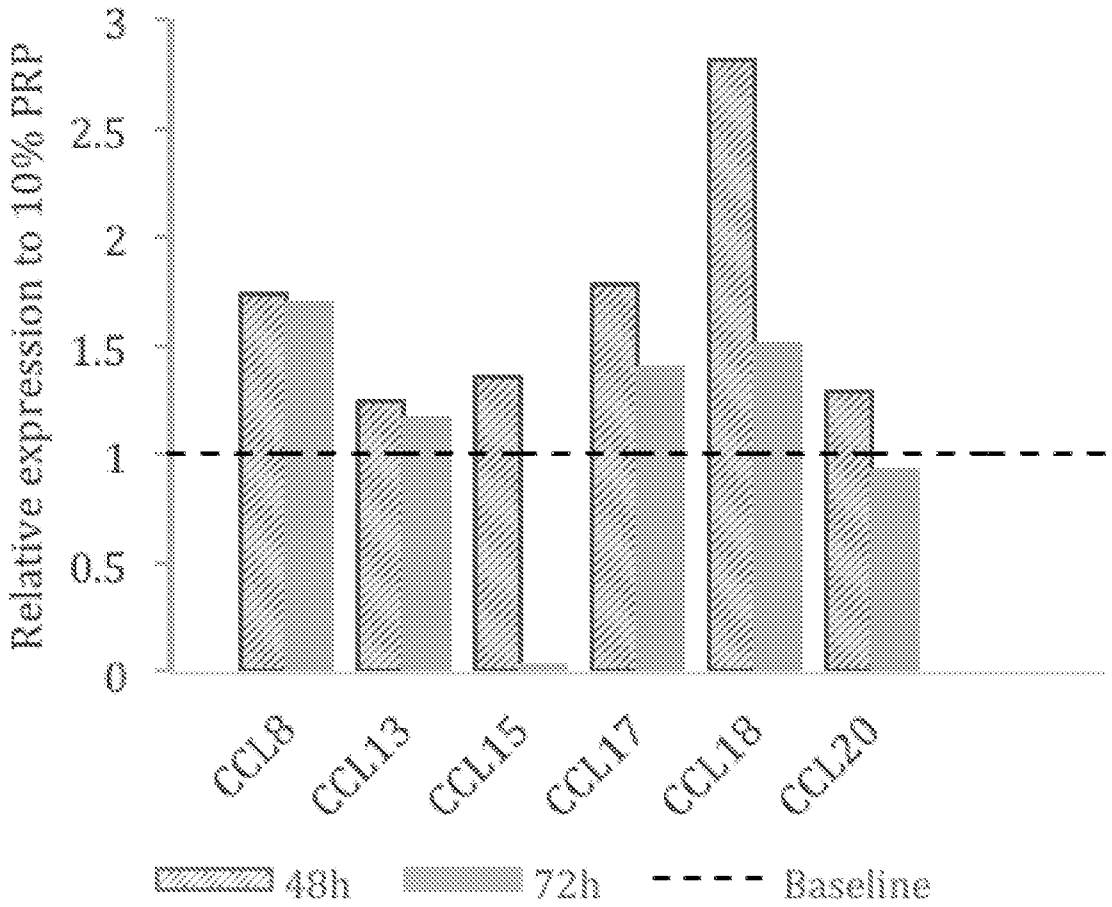
SEN-MSCs in a FPU
+ IL-2 Stimulation

FIG. 81



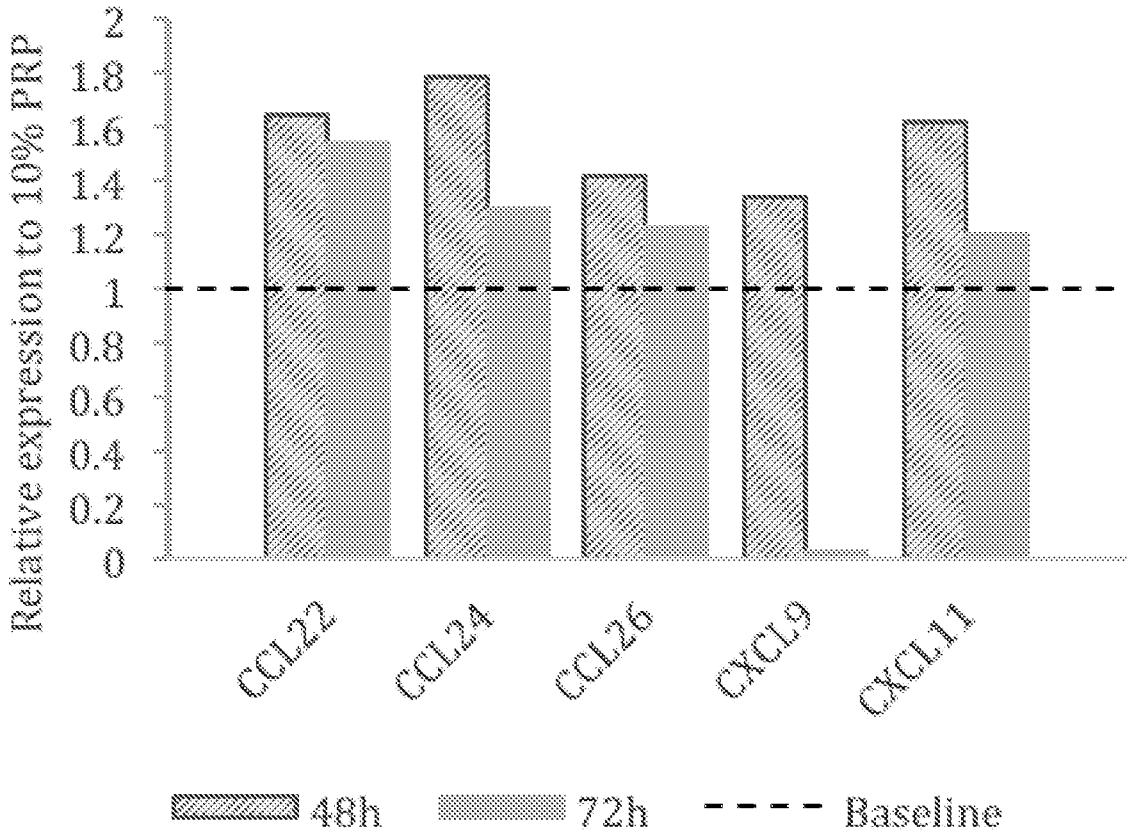
SEN-MSCs in a FPU
+ IL-2 Stimulation

FIG. 82



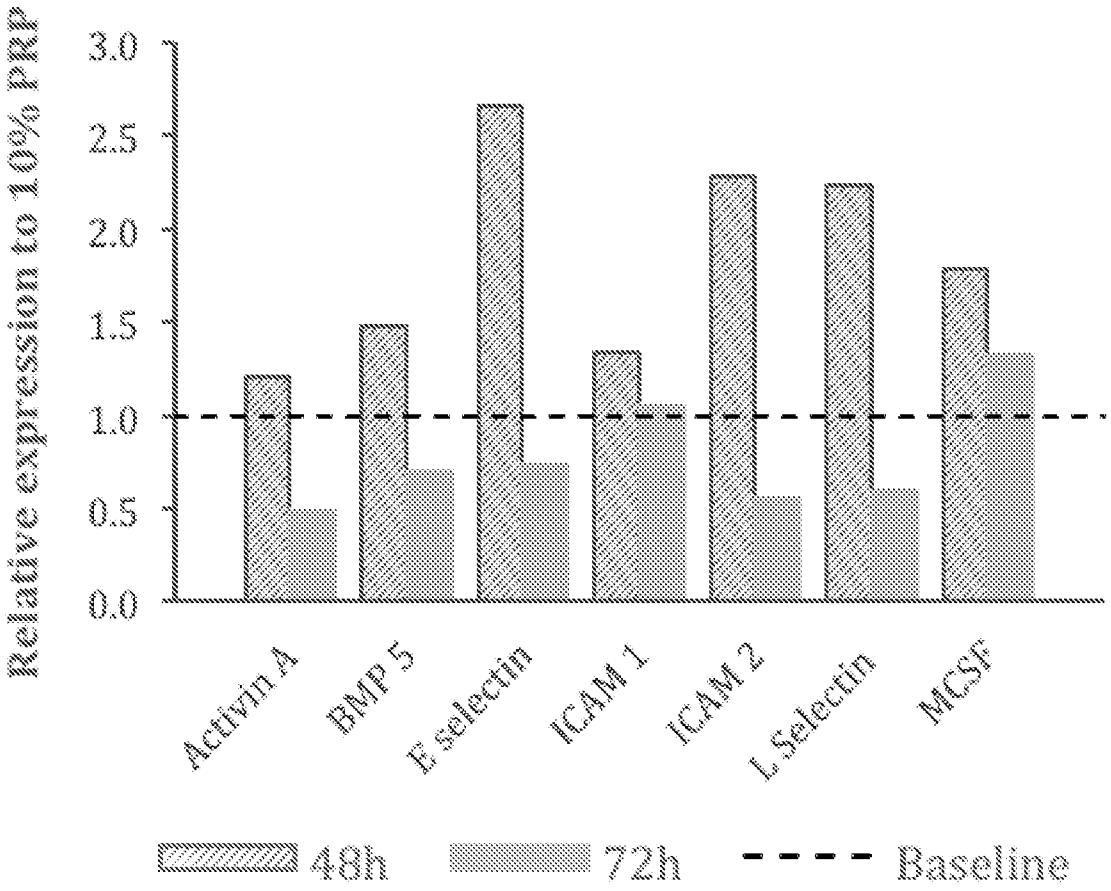
SEN-MSCs in a FPU
+ IL-2 Stimulation

FIG. 83



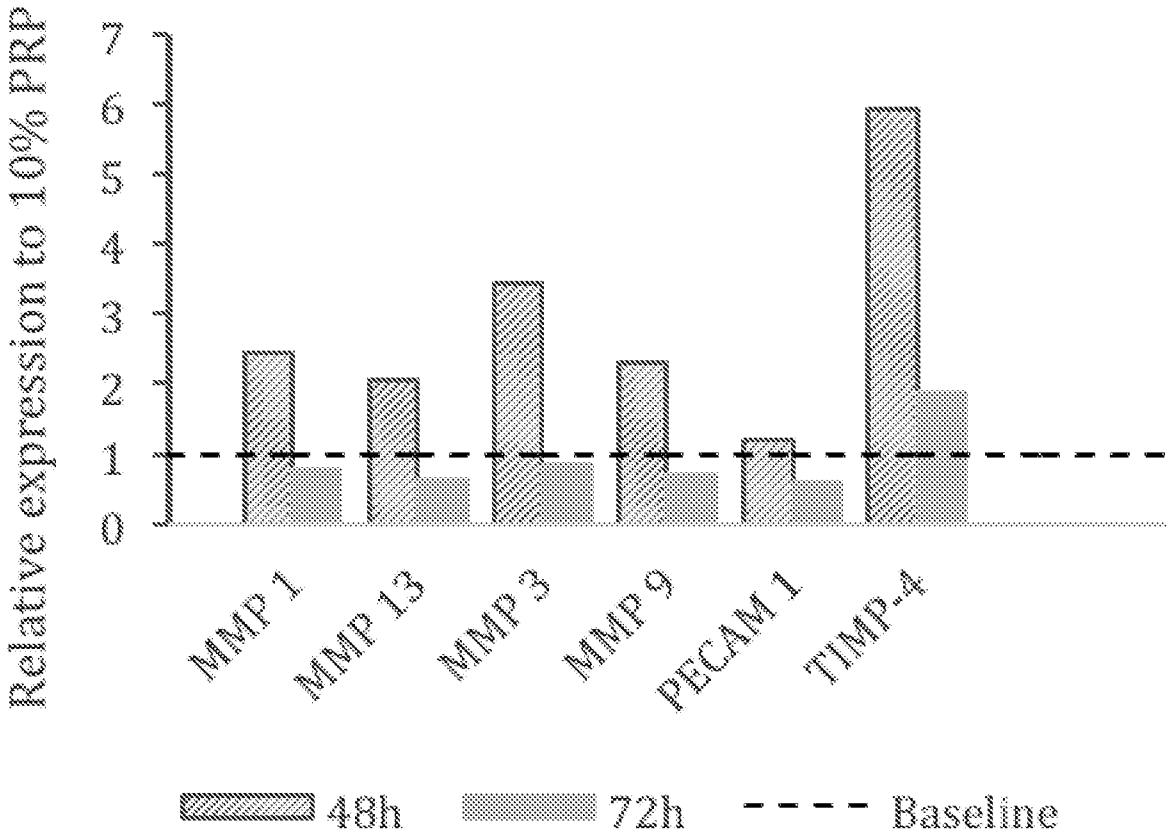
SEN-MSCs in a FPU
+ IL-2 Stimulation

FIG. 84



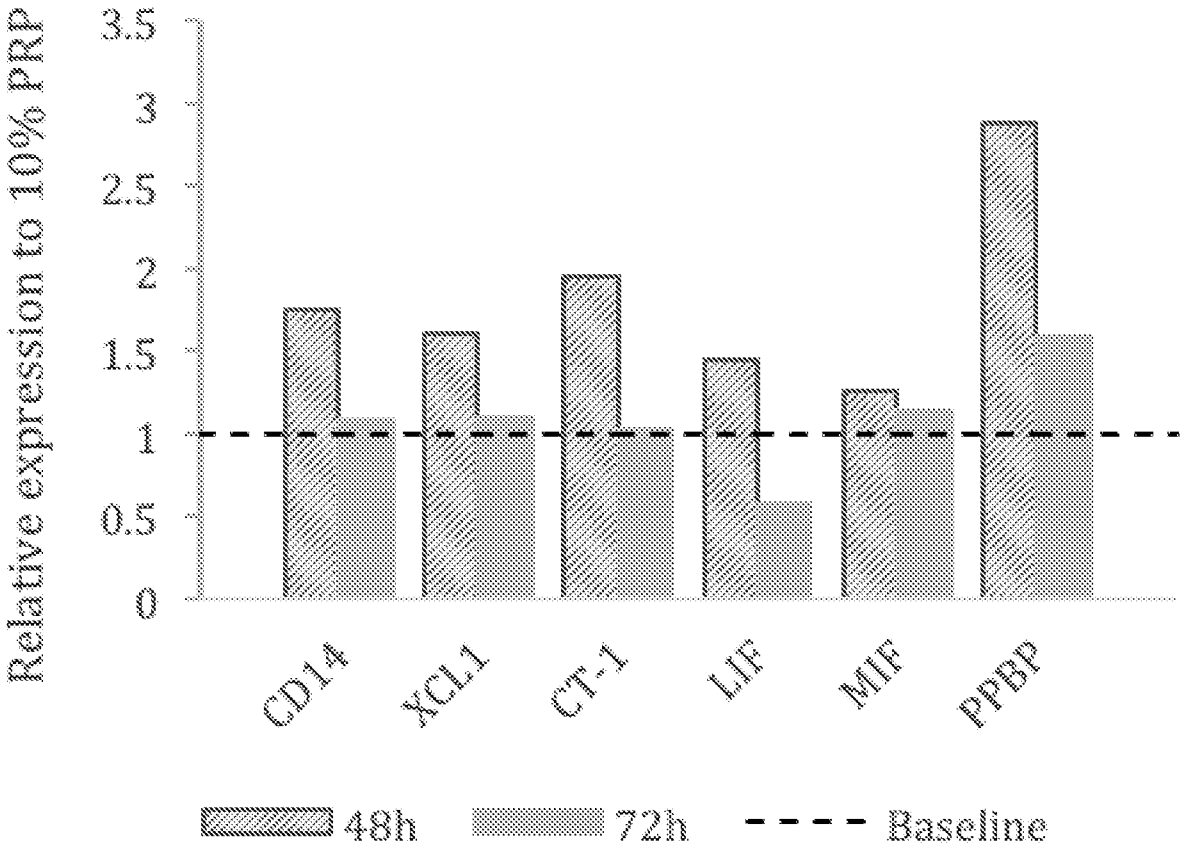
SEN-MSCs in a FPU
+ IL-2 Stimulation

FIG. 85



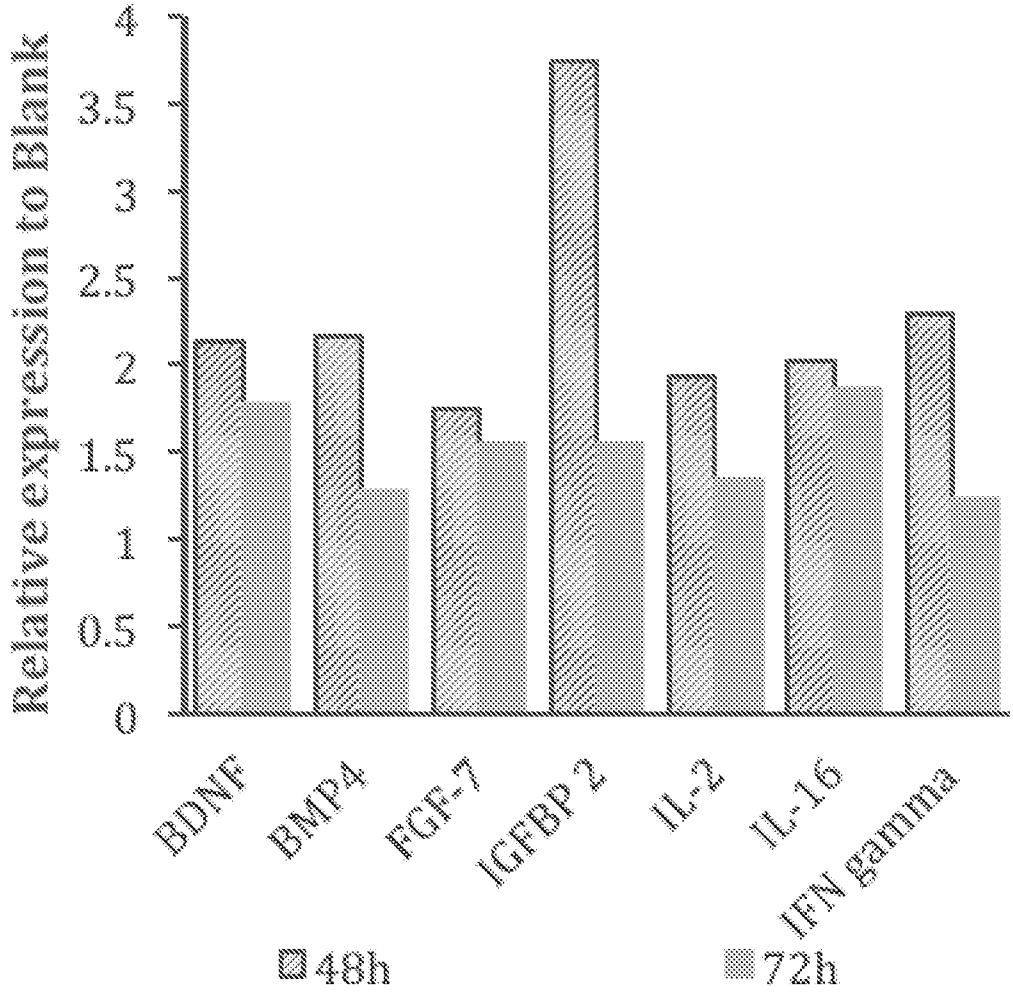
SEN-MSCs in a FPU
+ IL-2 Stimulation

FIG. 86



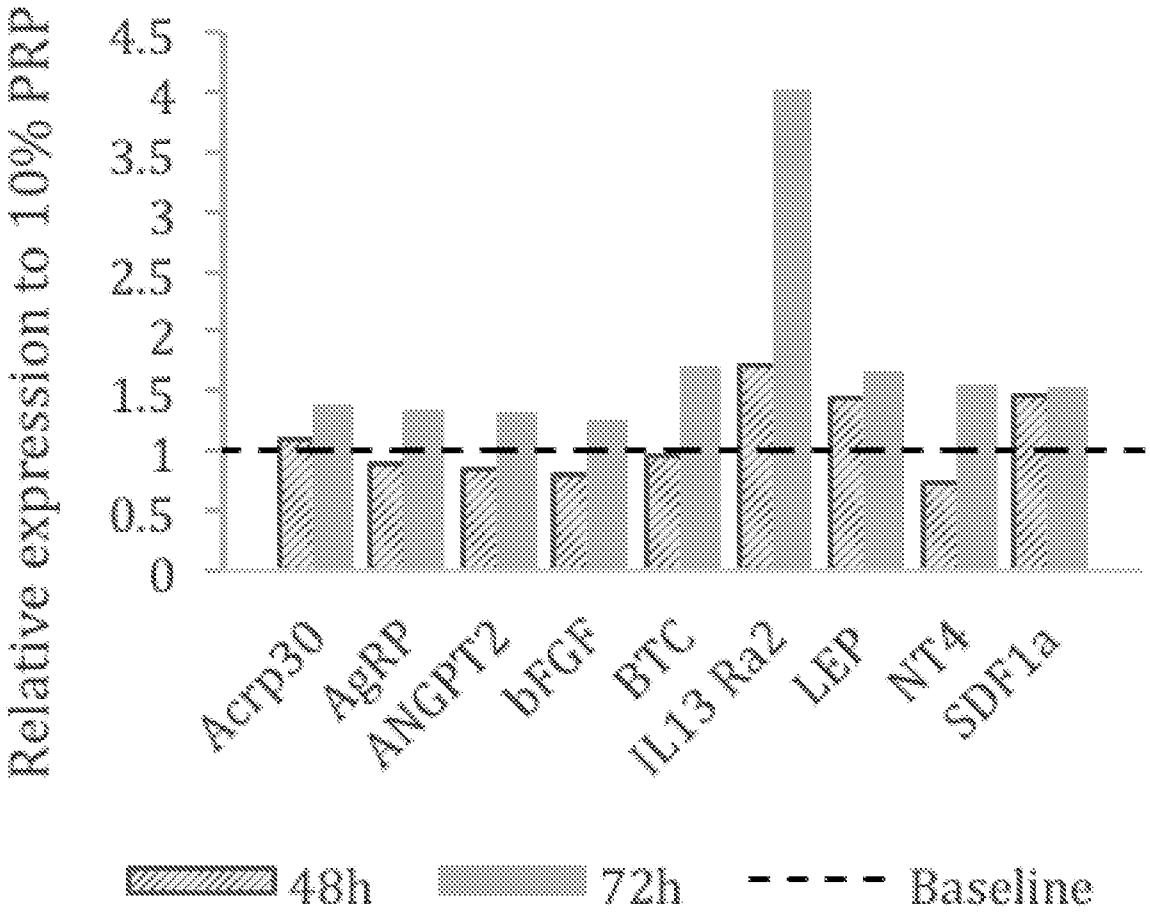
SEN-MSCs in a FPU
+ IL-2 Stimulation

FIG. 87



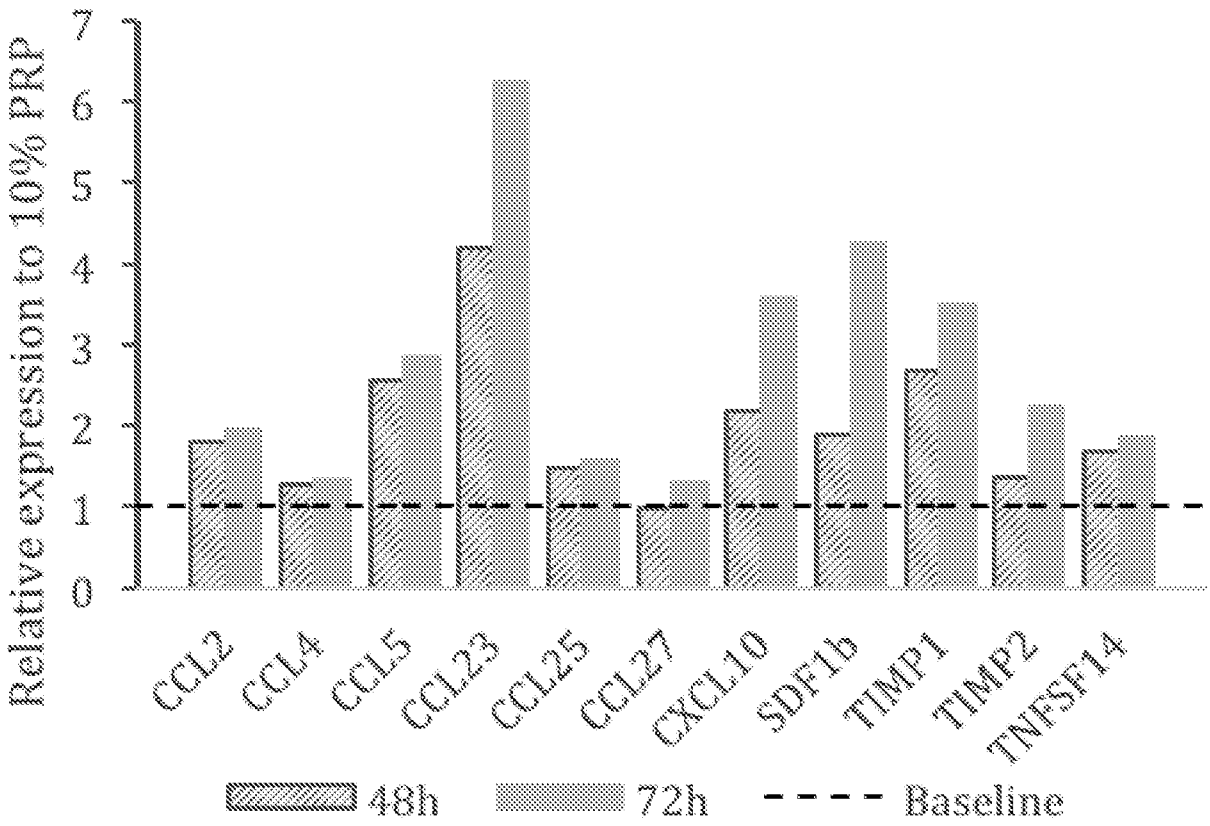
SEN-MSCs in a FPU
+ IL-2 Stimulation

FIG. 88



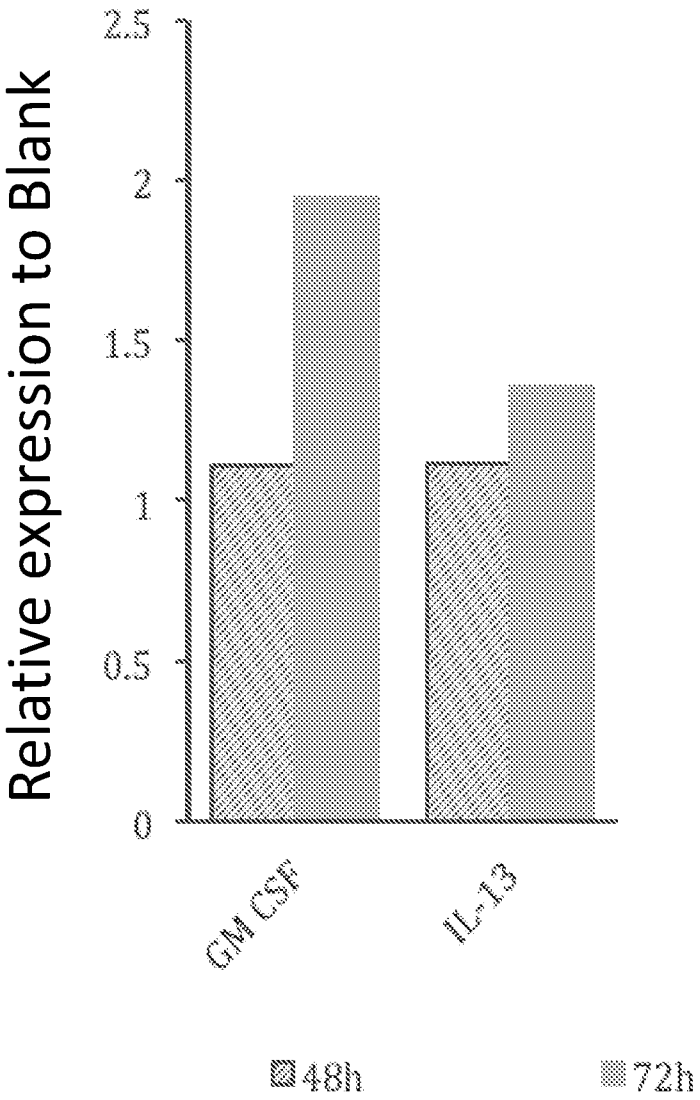
SEN-MSCs in a FPU
+ IL-2 Stimulation

FIG. 89



SEN-MSCs in a FPU
+ IL-2 Stimulation

FIG. 90



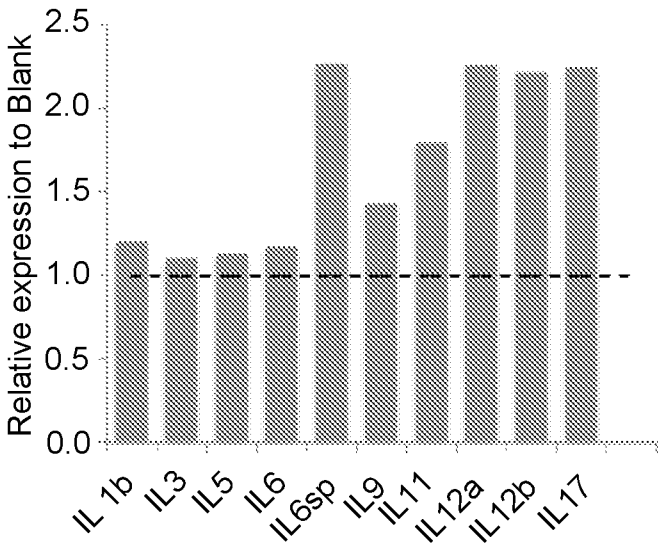
SEN-MSCs in a FPU
+ IL-2 Stimulation

FIG. 91

Interleukins

10% PRP

IL 1b	Interleukin 1 beta
IL3	Interleukin 3
IL5	Interleukin 5
IL6	Interleukin 6
IL6ST	Interleukin 6ST
IL9	Interleukin 9
IL11	Interleukin 11
IL12a	Interleukin 12 alpha
IL12b	Interleukin 12 beta
IL17	Interleukin 17



Interleukins Receptors

10% PRP

IL1Ra	Interleukin 1 receptor alpha
IL1R1	Interleukin 1 receptor
IL1R2	Interleukin 1 receptor 2
IL1R4	Interleukin 1 receptor 4
IL2Ra	Interleukin 2 receptor alpha
IL5Ra	Interleukin 5 receptor alpha
IL6R	Interleukin 6 receptor
IL10Rb	Interleukin 10 receptor beta
IL13Ra	Interleukin 13 receptor alpha
IL18Rb	Interleukin 18 receptor b
IL21R	Interleukin 21 receptor

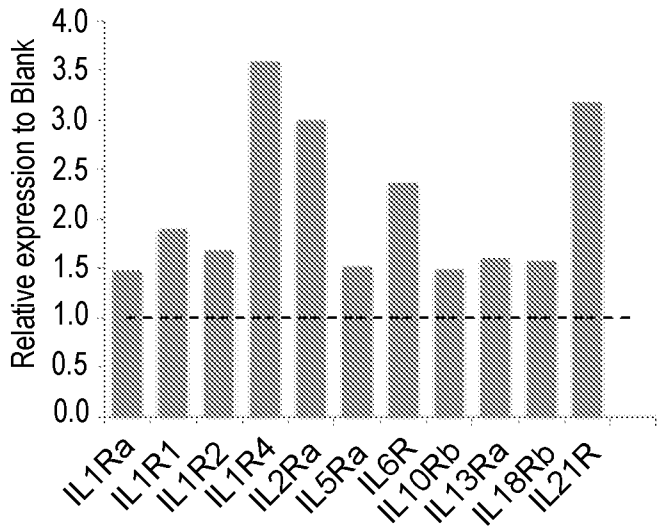
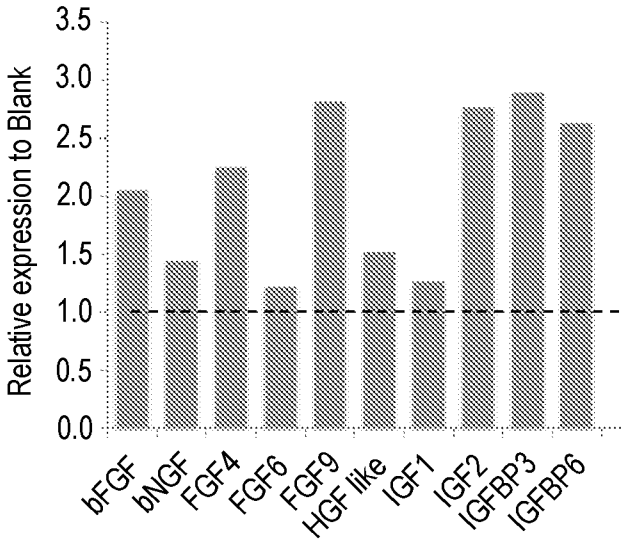


FIG. 92

Growth factors

10% PRP

bFGF	Basic fibroblast growth factor 2
bNGF	Beta-nerve growth factor
FGF4	Fibroblast growth factor 4
FGF6	Fibroblast growth factor 6
FGF9	Fibroblast growth factor 9
HGF like	Hepatocyte growth factor like
IGF1	Insulin growth factor 1
IGF2	Insulin growth factor 2
IGFBP3	Insulin growth factor binding protein 3
IGFBP6	Insulin growth factor binding protein 6
LAP	Transforming growth factor like
PDGFAA	Placenta derived growth factor A alpha
PDGFAB	Placenta derived growth factor A beta
PDGFBB	Placenta derived growth factor B beta
PLGF	Placenta growth factor
TGF b1	Transforming growth factor beta 1
TGF b2	Transforming growth factor beta 2
TGF b3	Transforming growth factor beta 3
VEGF	Vascular endothelial growth factor
VEGFD	Vascular endothelial growth factor D



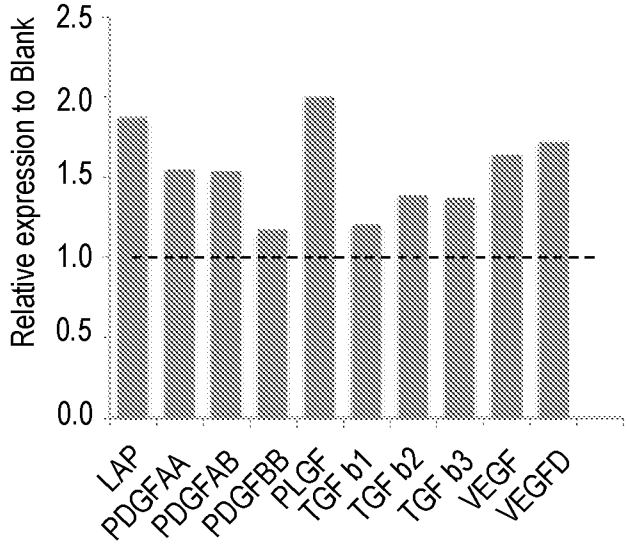
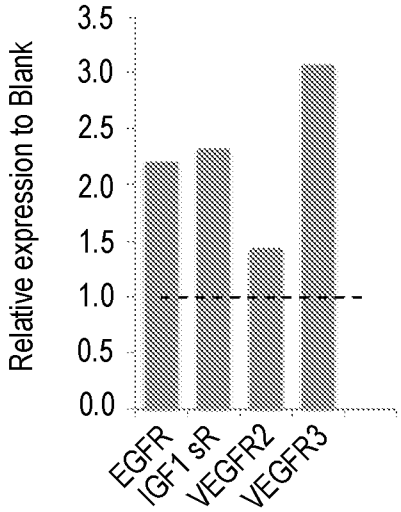


FIG. 93

Growth factor Receptors

10% PRP

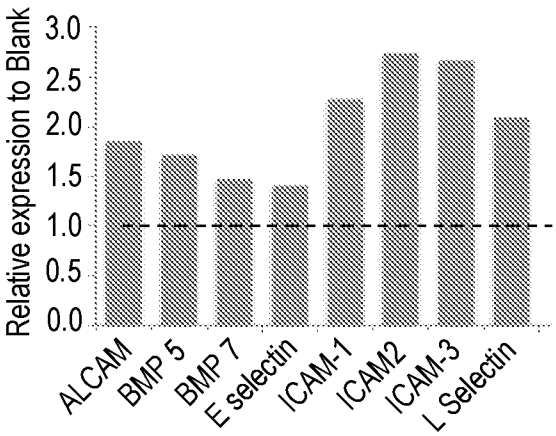
EGFR	Epithelial growth factor receptor
IGF1 sR	Interleukin 1 receptor 2
VEGFR2	Interleukin 1 receptor 4
VEGFR3	Interleukin 2 receptor alpha



Adhesion and proliferation

10% PRP

ALCAM	Activated leukocyte cell adhesion molecule
BMP 5	Bone morphogenic protein 5
BMP 7	Bone morphogenic protein 7
E selectin	Endothelial leukocyte adhesion molecule
ICAM-1	Intracellular adhesion molecule 1
ICAM2	Intracellular adhesion molecule 2
ICAM-3	Intracellular adhesion molecule 3
L Selectin	Lymphocytes adhesion molecule
MMP 1	Matrix metalloproteinase 1
MMP 3	Matrix metalloproteinase 3
MMP 9	Matrix metalloproteinase 9
MMP 13	Matrix metalloproteinase 13
PECAM 1	Platelet endothelial cell adhesion molecule
TIMP1	Metallopeptidase inhibitor 1
TIMP2	Metallopeptidase inhibitor 2



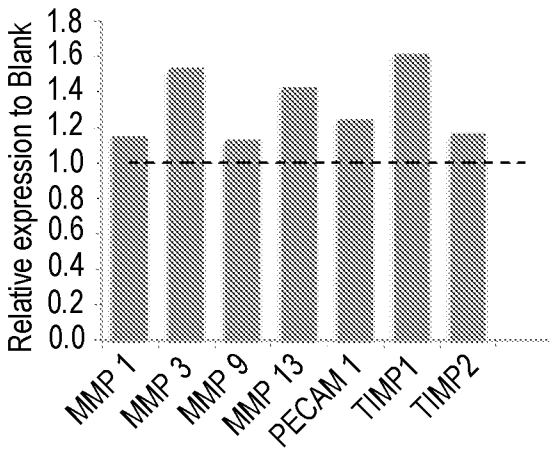


FIG. 94

Necrosis and neurotrophic factors

10% PRP

GDNF	Glial derived neurotrophic factor
GITR	TNF receptor family 18
GITR LG	TNF family 18
TNFa	Tumor necrosis factor alpha
TNFb	Tumor necrosis factor beta
TNFRSF10C	TNF receptor family 10C
TNFRSF10D	TNF receptor family 10D
TNFRSF6	TNF receptor family 6
TNFSF14	TNF family 14
TNFSF6	TNF family 6
TNFSRF1A	TNF receptor family 1A

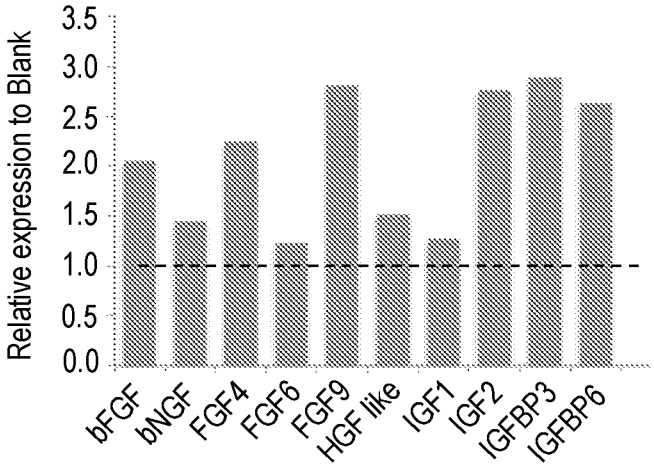
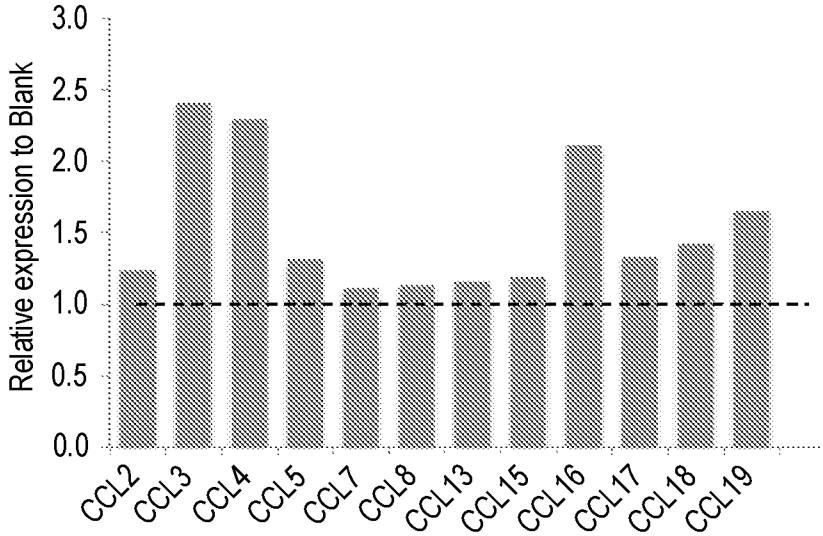


FIG. 95

Chemokines

10% PRP

CCL2	Chemokine ligand 2
CCL3	Chemokine ligand 3
CCL4	Chemokine ligand 4
CCL5	Chemokine ligand 5
CCL7	Chemokine ligand 7
CCL8	Chemokine ligand 8
CCL13	Chemokine ligand 13
CCL15	Chemokine ligand 15
CCL16	Chemokine ligand 16
CCL17	Chemokine ligand 17
CCL18	Chemokine ligand 18
CCL19	Chemokine ligand 19
CCL20	Chemokine ligand 20
CCL22	Chemokine ligand 22
CCL24	Chemokine ligand 24
CCL25	Chemokine ligand 25
CCL26	Chemokine ligand 26
CCL27	Chemokine ligand 27
CXCL1	Chemokine ligand 1
CXCL1/2/3	Chemokine ligand 1/2/3
CXCL5	Chemokine ligand 5
CXCL9	Chemokine ligand 9
CXCL10	Chemokine ligand 10
CXCL11	Chemokine ligand 11



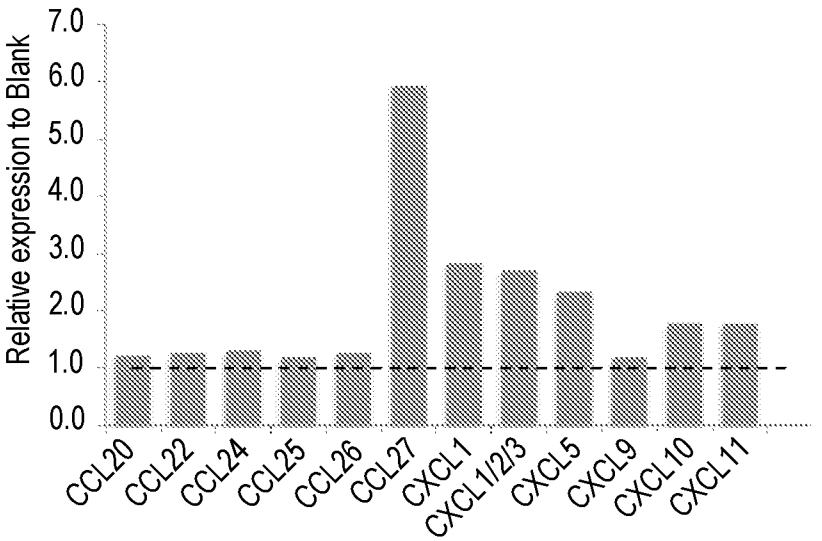


FIG. 96

Other factors

10% PRP

Activin A	Activin A
Adipoq	Adiponectin
AgRP	Agouti related protein
ANGPT2	Agiopoietin-2
AREG	Amphiregulin
Axl	Tyrosine-protein kinase receptor UFO
BTC	Betacellulin
CD14	Monocyte differentiation antigen
CD80	Monocyte differentiation antigen
CT-1	Cardiotropin-1
Dtk	Tyrosine-protein kinase receptor TYRO3
ENG	Endoglin
ErbB3	Receptor tyrosine-protein kinase erB-3
LEP	Leptin
LEPR	Leptin Receptor
LIF	Leukemia inhibitor factor
MIF	Macrophage migration inhibitory factor
NT-3	Neutrophin-3
NT-4	Neutrophin-4
OPG	Osteoprotegerin
OSM	Oncostatin M
PPBP	Platelet basic protein
PRL	Prolactin
SCF	Stem cell factor
SCF R	Stem cell factor receptor
SDF1a	Stromal derived factor 1 alpha
SDF1b	Stromal derived factor 1 beta
THPO	Thrombopoietin
TIE-1	Angiopoietin 1 receptor
TIE-2	Angiopoietin 1 receptor

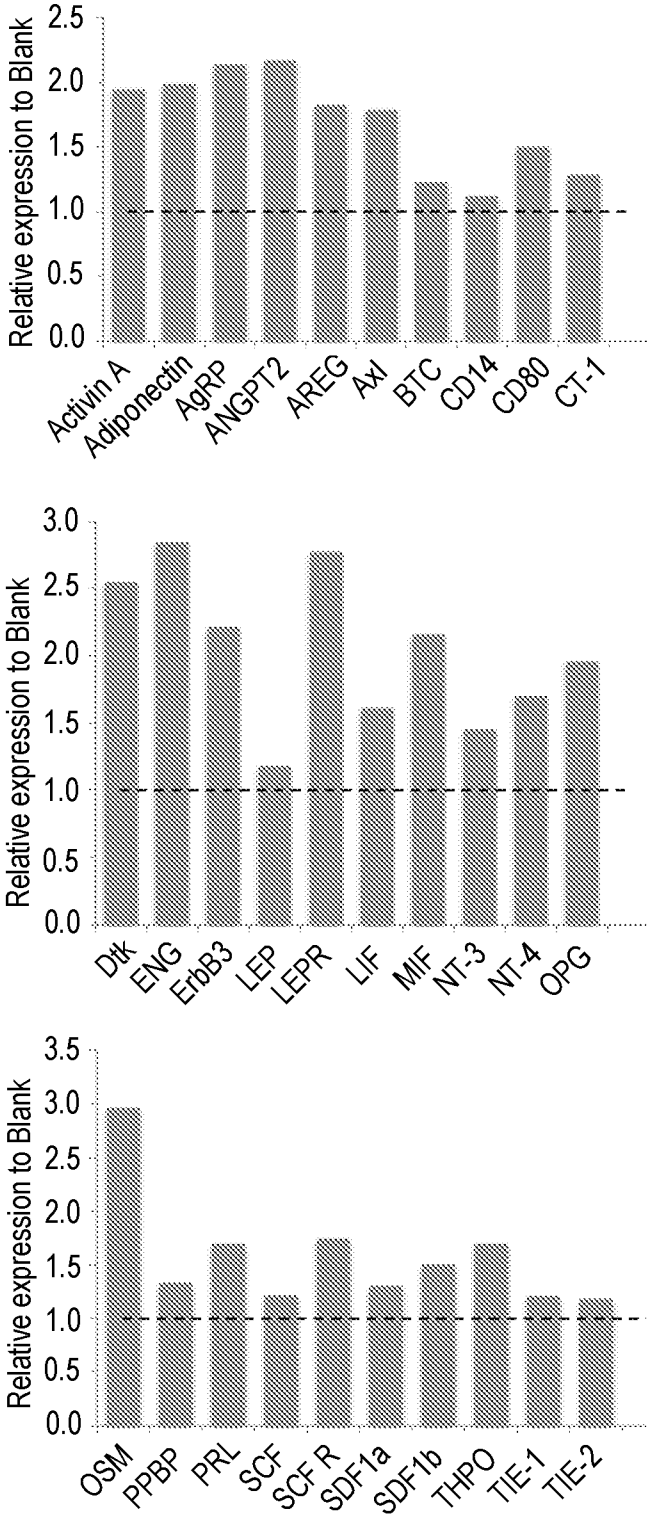
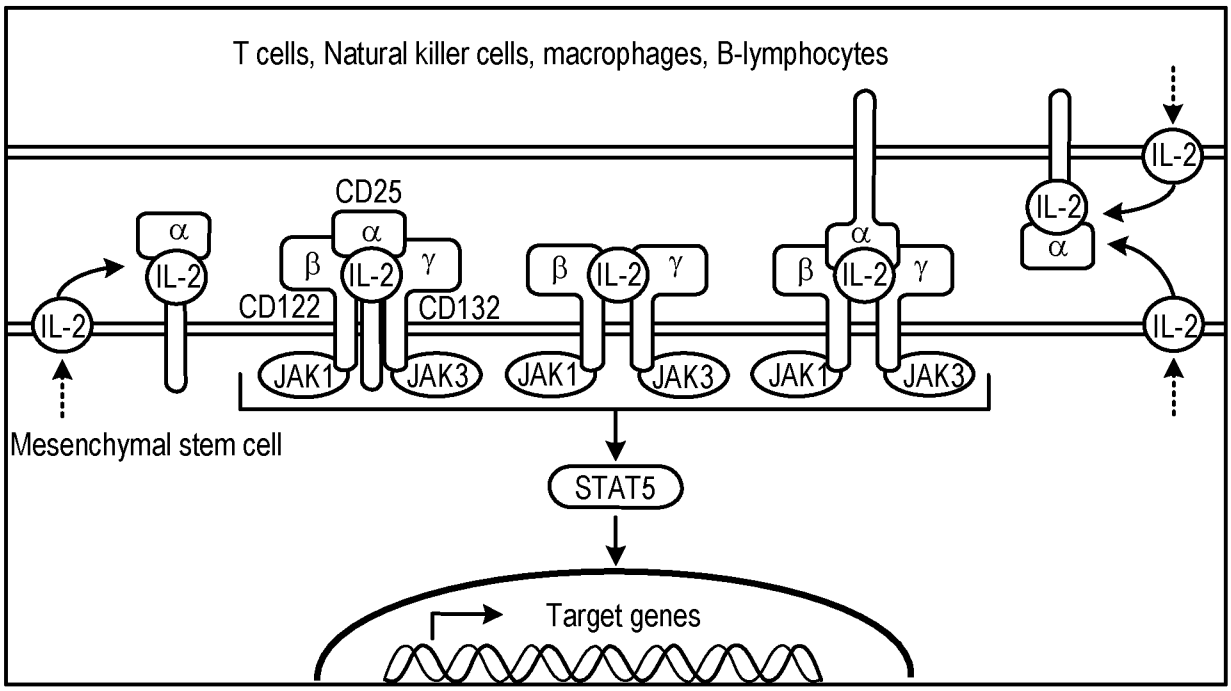


FIG. 97 **Transrepresentation of IL-2R alpha (CD25)**



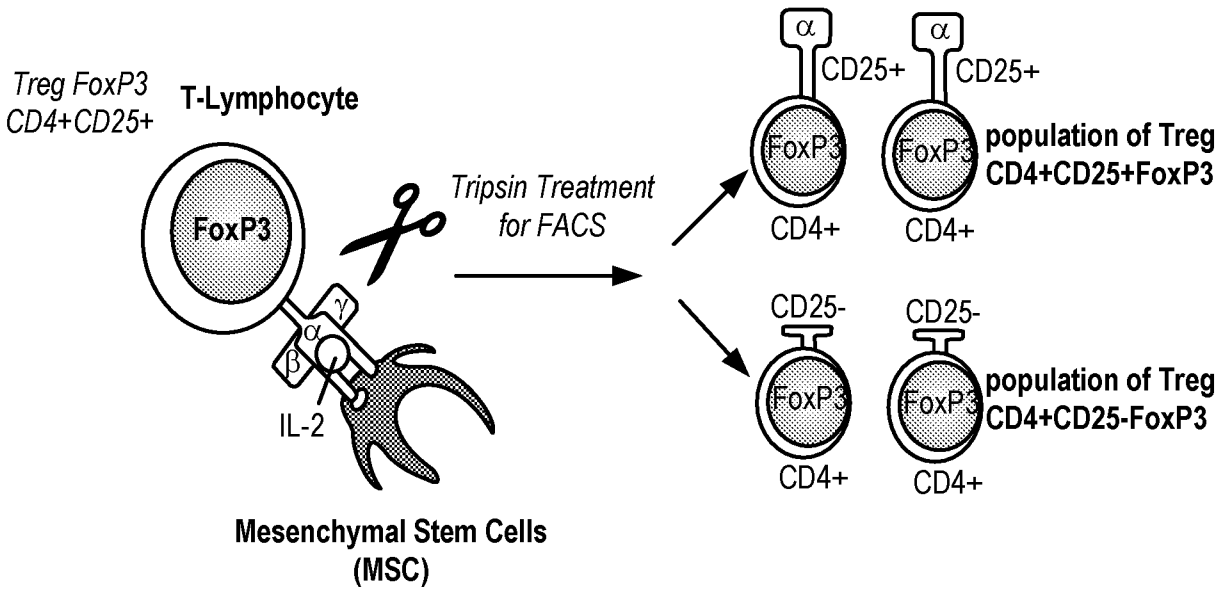


FIG. 97
(Continued)

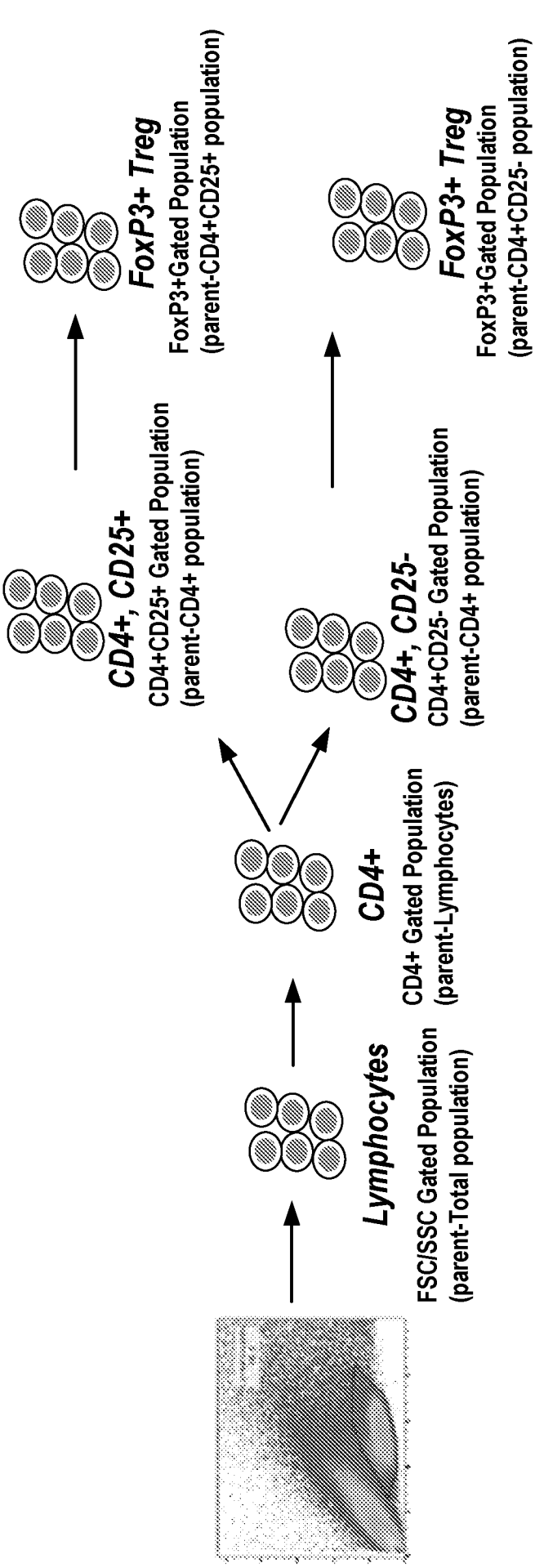


FIG. 98

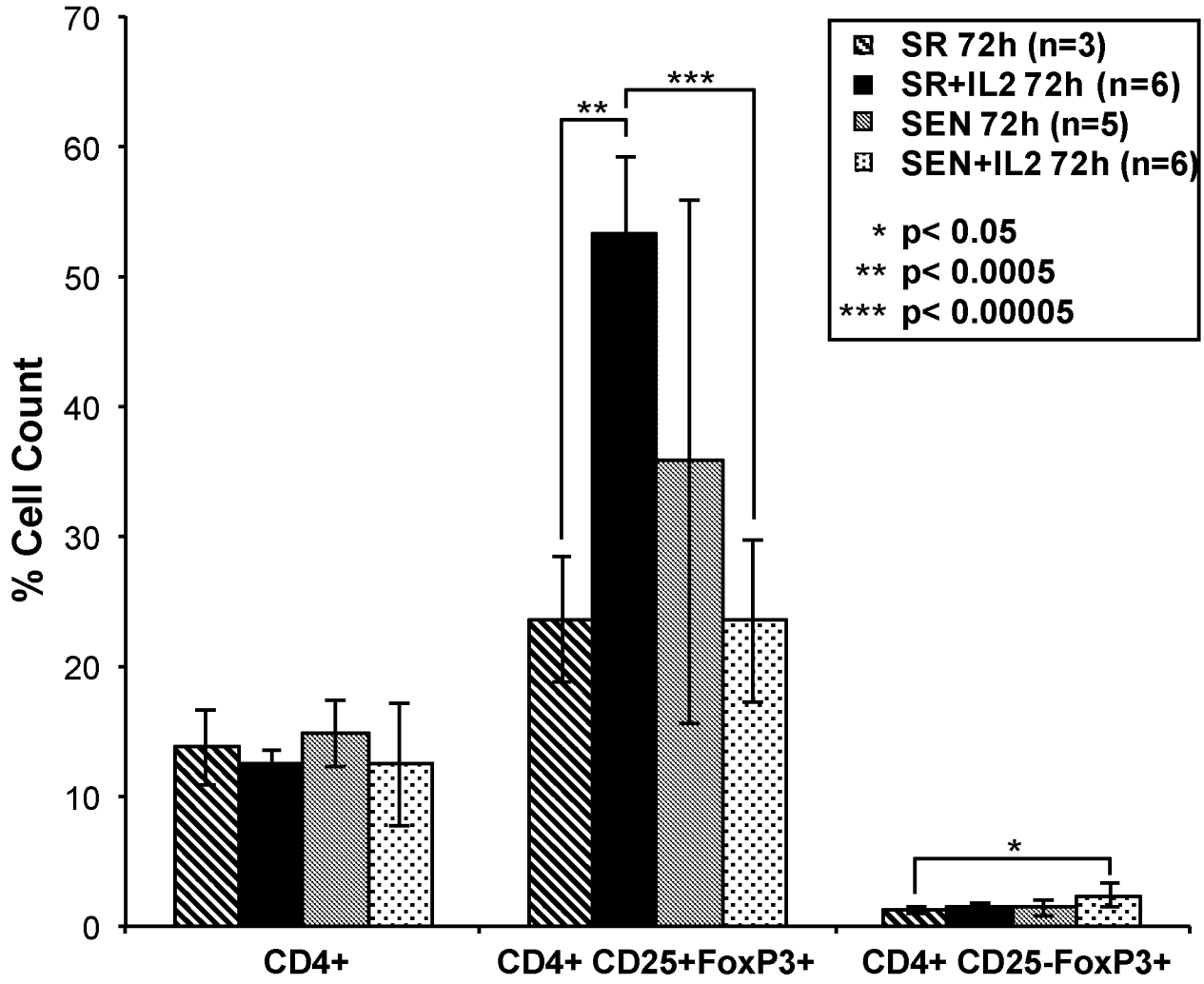
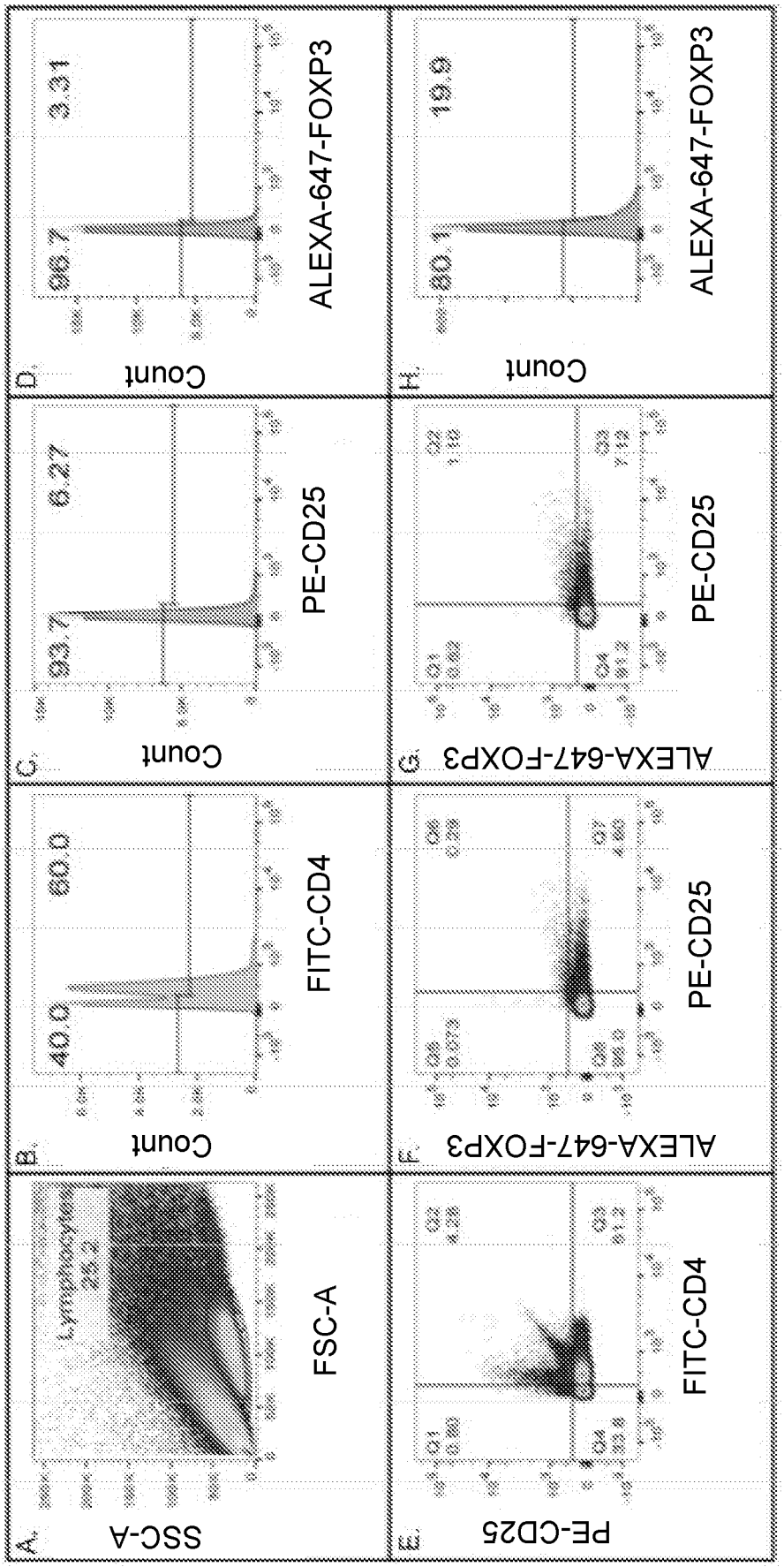

70
60
50
40
30
20
10
0
% Cell Count
SR 72h (n=3)
SR+IL2 72h (n=6)
SEN 72h (n=5)
SEN+IL2 72h (n=6)
* p< 0.05
** p< 0.0005
*** p< 0.00005
**
***
*
CD4+
CD4+ CD25+FoxP3+
CD4+ CD25-FoxP3+

FIG. 99



Full Gating Path	Count	Freq. of Parent	Freq. of Total
Ungated	6.37E5	100	100
Lymphocytes	160120	25.2	25.2
Lymphocytes/ALEXA-647-FOXP3(+)	5307	3.31	0.83
Lymphocytes/PE-CD25(+)	10047	6.27	1.58
Lymphocytes/FITC-CD4(+)	96122	60.0	15.1
Lymphocytes/FITC-CD4(+)/PE-CD25(+)	7896	8.21	1.24
Lymphocytes/FITC-CD4(+)/PE-CD25(+)/ALEXA-647-FOXP3(+)	1571	19.9	0.25
Lymphocytes/FITC-CD4(+)/PE-CD25(-)/ALEXA-647-FOXP3(+)	2442	2.77	0.38

FIG. 100

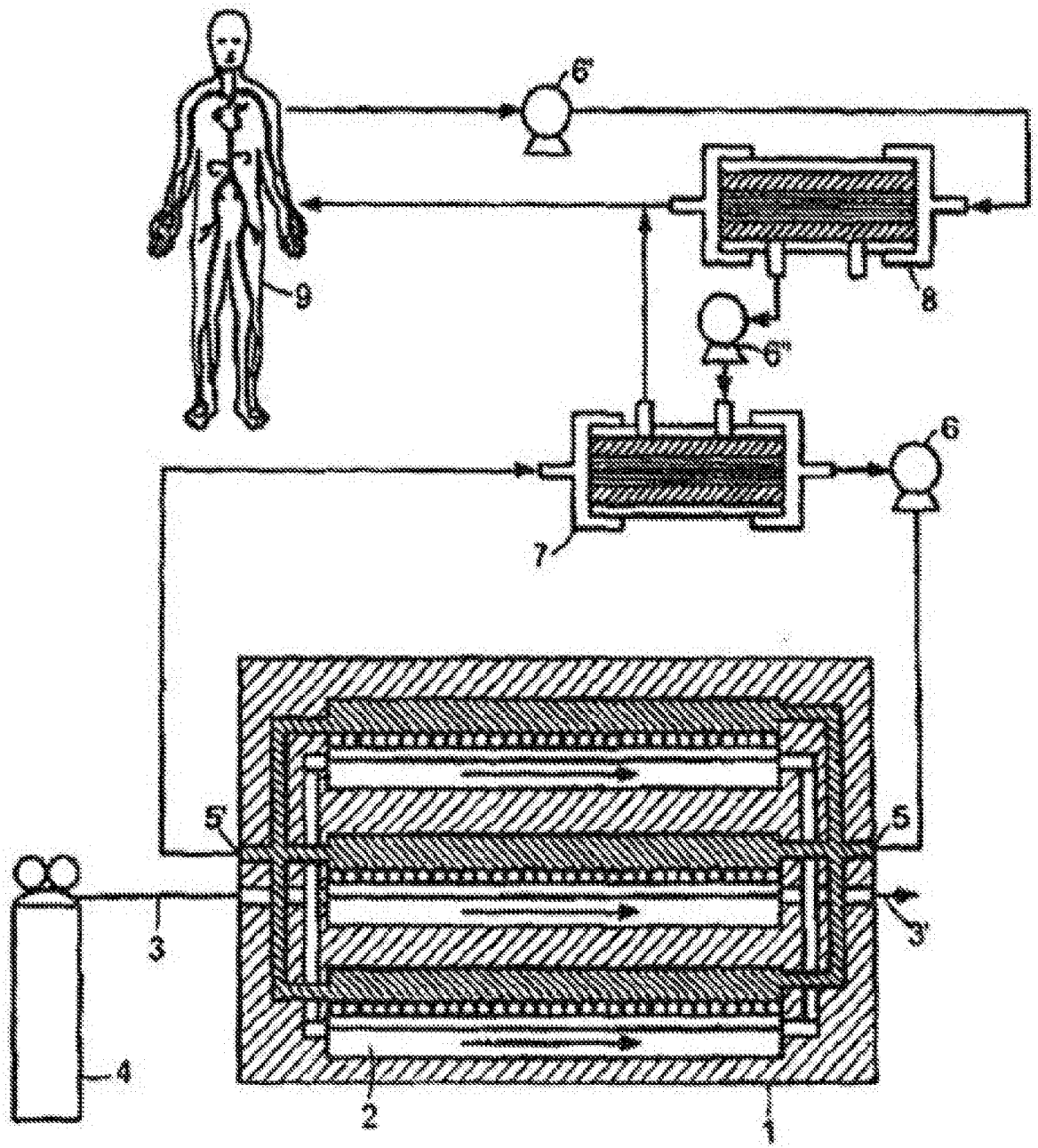


FIG. 101

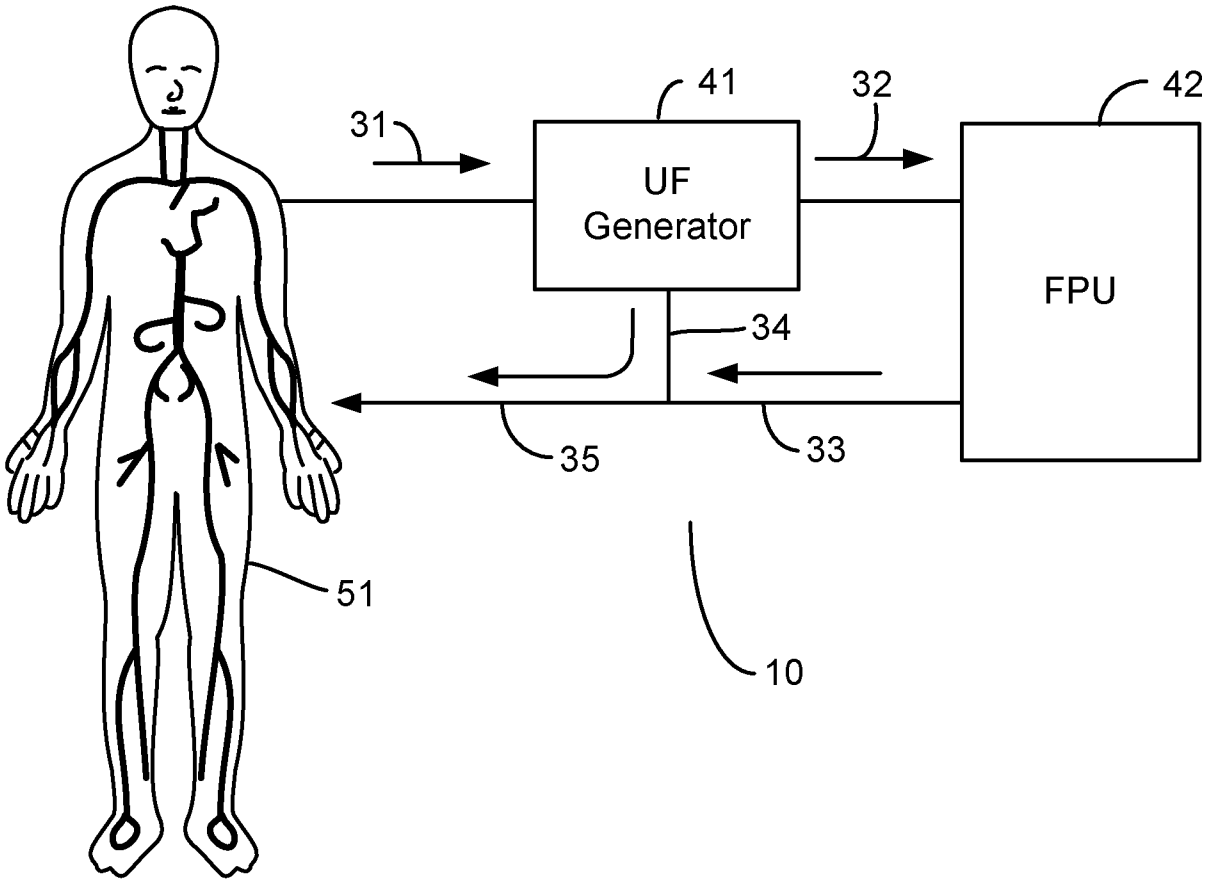


FIG. 102

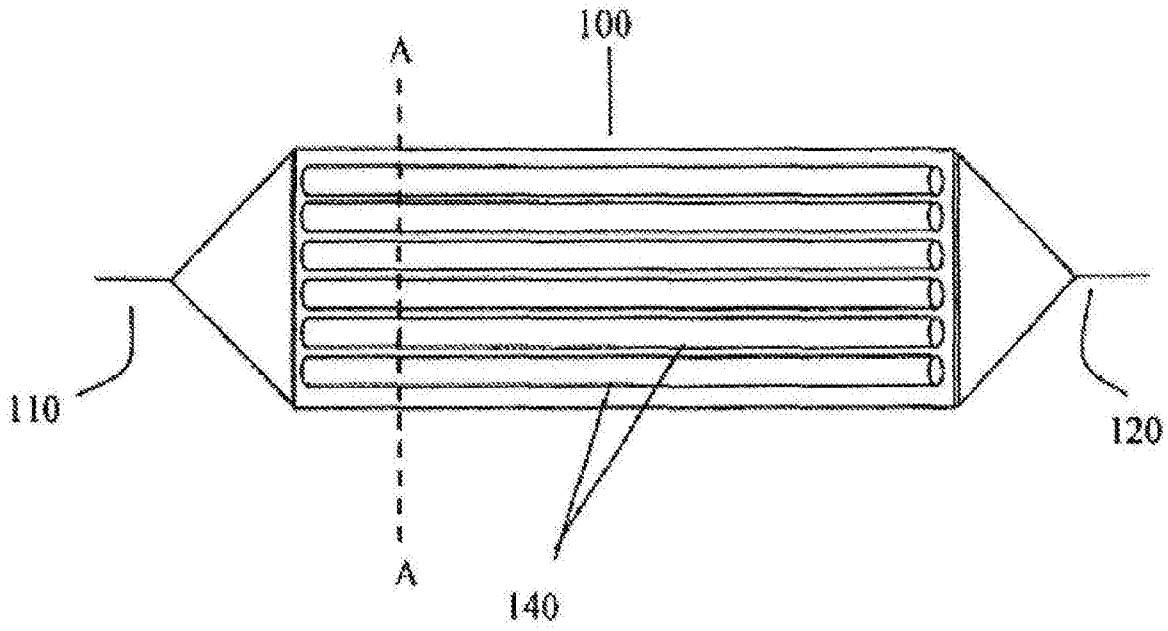


FIG. 103

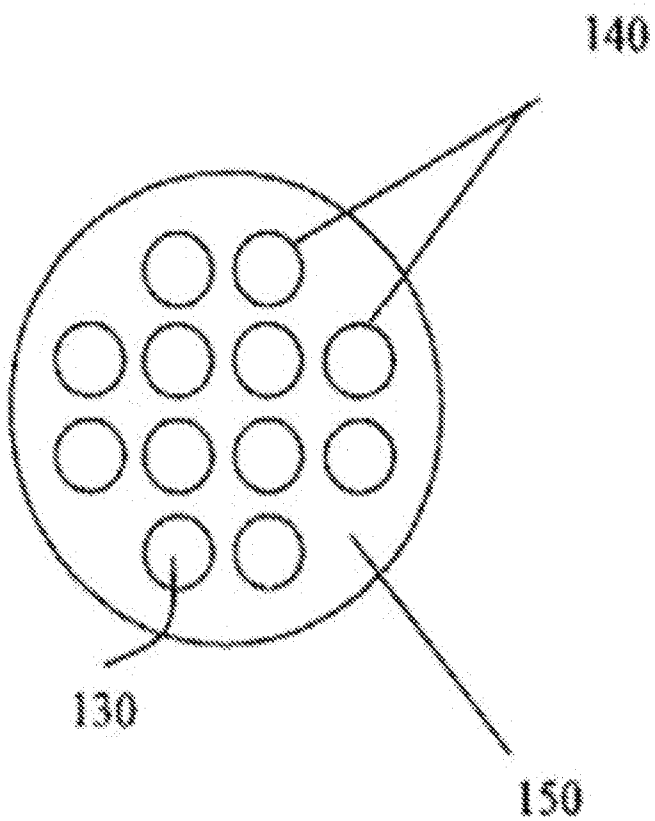


FIG. 104

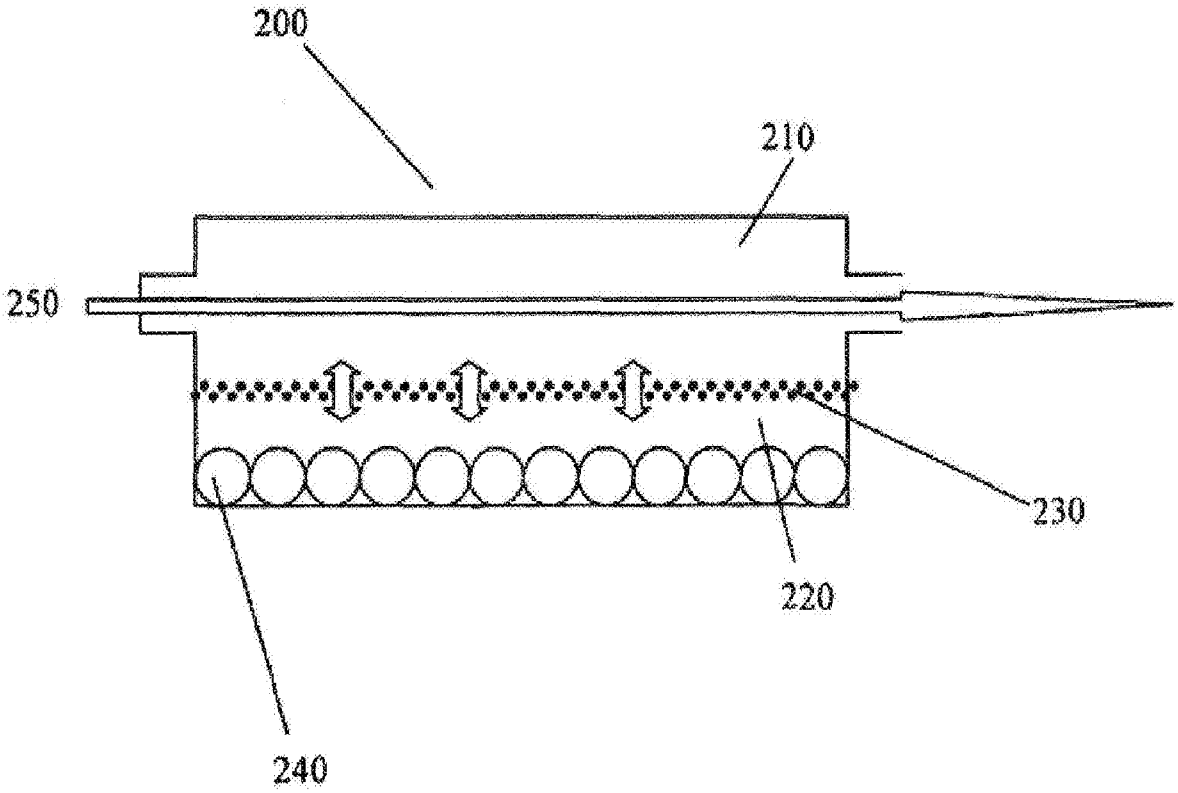
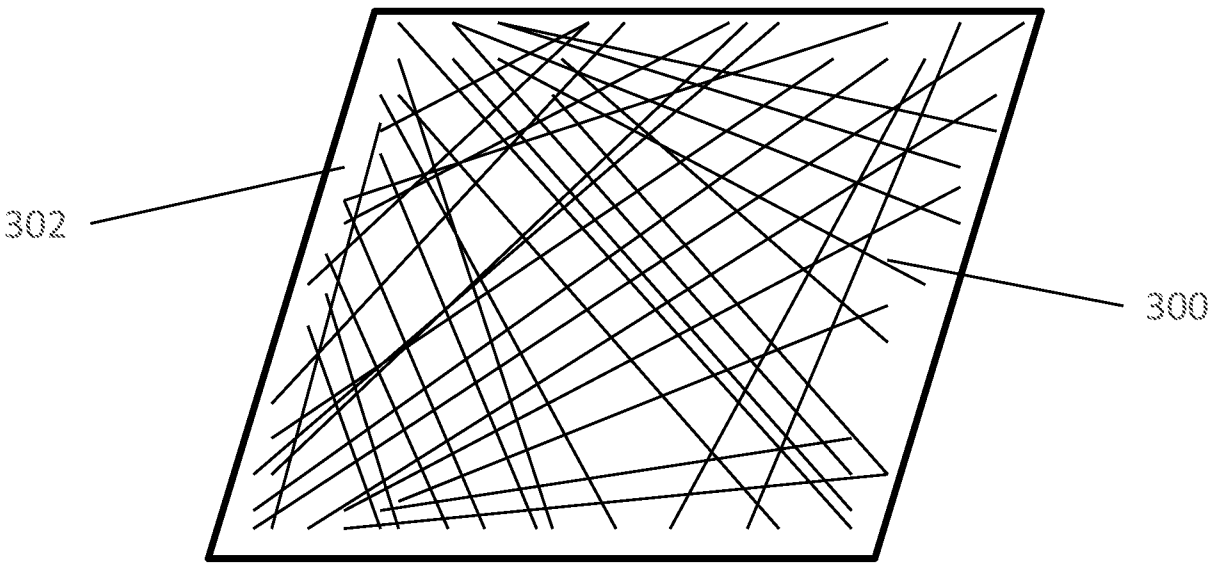


FIG. 105



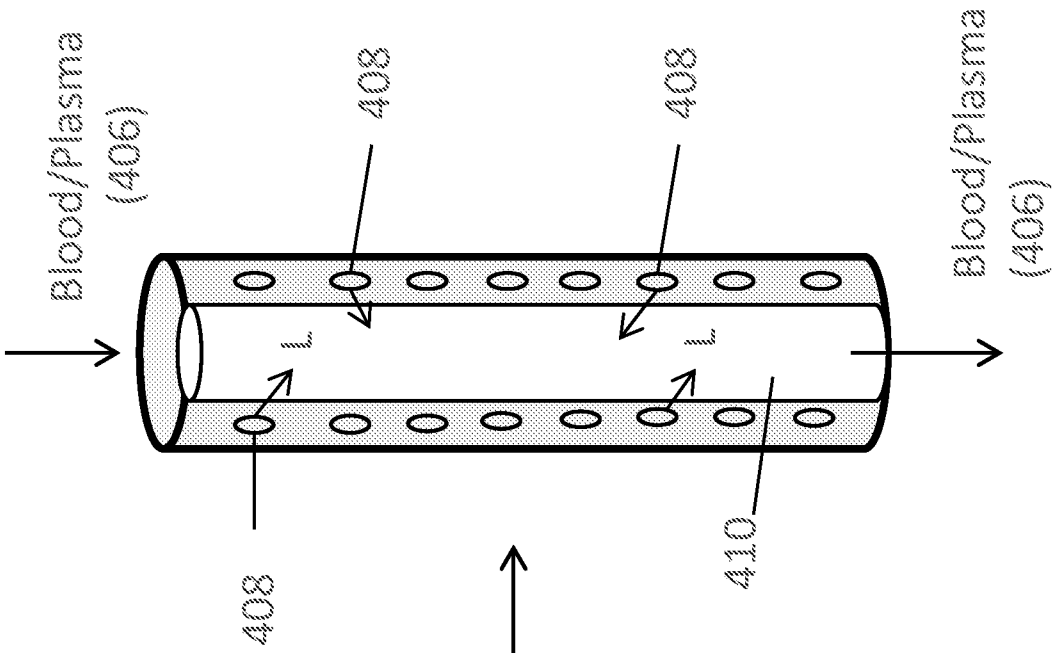


FIG. 106B

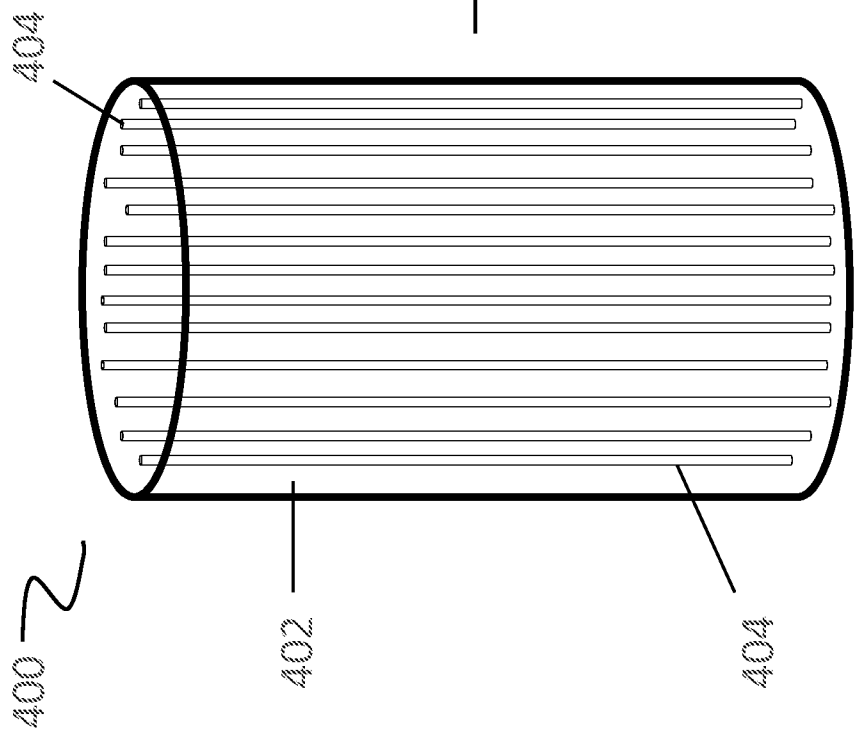


FIG. 106A

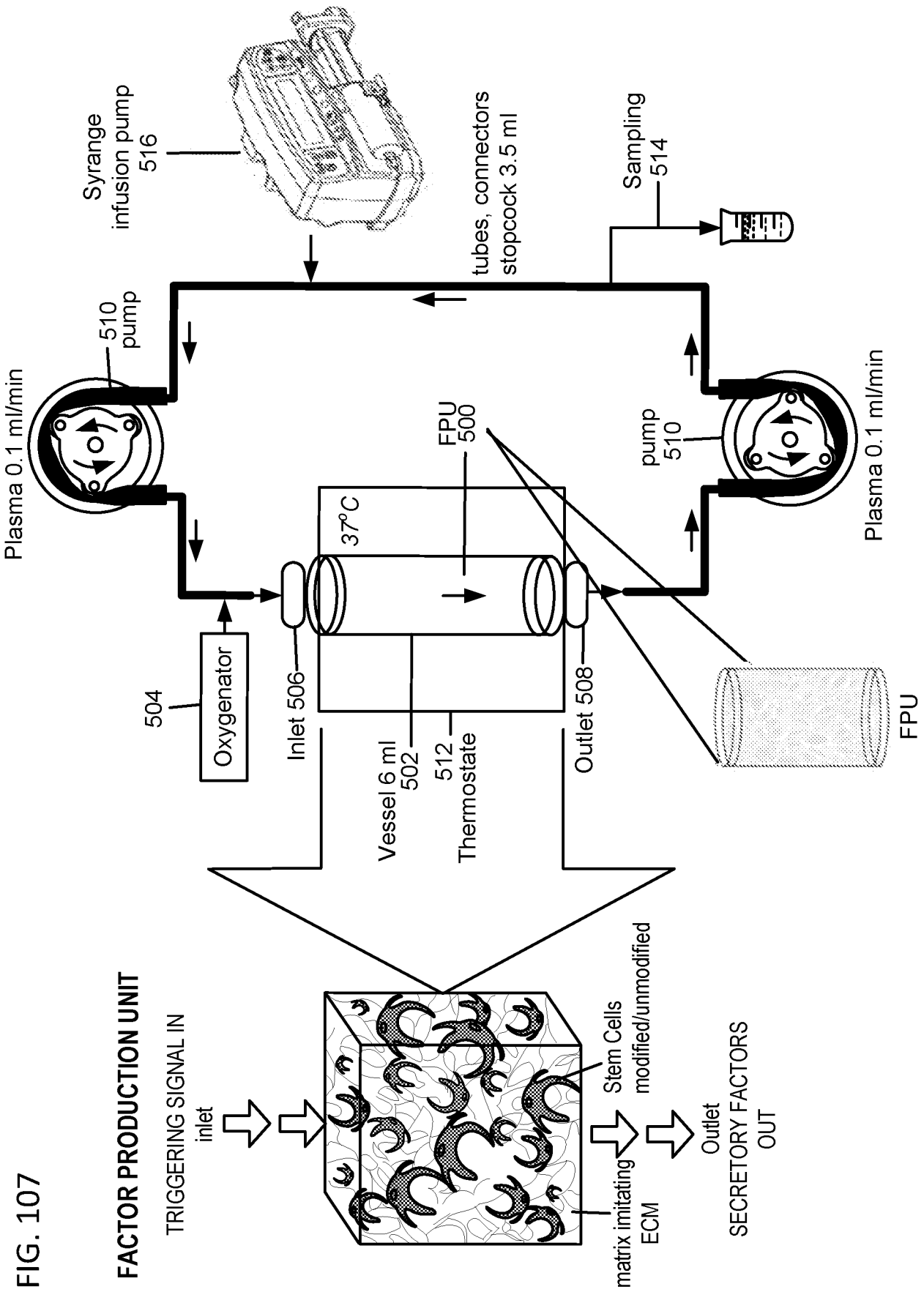
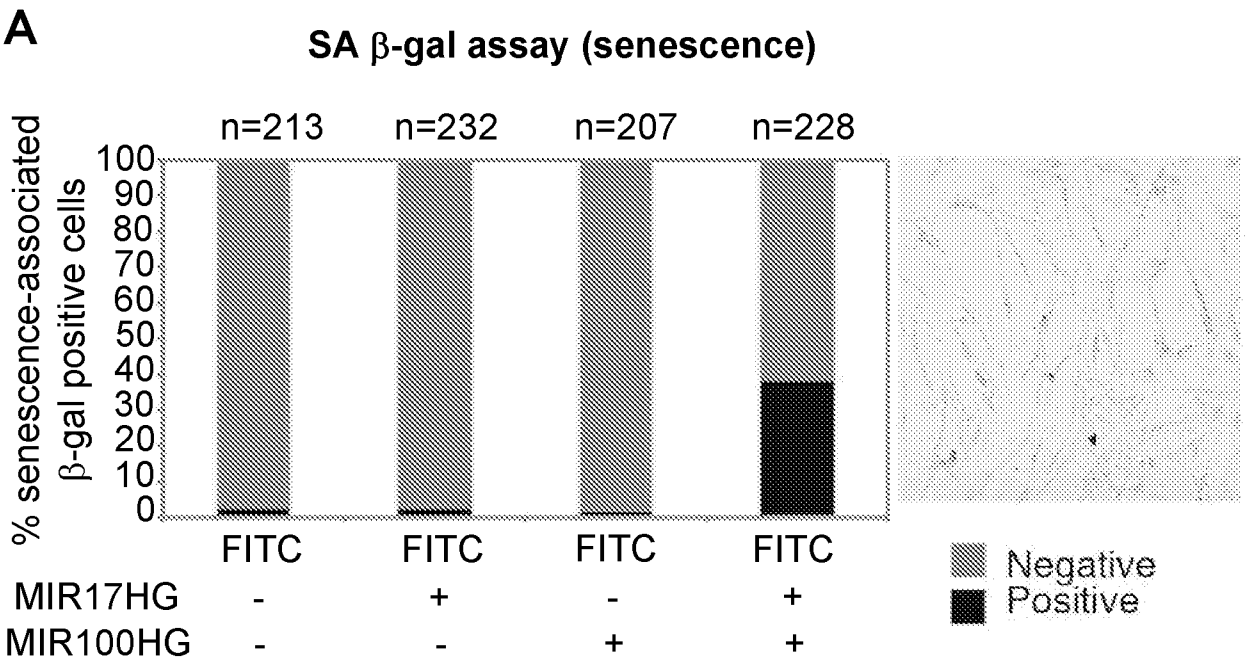

Syrange infusion pump 516
tubes, connectors stopcock 3.5 ml
Sampling 514
510 pump
Plasma 0.1 ml/min
FPU 500
pump 510
Plasma 0.1 ml/min
37°C
504
Oxygenator
Inlet 506
Vessel 6 ml 502
512 Thermostate
Outlet 508
FPU
FACTOR PRODUCTION UNIT
TRIGGERING SIGNAL IN
inlet
Stem Cells modified/unmodified
matrix imitating ECM
Outlet SECRETORY FACTORS OUT

FIG. 107

FIG. 108


A
SA β-gal assay (senescence)
n=213
n=232
n=207
n=228
% senescence-associated β-gal positive cells
100
90
80
70
60
50
40
30
20
10
0
FITC
FITC
FITC
FITC
MIR17HG - + - +
MIR100HG - - + +
Negative
Positive

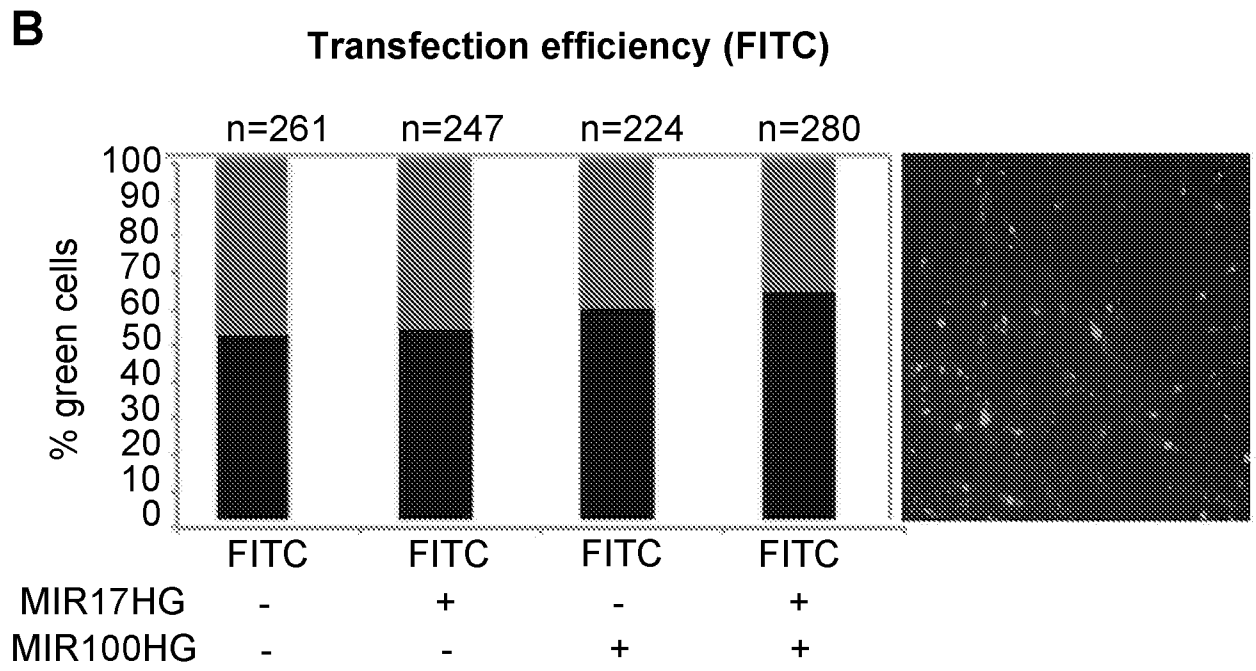

B
Transfection efficiency (FITC)
n=261
n=247
n=224
n=280
% green cells
100
90
80
70
60
50
40
30
20
10
0
FITC
FITC
FITC
FITC
MIR17HG - + - +
MIR100HG - - + +

FIG. 109

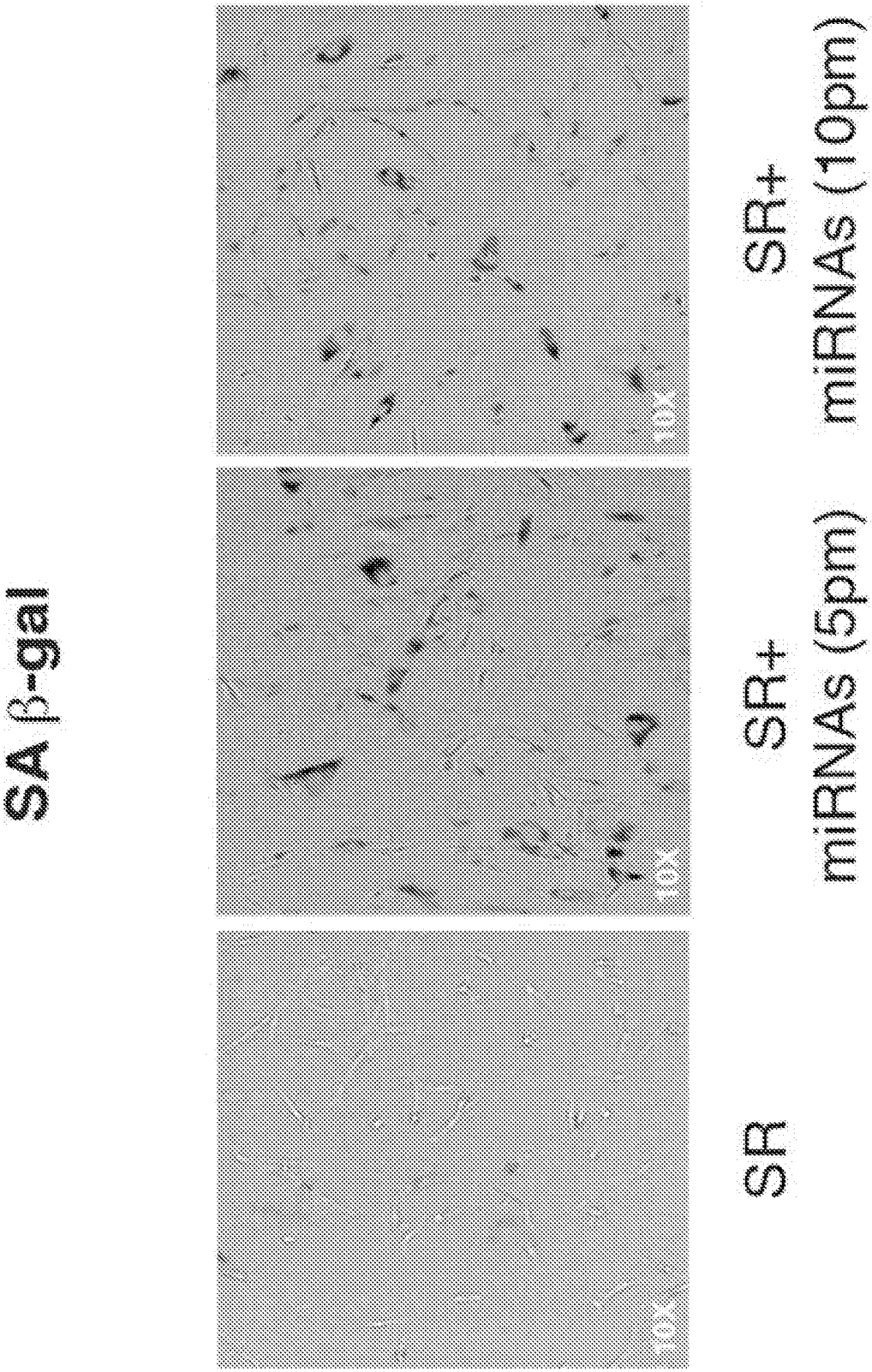


FIG. 110

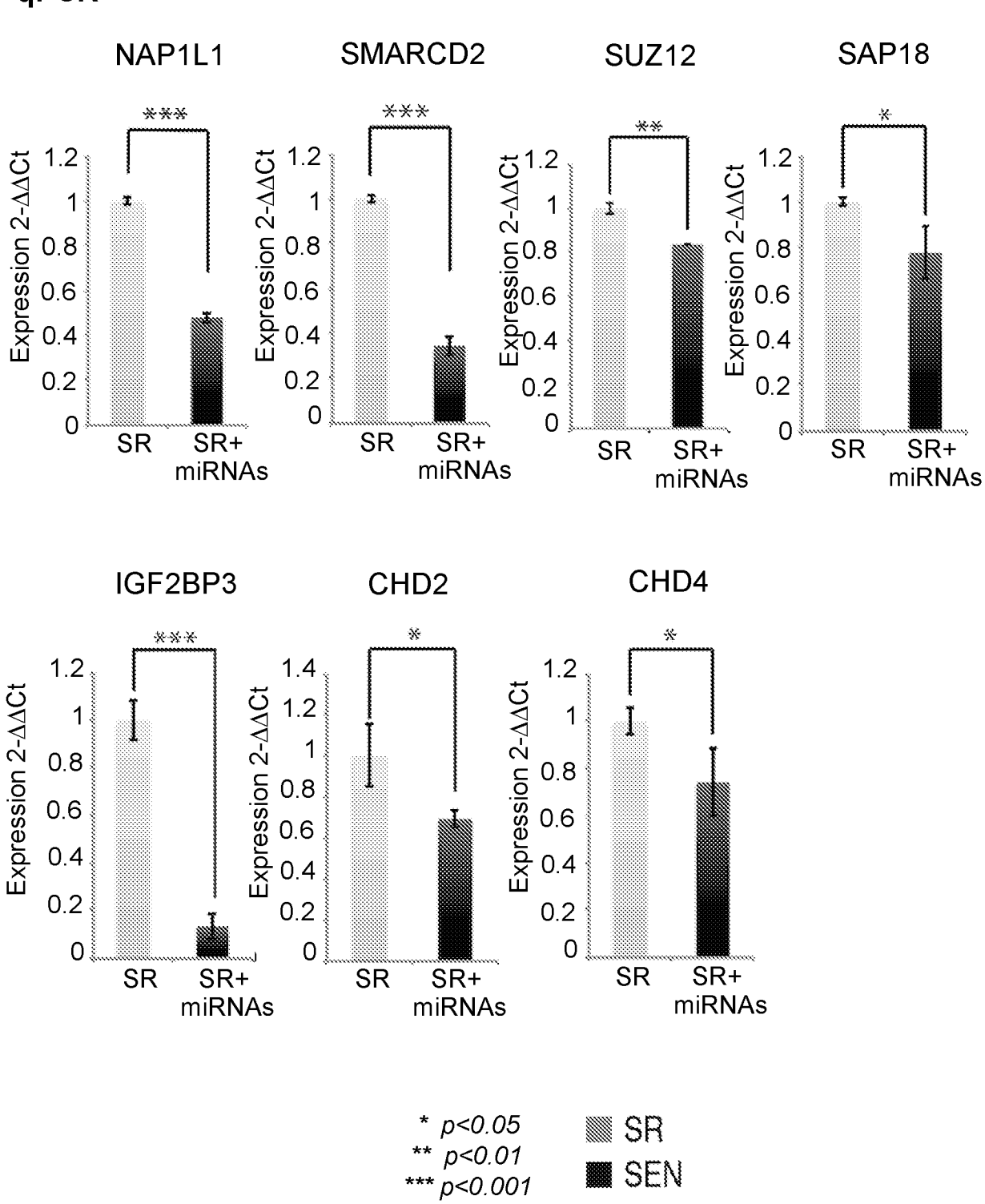
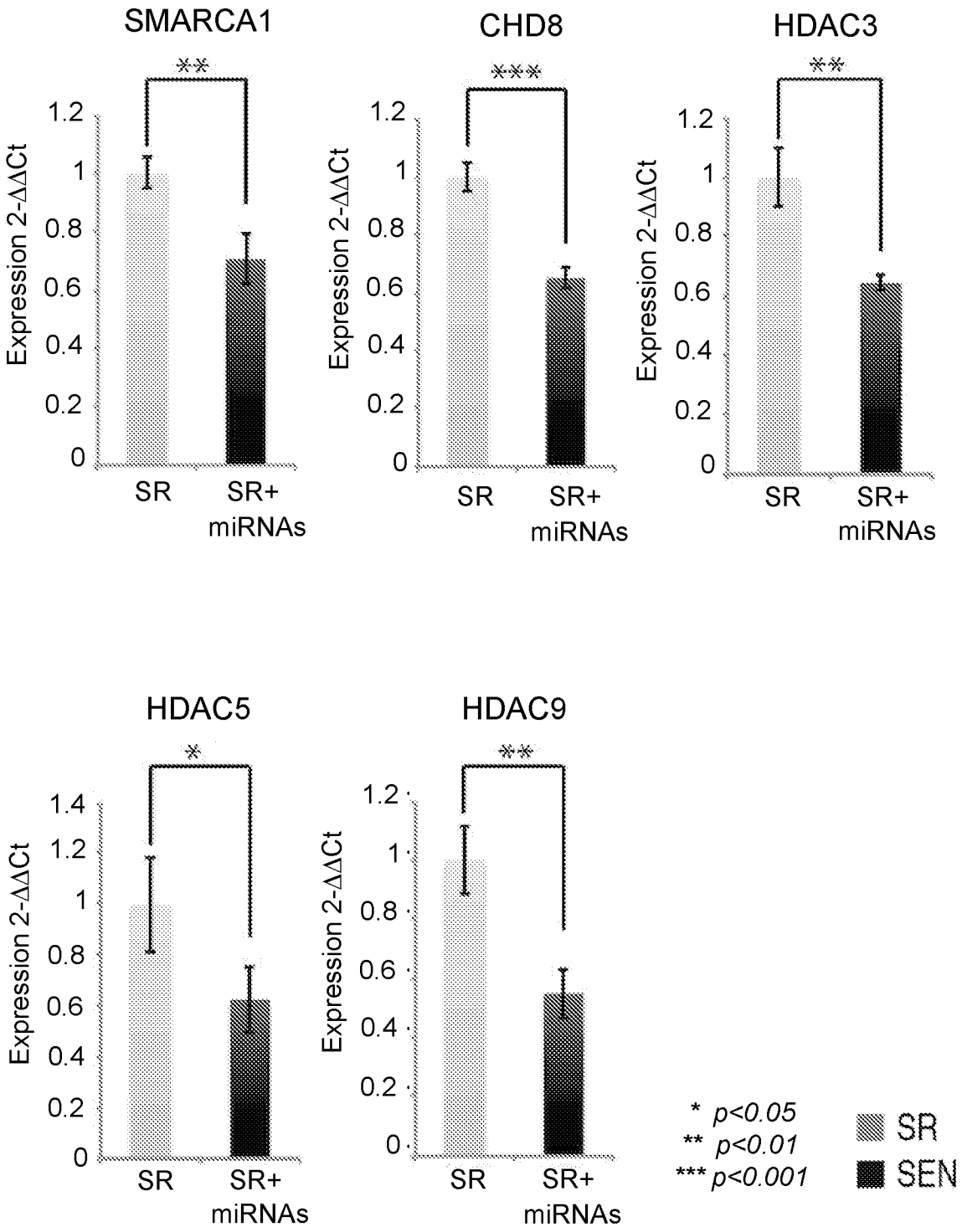

qPCR
NAP1L1
SMARCD2
SUZ12
SAP18
IGF2BP3
CHD2
CHD4
Expression 2-ΔΔCt
SR
SR+ miRNAs
* p<0.05
** p<0.01
*** p<0.001
SR
SEN

FIG. 111


SMARCA1
CHD8
HDAC3
HDAC5
HDAC9
Expression 2-ΔΔCt
SR
SR+ miRNAs
* p<0.05
** p<0.01
*** p<0.001
SR
SEN

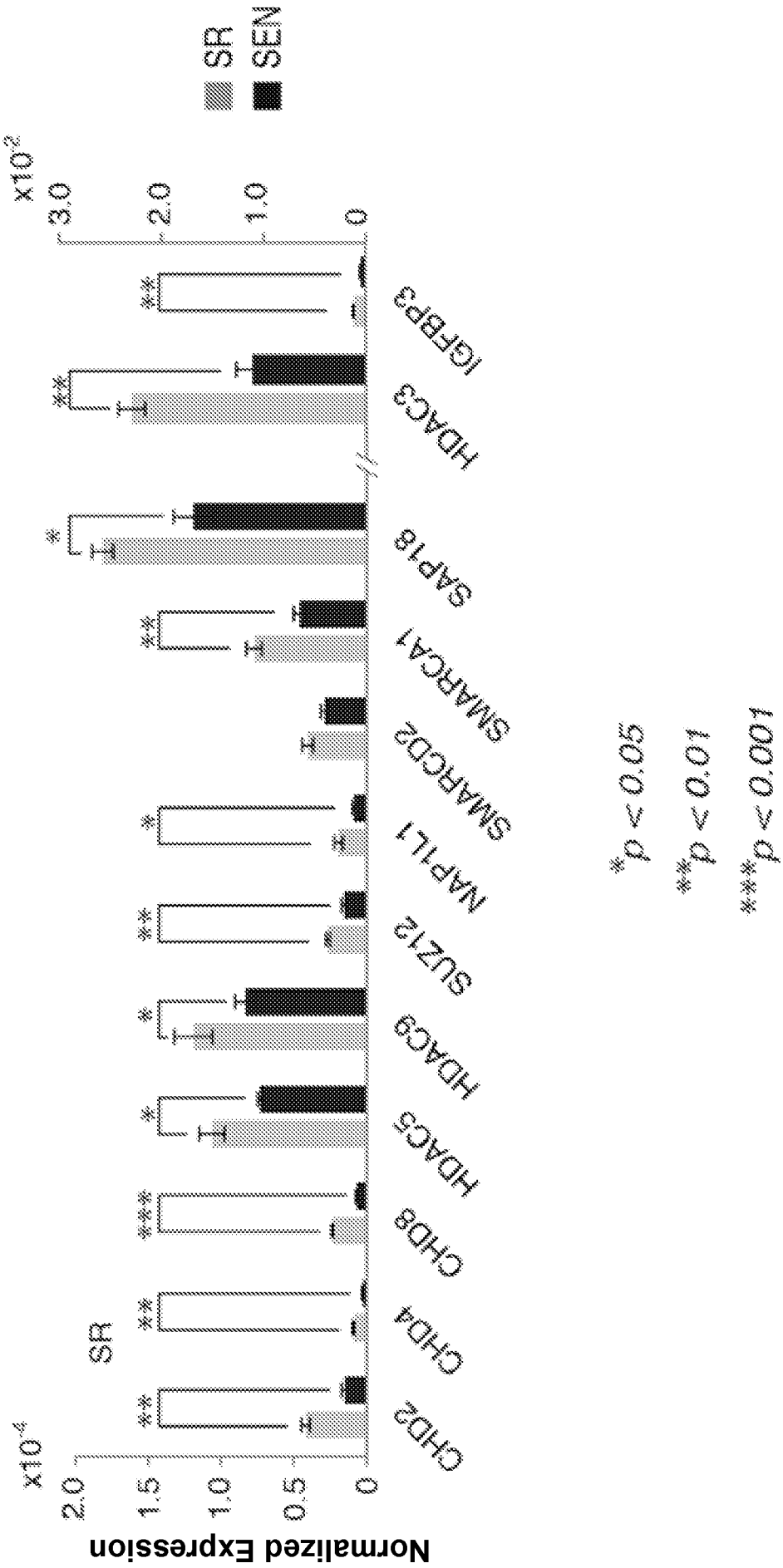
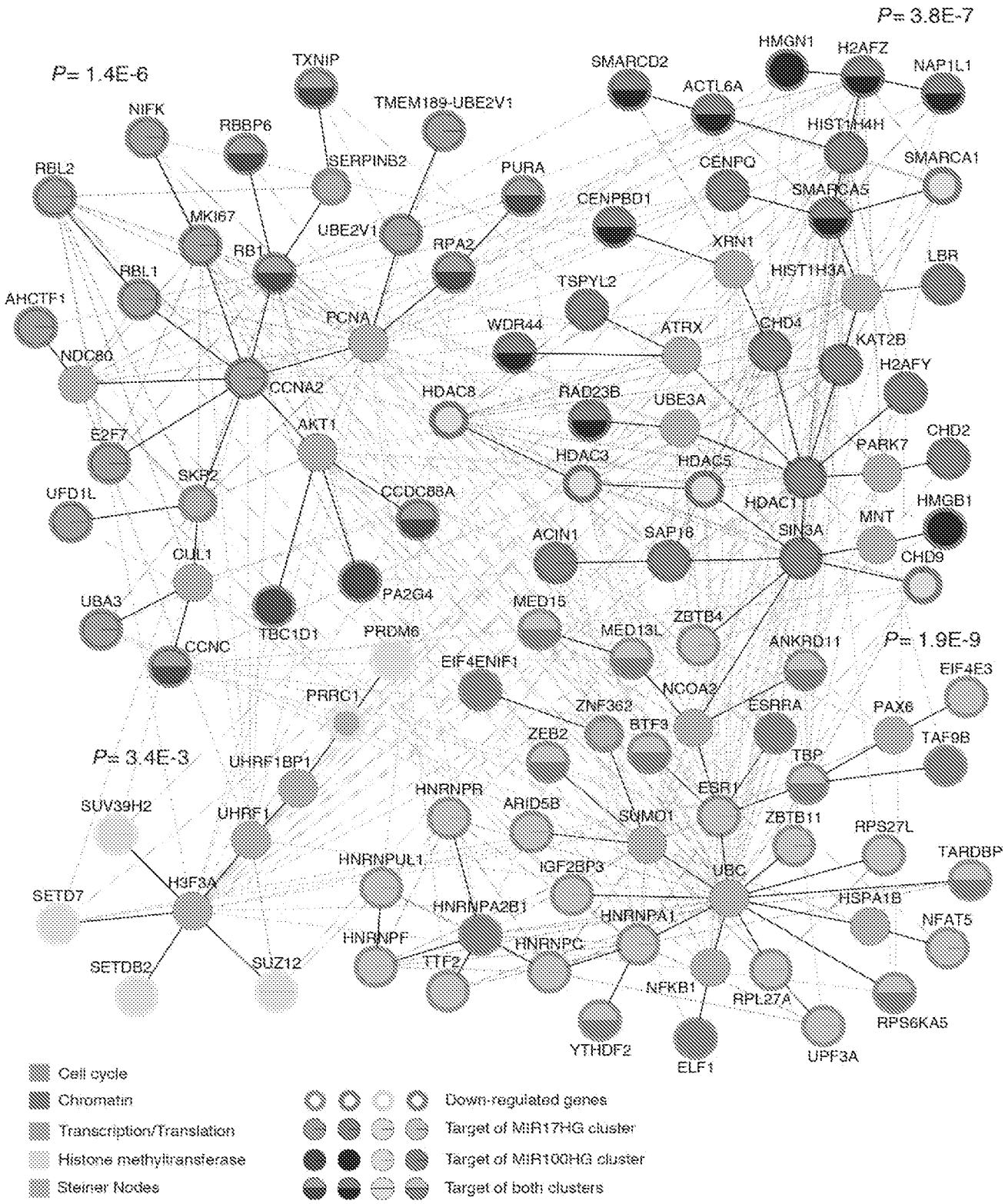

SR
SEM
x10-2
3.0
2.0
1.0
0
IGFBP3
HDAC3
SAP18
SMARCA1
SMARCD2
NAP1L1
SUZ12
HDAC9
HDAC5
CHD8
CHD4
CHD2
x10-4
2.0
1.5
1.0
0.5
0
SR
Normalized Expression
*p < 0.05
**p < 0.01
***p < 0.001

FIG. 112

FIG. 113


P= 3.8E-7
P= 1.4E-6
P= 1.9E-9
P= 3.4E-3
TXNIP
NIFK
RBBP6
TMEM189-UBE2V1
SERPINB2
RBL2
PURA
MKI67
UBE2V1
RB1
RPA2
RBL1
AHCTF1
PCNA
NDC80
CCNA2
E2F7
AKT1
SKP2
UFD1L
CCDC88A
CUL1
UBA3
TBC1D1
PA2G4
CCNC
PRDM6
PRRC1
UHRF1BP1
SUV39H2
UHRF1
SETD7
H3F3A
SETDB2
SUZ12
SMARCD2
HMGN1
H2AFZ
NAP1L1
ACTL6A
HIST1H4H
CENPQ
SMARCA1
SMARCA5
CENPBD1
XRN1
LBR
HIST1H3A
TSPYL2
WDR44
ATRX
CHD4
KAT2B
H2AFY
HDAC8
RAD23B
UBE3A
CHD2
PARK7
HDAC3
HDAC5
HDAC1
HMGB1
MNT
ACIN1
SAP18
SIN3A
CHD9
MED15
ZBTB4
MED13L
ANKRD11
EIF4ENIF1
EIF4E3
NCOA2
ZNF362
ESRRA
PAX6
ZEB2
BTF3
TAF9B
TBP
HNRNPR
ARID5B
SUMO1
ESR1
ZBTB11
RPS27L
TARDBP
HNRNPUL1
IGF2BP3
UBC
HSPA1B
HNRNPA2B1
HNRNPA1
NFAT5
HNRNPF
HNRNPC
TTF2
NFKB1
RPL27A
RPS6KA5
YTHDF2
ELF1
UPF3A
Cell cycle
Chromatin
Transcription/Translation
Histone methyltransferase
Steiner Nodes
Down-regulated genes
Target of MiR17HG cluster
Target of MiR100HG cluster
Target of both clusters

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 16/35487

A. CLASSIFICATION OF SUBJECT MATTER
IPC(8) - A61K 39/00, A61K 38/43 (2016.01)
CPC - A61K 35/545, A61K 38/00, A61K 35/28
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)
IPC(8): A61K 39/00, A61K 38/43 (2016.01)
CPC: A61K 35/545, A61K 38/00, A61K 35/28

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
USPC: 424/520, 514/7.6, 424/94.1

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
PatBase, Google Patents, Google Scholar, Google Web, search terms: stem cells, secreted factors, cytokines, secreted proteins, conditioned medium senescent cells, mesenchymal stem cell, IL-2, vesicular, stromal, plasma, blood, T-cells, treat, administer, injection, intravenous, dermatological

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X — Y	WO 2014/054004 A1 (CORION BIOTECH S.R.L) 10 April 2014 (10.04.2014) pg 4, ln 13-15, pg 6, ln 20-29, pg 7, ln2-3, ln 5-6, pg 8, ln 3-7, pg 9, ln 7-11	1-2, 11, 13, 16, 21 --- 3-10, 12, 14-15, 17-20, 22-24
Y	US 2012/0165216 A1 (SAMPER et al.) 28 June 2012 (28.06.2012) para [0001], [0004], [0022], [0095]	3-5, 9-10
Y	US 2014/0205563 A1 (MAGUIRE et al.) 24 July 2014 (24.07.2014) para [0014], [0055], [0069]	6-10, 12
Y	US 2011/0003008 A1 (LIM) 6 January 2011 (06.01.2011) para [0003], [0008], [0012], [0029], [0117], tables D3-D5	14-15, 20
Y	WO 2014/128634 A1 (PLURISTEM LTD) 28 August 2014 (28.08.2014) para [001], [002], [035], [0142], [0179], [0180], Tables 13-15	15, 17-20
Y	US 2013/0251670 A1 (RIORDAN et al.) 26 September 2013 (26.09.2013) abstract , para [0019]	22-24

☒ Further documents are listed in the continuation of Box C. ☐

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
19 October 2016	07 NOV 2016
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-8300	Authorized officer: Lee W. Young PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 16/35487

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	GLENN et al. Mesenchymal stem cells: Emerging mechanisms of immunomodulation and therapy. World J Stem Cells (26 November 2014) vol 6, no 5, pp 526-539, pg 530, col 2, para 1, Figs 3, 5	8
Y	FAN et al. Comparative study of regulatory T cells expanded ex vivo from cord blood and adult peripheral blood. Immunology (June 2012) Vol 136, no 2, pp 218?230, abstract, pg 219, col 1, para 1	23-24

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 16/35487

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

---------- see extra sheet ----------

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-24

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 16/35487

Continuation of Box No. III, Observations where unity of invention is lacking:

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I: Claims 1-24, directed to a method of treating a disease or disorder in an individual comprising delivering one or more factors produced by a population of stem cells to the individual or to a biological fluid from the individual.

Group II: Claims 25-45, 73-74, directed to a method of producing one or more factors comprising adding an inducing agent to a population of stem cells.

Group III: Claims 46-67 directed to a composition comprising a factor production unit.

Group IV: Claims 68-72, directed to a factor composition.

The inventions listed as Groups I through IV do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Special Technical Features

Group I requires a method of treating a disease or disorder, not required by groups II-IV.

Group II requires a method of inducing stem cells to produce one or more factors, not required by groups I, III-IV.

Group III requires a factor production unit comprising a substrate and a population of input stem cells, not required by groups I, II, IV.

Group IV requires a factor composition, not required by groups I-III.

Common Technical Features

The common technical feature shared by Groups I-IV is factors produced by stem cells.
The common technical feature shared by Groups II and III is a factor production unit.
The common technical feature shared by Groups I and II is a method of applying factors produced by stem cells to effect a biological functions.

However, these shared technical feature do not represent a contribution over prior art, in view of WO 2014/054004 A1 to CORION BIOTECH S.R.L. (hereinafter Corion). Corion teaches factors produced by stem cells; a factor production unit; and a method of applying factors produced by stem cells to effect a biological functions (pg 3, ln 22-26 "the present inventors observed that conditioned medium (CM) produced by culturing in a liquid culture media placental mesenchymal stem cells ... exerts a surprising inhibitory effect on tumoral proliferation and angiogenesis", pg 4, ln 5-9 "the experimentally demonstrated inhibitory effect exerted on ... tumoral cells proliferation, which turned out to be particularly effective also on cancer tissues at an advanced stage, is strongly indicative of the clinical anti-tumoral effectiveness of the conditioned medium obtainable by culturing in a liquid culture medium placental mesenchymal stem cells", pg 5 ln 16 to pg 6, ln 7 "The conditioned medium which is the subject-matter of the present invention, comprises at least IP- 10 and TARC, secreted proteins that are renowned for their anti-tumoral activity. ... IP- 10 is able to attract CD8+ T lymphocytes and macrophages to the tumor site and it is able to exert an anti-angiogenic effect. Similarly, a role of chemotactic attraction is exerted by TARC chemokine, which is responsible for the selective migration of activated Th2 effector cells" pg 8, ln 18-19 "the separation of the conditioned medium of the invention from the cellular components is performed by filtration or centrifugation or combination of both.").

As the technical features was known in the art at the time of the invention, they cannot be considered a special technical feature that would otherwise unify the groups.

Groups I through IV therefore lack unity under PCT Rule 13 because they do not share a same or corresponding special technical feature.

Note: Claim 42 lacks antecedent basis ["The factor production unit"] for claims 47-49 53, 56-59, 61, 63, 65 and 67 For purposes of this search and opinion, claims 47-49 53, 56-59, 61, 63, 65 and 67 are considered to be dependent from claim 46 (A factor production unit comprising a substrate and a population of input stem cells.).