



(11) **EP 1 870 455 A1**

(12) **EUROPEAN PATENT APPLICATION**
published in accordance with Art. 153(4) EPC

(43) Date of publication:
26.12.2007 Bulletin 2007/52

(21) Application number: **06730606.8**

(22) Date of filing: **30.03.2006**

(51) Int Cl.:
C12N 15/00 (2006.01) **C07K 16/18** (2006.01)
C07K 16/22 (2006.01) **C07K 16/24** (2006.01)
C07K 16/28 (2006.01) **C07K 16/40** (2006.01)
C07K 16/44 (2006.01) **C12M 1/00** (2006.01)
C12N 5/06 (2006.01) **C12N 15/09** (2006.01)
C12Q 1/04 (2006.01) **C12Q 1/68** (2006.01)
G01N 33/53 (2006.01) **G01N 37/00** (2006.01)
A61L 27/00 (2006.01) **C07K 14/47** (2006.01)
C07K 14/475 (2006.01) **C07K 14/52** (2006.01)
C07K 14/54 (2006.01) **C07K 14/705** (2006.01)
C07K 14/81 (2006.01)

(86) International application number:
PCT/JP2006/306658

(87) International publication number:
WO 2006/106823 (12.10.2006 Gazette 2006/41)

(84) Designated Contracting States:
AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HU IE IS IT LI LT LU LV MC NL PL PT RO SE SI SK TR

(30) Priority: **31.03.2005 JP 2005104563**

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(54) **METHOD FOR DISTINGUISHING MESENCHYMAL STEM CELL USING MOLECULAR MARKER AND USE THEREOF**

(57) Disclosed is a method for distinguishing a mesenchymal stem cell comprising, using at least one gene selected from the genes having the nucleotide sequences indicated by the accession numbers shown in Table 1 as a distinguish marker, detecting the difference in expression of the distinguish marker between a mesenchymal stem cell and a connective tissue cell to distinguish the mesenchymal stem cell from the connective tissue

cell. This method enables to distinguish an undifferentiated mesenchymal stem cell from other connective tissue cell such as fibroblasts, osteoblasts, chondrocytes and adipose cells with good accuracy. A mesenchymal stem cell given by this method or a composition comprising the mesenchymal stem cell can be used as a therapeutic for use in the regenerative medicine.

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Description

TECHNICAL FIELD

5 **[0001]** The present invention relates to a method for detecting, distinguishing, and separating mesenchymal stem cells, especially, to a method for distinguishing mesenchymal stem cells from connective tissue cells such as fibroblasts, osteoblasts, chondrocytes, adipose cells, etc. by using a gene marker, a protein marker, and/or the like marker for detecting mesenchymal stem cells, the markers being expressed in a different way in mesenchymal stem cells and in the other connective tissue cells.

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BACKGROUND ART

15 **[0002]** Mesenchymal stem cells are present in mammalian marrows etc. and known as pluripotential stem cells, which can differentiate into adipose cells, cartilage cells, and bone cells. Due to its pluripotency, mesenchymal stem cells are highly expected as transplantation material for use in regenerative medicine for many kinds of tissues. That is, the use of mesenchymal stem cell enables "regenerative medicine by cell transplantation" for regenerating lost tissues lost due to diseases or impairment and have not been able to be regenerated by a conventional remedy method. More specifically, therapeutic treatments have been started or planned, which are for example, transplantation of marrow mesenchymal stem cells to a patient of lower limb ischemia (Buerger's disease), transplantation of marrow mesenchymal stem cells to a patient of a periodontal disease, transplantation of marrow mesenchymal stem cells to a patient of osteoarthritis, transportation of amniotic epithelium sheet to burn injured portion, transportation of amniotic stem cells to a patient of diabetes mellitus, and the other transplantation.

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25 **[0003]** In order to use mesenchymal stem cells for regenerative medicine, the stem cells should be collected from a living tissue and then multiplied without differentiation, and the multiplied and undifferentiated stem cells should be induced to differentiate to desired cells in order to prepare tissue for the regenerative medicine.

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30 **[0004]** The inventors of the present invention have reported a method of easily collecting mesenchymal stem cells by separating mesenchymal stem cells from an oral cavity tissue, which method is safe for an individual from which the mesenchymal stem cells are collected (see Patent Citation 1). Moreover, the inventors of the present invention have reported a culturing method, which can give a significantly larger amount of mesenchymal stem cells than can a conventional culturing method. The culturing method having been reported by the inventors of the present invention is based on a fact found by the inventors that mesenchymal stem cells can be multiplied at a dramatically fast rate by culturing the mesenchymal stem cells in the presence of an extracellular matrix of a basement membrane or in a medium containing fibroblast growth factor (FGF) etc. and this culturing method can multiply mesenchymal stem cells without the differentiating ability thereof (see Patent Citation 2).

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35 **[0005]** These arts are not enough to make the regenerative medicine using the mesenchymal stem cells practically applicable. To speak specifically, for the preparation of the tissue for regenerative medicine by inducing the differentiation of the cultured and multiplied mesenchymal stem cells to desired cells, the cultured cells should be confirmed beforehand that they are mesenchymal stem cells. That is, it is necessary to develop a method of detecting and distinguishing the mesenchymal stem cells after the culturing and multiplication.

35

40 **[0006]** To solve this technical problem, the inventors of the present invention have developed a method of effectively identifying and separating mesenchymal stem cells and fibroblast, which are morphologically similar and thus difficult to be distinguish, the method using a gene maker and/or a protein marker for detecting mesenchymal stem cells (see Patent Citation 3).

40

45 [Patent Citation 1]

Japanese Patent Application Publication, Tokukai, No. 2003-52365 (published on February 25, 2003).

[Patent Citation 2]

Japanese Patent Application Publication, Tokukai, No. 2003-52360 (published on February 25, 2003).

[Patent Citation 3]

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Japanese Patent Application Publication, Tokukai, No. 2005-27579 (published on February 3, 2005).

DISCLOSURE OF INVENTION

[Technical Problems]

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[0007] As described above, mesenchymal stem cells, which differentiate to bones, cartilages, fats, muscles, tendons/ligaments, nerves, etc., have been highly expected to be applicable to the regenerative medicine as cells for transplantation to remedy impairment of these tissues. Conventionally, the confirmation of the mesenchymal stem cells can be

carried out *in vitro* or by providing the differentiation ability thereof *in vivo*. The practical use of the tissue regenerative medicine of the mesenchymal stem cells cannot be attained without exact, accurate, and easy method to confirm that the cells are mesenchymal stem cells and the mesenchymal stem cells keep its pluripotency.

[0008] It is true that the method disclosed in Patent Citation 3 is sufficient to identify and distinguish the mesenchymal stem cells and fibroblast. However, bone marrows etc. contain many other connective tissue cells other than fibroblasts, such as osteoblasts, chondrocytes, adipose cells, etc.

[0009] Therefore, the art to distinguish the mesenchymal stem cells from fibroblast is not enough to realize practical regenerative medicine using the mesenchymal stem cells. Accordingly, there have been a high demand to develop an art to distinguish and separate the undifferentiated mesenchymal stem cells from the other connective tissue cells such as fibroblasts, osteoblasts, chondrocytes, adipose cells, etc. with exactness, accuracy, and easiness. The development of the art will be beneficial for the regenerative medicine because the art can distinguish the mesenchymal stem cells that keep the pluripotency thereof, from the undifferentiated mesenchymal stem cells mass-produced.

[0010] The present invention was accomplished in view of the aforementioned problem. An object of the present invention is to provide a method of exactly and accurately distinguishing and/or separating mesenchymal stem cells from the connective tissue cells such as fibroblasts, osteoblasts, chondrocytes, adipose cells, etc., and use of the same method.

[Technical Solution]

[0011] The inventors of the present invention diligently worked to attain the object. The inventors studied expression profiles of genes in mesenchymal stem cells and connective tissue cells such as fibroblasts and others. As a result, the inventors newly found that there are genes whose expression is specific to mesenchymal stem cells but whose expressions in the connective tissue cells such as fibroblast and others are clearly different from the expression in mesenchymal stem cells. Based on this novel finding, the present invention was accomplished. The present invention, based on this novel finding, encompass the following inventions.

(1) A method of distinguishing mesenchymal stem cells, including:

distinguishing the mesenchymal stem cells from connective tissue cells by detecting a difference between expression in the mesenchymal stem cells and expression in the connective tissue cells by using a distinguishing marker(s), the distinguishing marker(s) being at least one of genes having the base sequences identified with accession numbers listed in Table 1 a to 1j.

[Table 1a]

| Classification 1 | Gene symbol | Gene title | Genbank number |
|--------------------|-------------|---|----------------|
| ATP/GTP binding -1 | BRIP1 | BRCA1 interacting protein C-terminal helicase 1 | NM_032043 |
| ATP/GTP binding -2 | PASK | PAS domain containing serine/threonine kinase | NM_015148 |
| ATP/GTP binding -3 | RAC2 | ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) | NM_002872 |
| ATP/GTP binding -4 | KIF18A | kinesin family member 18A | NM_031217 |
| ATP/GTP binding -5 | NEK7 | NIMA (never in mitosis gene a)-related kinase 7 | NM_133494 |
| ATP/GTP binding -6 | ARL4C | ADP-ribosylation factor-like | NM_005737 |
| ATP/GTP binding -7 | EDEM1 | ER degradation enhancer, mannosidase alpha-like 1 | NM_014674 |
| ATP/GTP binding -8 | CAMK2D | calcium/calmodulin-dependent protein kinase (CaM kinase) II delta | NM_172127 |
| Classification 2 | Gene symbol | Gene title | Genbank number |
| binding -1 | PDE5A | phosphodiesterase 5A, cGMP-specific | NM_001083 |
| binding -2 | RGS4 | regulator of G-protein signalling 4 | NM_005613 |
| binding -3 | EGFL3 | EGF-like-domain, multiple 3 | NM_001409 |
| binding -4 | FHL2 | four and a half LIM domains | NM_001450 |

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(continued)

| Classification 2 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| binding -5 | HRB2 | HIV-1 rev binding protein 2 | NM_007043 |
| binding -6 | CAPZA1 | capping protein (actin filament) muscle Z-line, alpha 1 | NM_006135 |
| binding -7 | PAPPA2 | pappalysin 2 | NM_020318 |
| binding -8 | LOXL2 | lysyl oxidase-like 2 | NM_002318 |
| binding -9 | LOX | lysyl oxidase | NM_002317 |
| binding -10 | ADAMTS5 | ADAM metalloproteinase with thrombospondin type 1 motif, 5 (aggrecanase-2) | NM_007038 |

[Table 1b]

| Classification 3 | Gene symbol | Gene title | Genbank number |
|-----------------------------------|-------------|---|----------------|
| cell growth and/or maintenance-1 | CCND1 | cyclin D1 (PRAD1: parathyroid adenomatosis 1) | NM_053056 |
| cell growth and/or maintenance-2 | CDC25A | cell division cycle 25A | NM_001789 |
| cell growth and/or maintenance-3 | IER3 | immediate early response 3 | NM_052815 |
| cell growth and/or maintenance-4 | BCL2 | B-cell CLL/lymphoma 2 | NM_000633 |
| cell growth and/or maintenance-5 | NALP1 | NACHT, leucine rich repeat and PYD containing 1 | NM_033004 |
| cell growth and/or maintenance-6 | PAK3 | p21 (CDKN1A)-activated kinase 3 | NM_002578 |
| cell growth and/or maintenance-7 | PODXL | podocalyxin-like | NM_001018 111 |
| cell growth and/or maintenance-8 | CCL26 | chemokine (C-C motif) ligand 26 | NM_006072 |
| cell growth and/or maintenance-9 | FBLN1 | fibulin 1 | NM_006486 |
| cell growth and/or maintenance-10 | LAMA1 | laminin, alpha 1 | NM_005559 |
| cell growth and/or maintenance-11 | NTNG1 | netrin G1 | NM_014917 |

[Table 1c]

| Classification 4 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| cytokine -1 | GDF15 | growth differentiation factor 15 | NM_004864 |
| cytokine -2 | IL6 | interleukin 6 (interferon, beta 2) | NM_000600 |
| cytokine -3 | CTGF | connective tissue growth factor | NM_001901 |
| cytokine -4 | VEGF | vascular endothelial growth factor | NM_001025 366 |
| cytokine -5 | VEGFC | vascular endothelial growth factor C | NM_005429 |
| cytokine -6 | HGF | hepatocyte growth factor (hepapoietin A; scatter | NM_000601 |
| Classification 5 | Gene symbol | Gene title | Genbank number |
| cytoskeleton-1 | KRT19 | keratin 19 | NM_002276 |
| cytoskeleton-2 | KRTAP1-5 | keratin associated protein 1- | NM_031957 |
| cytoskeleton-3 | KRTAP2-1 | keratin associated protein 2- | BC012486 |
| cytoskeleton-4 | KRTHA4 | keratin, hair, acidic, 4 | NM_021013 |

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(continued)

| Classification 5 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| cytoskeleton-5 | CKAP2 | cytoskeleton associated protein 2 | NM_018204 |
| cytoskeleton-6 | KRTAP1-1 | keratin associated protein 1- | NM 030967 |
| cytoskeleton-7 | KRT18 | keratin 18 | NM 000224 |
| cytoskeleton-8 | KAP2.1B | keratin associated protein 2.1B | AJ406929 |
| cytoskeleton-9 | SSH1 | slingshot homolog 1 (Drosophila) | NM_018984 |
| | | | |
| Classification 6 | Gene symbol | Gene title | Genbank number |
| enzyme-1 | LXN | latexin | NM 020169 |
| enzyme-2 | IFI30 | interferon, gamma-inducible protein 30 | NM 006332 |
| enzyme-3 | CPA4 | carboxypeptidase A4 | NM 016352 |

[Table 1d]

| Classification 7 | Gene symbol | Gene title | Genbank number |
|--------------------------------|-------------|--|----------------|
| extracellular matrix-1 | CHI3L1 | chitinase 3-like 1 (cartilage glycoprotein-39) | NM_001276 |
| extracellular matrix-2 | KRT23 | keratin 23 (histone deacetylase inducible) | NM_015515 |
| extracellular matrix-3 | FLG | filaggrin | NM 002016 |
| extracellular matrix-4 | ADAMTS1 | a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 | NM_006988 |
| extracellular matrix-5 | FRMD5 | FERM domain containing 5 | NM_001031 729 |
| Classification 8 | Gene symbol | Gene title | Genbank number |
| growth factor or receptor-1 | IGFBP1 | insulin-like growth factor binding protein 1 | NM_000596 |
| growth factor or receptor-2 | CFI | complement factor I | NM_000204 |
| growth factor or receptor-3 | ESM1 | endothelial cell-specific molecule 1 | NM_007036 |
| growth factor or receptor-4 | F2RL1 | coagulation factor II (thrombin) receptor-like 1 | NM_005242 |
| growth factor or receptor-5 or | MET | met proto-oncogene (hepatocyte growth factor receptor) | NM_000245 |
| growth factor or receptor-6 | HTR7 | 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) | NM_000872 |
| growth factor or receptor-7 | IGFBP3 | insulin-like growth factor binding protein 3 | NM_001013 398 |

[Table 1e]

| Classification 9 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| membrane -1 | ABHD2 | abhydrolase domain containing 2 | NM_007011 |
| membrane -2 | ITGA2 | integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) | NM_002203 |
| membrane -3 | LAMA3 | laminin, alpha 3 | NM 198129 |
| membrane -4 | NETO2 | neuropilin (NRP) and tolloid (TLL)-like 2 | NM_018092 |

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| Classification 9 | Gene symbol | Gene title | Genbank number |
|----------------------------|-------------|---|------------------|
| membrane -5 | NTN4 | netrin 4 | NM_021229 |
| membrane-6 | PTGER1 | prostaglandin E receptor 1 (subtype EP1), 42kDa | NM_000955 |
| membrane -7 | EPHB2 | EPH receptor B2 | NM 017449 |
| membrane -8 | SFRP1 | secreted frizzled-related protein 1 | NM_003012 |
| membrane -9 | CD33L3 | CD33 antigen-like 3 | NM 213602 |
| membrane -10 | GLIPR1 | GLI pathogenesis-related 1 (glioma) | NM_006851 |
| membrane -11 | UGCG | UDP-glucose ceramide glucosyltransferase | NM_003358 |
| membrane -12 | ADORA1 | adenosine A1 receptor | NM 000674 |
| | | | |
| Classification 10 | Gene symbol | Gene title | Genbank number |
| membrane binding protein-1 | ANXA10 | annexin A10 | NM 007193 |
| membrane binding protein-2 | RARRES1 | retinoic acid receptor responder (tazarotene induced) 1 | NM_206963 |
| membrane binding protein-3 | HNT | neurotrimin | NM_016522 |
| membrane binding protein-4 | CNINAP3 | contactin associated protein- | NM_033655 like 3 |

[Table 1f]

| Classification 11 | Gene symbol | Gene title | Genbank number |
|---------------------|-------------|--|----------------|
| protein binding -1 | SYT1 | synaptotagmin I | NM 005639 |
| protein binding -2 | MLF1 | myeloid leukemia factor 1 | NM 022443 |
| protein binding -3 | CDCP1 | CUB domain-containing protein 1 | NM_022842 |
| protein binding -4 | KIAA0746 | KIAA0746 protein | NM_015187 |
| protein binding -5 | PSCDBP | pleckstrin homology, Sec7 and coiled-coil domains, binding protein | NM_004288 |
| protein binding -6 | SKI | v-ski sarcoma viral oncogene homolog (avian) | NM_003036 |
| protein binding -7 | SNX25 | sorting nexin 25 | NM_031953 |
| protein binding -8 | CDH6 | cadherin 6, type 2, K-cadherin (fetal kidney) | NM_004932 |
| protein binding -9 | DCBLD2 | discoidin, CUB and LCCL domain containing 2 | NM_080927 |
| protein binding -10 | ENG | endoglin (Osler-Rendu-Weber syndrome 1) | NM_000118 |

[Table 1g]

| Classification 12 | Gene symbol | Gene title | Genbank number |
|------------------------|-------------|---|----------------|
| protein modification-1 | SH3RF1 | SH3 domain containing ring finger 1 | NM_020870 |
| protein modification-2 | SMLTRF2 | SMAD specific E3 ubiquitin protein ligase 2 | NM_022739 |
| protein modification-3 | TFPI2 | tissue factor pathway inhibitor 2 | NM_006528 |
| protein modification-4 | ITGB3 | integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) | NM_000212 |

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(continued)

| Classification 12 | Gene symbol | Gene title | Genbank number |
|------------------------|-------------|---|----------------|
| protein modification-5 | MYPN | myopalladin | NM_032578 |
| protein modification-6 | LRP2BP | LRP2 binding protein | NM_018409 |
| protein modification-7 | HECW2 | HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2 | NM_020760 |
| protein modification-8 | PKIA | protein kinase (cAMP-dependent, catalytic) inhibitor alpha | NM_006823 |
| | | | |
| Classification 13 | Gene symbol | Gene title | Genbank number |
| signal molecule-1 | LVPD1 | LY6/PLAUR domain containing 1 | NM_144586 |
| signal molecule-2 | GATA6 | GATA binding protein 6 | NM_005257 |
| signal molecule-3 | RAB27B | RAB27B, member RAS | NM_004163 |
| signal molecule-4 | SOX11 | SRY (sex determining region Y)-box 11 | NM_003108 |
| signal molecule-5 | ARHGAP2 | Rho GTPase activating 2 protein 22 | NM_021226 |

[Table 1h]

| Classification 14 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| transcription-1 | ETV1 | ets variant gene 1 | NM_004956 |
| transcription-2 | ETV5 | ets variant gene 5 (ets-related molecule) | NM_004454 |
| transcription-3 | FOXP1 | forkhead box P1 | NM_032682 |
| transcription-4 | HMGA2 | high mobility group AT-hook 2 | NM_003483 |
| transcription-5 | KLF12 | Kruppel-like factor 12 | NM_007249 |
| transcription-6 | PRDM16 | PR domain containing 16 | NM_022114 |
| transcription-7 | SIM2 | single-minded homolog 2 (Drosophila) | NM_009586 |
| transcription-8 | SUHW2 | suppressor of hairy wing homolog 2 (Drosophila) | NM_080764 |
| transcription-9 | ENO1 | enolase 1 | NM_001428 |
| transcription-10 | MITF | microphthalmia-associated transcription factor | NM_198159 |
| transcription-11 | TCF3 | transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) | NM_003200 |
| transcription-12 | SMYD3 | SET and MYND domain containing 3 | NM_022743 |

[Table 1i]

| Classification 15 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| transport-1 | ATP6V1G3 | ATPase, H ⁺ transporting, lysosomal 13kDa, V1 subunit G isoform 3 | NM_133262 |
| transport-2 | KCTD16 | potassium channel tetramerisation domain containing 16 | NM_020768 |
| transport-3 | NUPL1 | nucleoporin like 1 | NM_014089 |
| transport-4 | SLC14A1 | solute carrier family 14 (urea transporter), member 1 (Kidd blood group) | NM_015865 |

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| Classification 15 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|---|----------------|
| transport-5 | SLC16A4 | solute carrier family 16 (monocarboxylic acid transporters), member 4 | NM_004696 |
| transport-6 | SLC4A4 | solute carrier family 4, sodium bicarbonate cotransporter, member 4 | NM_003759 |
| transport-7 | SLC9A7 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 7 | NM_032591 |
| transport-8 | TRPC4 | transient receptor potential cation channel, subfamily C, member 4 | NM_016179 |
| transport-9 | MCFD2 | multiple coagulation factor deficiency 2 | NM_139279 |
| transport-10 | SLC26A4 | solute carrier family 26, member 4 | NM_000441 |
| transport-11 | MCOLN3 | mucolipin 3 | NM_018298 |
| transport-12 | SLC25A37 | solute carrier family 25, member 37 | NM_016612 |
| transport-13 | SLC30A7 | solute carrier family 30 (zinc transporter), member 7 | NM_133496 |

[Table 1j]

| Classification 16 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| others -1 | FLJ38725 | hypothetical protein FLJ38725 | NM_153218 |
| others -2 | KIAA1913 | KLAA1913 | NM_052913 |
| others -3 | PHLDB2 | pleckstrin homology-like domain, family B, member 2 | NM_145753 |
| others -4 | PLCXD2 | phosphatidylinositol-specific phospholipase C, X domain containing 2 | NM_153268 |
| others -5 | SAMD3 | sterile alpha motif domain containing 3 | NM_001017 373 |
| others -6 | ZNF423 | zinc finger protein 423 | NM_015069 |
| others -7 | FLJ33996 | hypothetical protein FLJ33996 | NM_175894. 2 |
| others -8 | PLEKHK1 | pleckstrin homology domain containing, family K member 1 | NM_145307 |
| others -9 | PTOV1 | prostate tumor overexpressed gene 1 | NM_017432 |
| others -10 | FAM40B | family with sequence similarity 40, member B | NM_020704 |
| others -11 | ABI3BP | ABI gene family, member 3 (NESH) binding protein | NM_015429 |
| others -12 | NHS | Nance-Horan syndrome (congenital cataracts and dental anomalies) | NM_198270 |
| others -13 | DTL | denticleless homolog (Drosophila) | NM_016448 |
| others -14 | C1GALT1 | core 1 synthase, glycoprotein-N- acetylgalactosamine 3-beta- | NM_020156 |
| others -15 | CPNE8 | copine VIII | NM_153634 |
| others -16 | TMEM49 | transmembrane protein 49 | NM_030938 |

(2) The method as set forth in (1), wherein the distinguishing marker(s) is at least one of the genes listed the classifications 6, 7, 8, 10, and 13 in Tables 1a to 1j.

(3) The method as set forth in (2), wherein the distinguishing markers are a combination of one or more genes from each of the classifications 6, 7, 8, 10, and 13 in Tables 1a to 1j.

(4) The method as set forth in any one of (1) to (3), wherein the distinguishing marker is at least one of the genes listed

in Table 2.

| Gene symbol | Gene title | Genbank number |
|-------------|--|----------------|
| CHI3L1 | chitinase 3-like 1 (cartilage glycoprotein-39) | NM_001276 |
| FLG | filaggrin | NM_002016 |
| CFI | complement factor I | NM_000204 |
| ANXA10 | annexin A10 | NM_007193 |
| LYPDC1 | LY6/PLAUR domain containing 1 | NM_144586 |
| GATA6 | GATA binding protein 6 | NM_005257 |

(5) The method as set forth in any one of (1) to (4), wherein the detection of the difference in the expressions of the distinguishing markers is carried out by detecting expression of the gene or expression of a protein encoded by the gene.
 (6) A microarray for distinguishing mesenchymal stem cells, the microarray including at least one of (a) to (d) immobilized thereon:

- (a) at least one of genes having the base sequences identified with the accession numbers listed in Tables 1a to 1j;
- (b) an antisense chain of at least one of genes having the base sequences identified with the accession numbers listed in Tables 3a to 3j;
- (c) a partial base sequence of (a) or (b); and
- (d) a polynucleotide that is capable of hybridizing, under stringent conditions, with a polynucleotide having the base sequence described in any one of (a) to (c).

(7) An antibody, being inducible with a polypeptide described in (e) or (f), and bindable specifically with the polypeptide specifically:

- (e) a polypeptide encoded by any one of the genes having the base sequences identified with the accession numbers listed in Tables 1a to 1j; and
- (f) a partial polypeptide of the polypeptide described in (e).

(8) A kit for distinguishing and separating mesenchymal stem cells, including any one of (g) to (i):

- (g) a microarray as set forth in (6);
- (h) an antibody as set forth in claim (7); and
- (i) a probe for detecting whether the distinguishing marker gene for mesenchymal stem cells is expressed or not, the distinguishing marker gene comprising a polynucleotide, which, under strigent condition, hybridizes with a gene or a partial sequence thereof, the gene having a base sequence identified with the accession number listed in any one of Tables 1a to 1j.

(9) A method for distinguishing and separating mesenchymal stem cells, the method including:

separating the mesenchymal stem cells distinguished by a method as set forth in any one of (1) to (5).

(10) A cell-containing composition including:

mesenchymal stem cells separated by a method as set forth in (9); or
 a multiplied culture of the mesenchymal stem cells.

(11) A drug for regenerative medicine, including:

a cell-containing composition as set forth in (10).

(12) A distinguishing marker for distinguishing mesenchymal stem cells, the distinguishing marker being at least one of genes having the base sequences identified with the accession numbers listed in Tables 1a to 1j.

(13) A distinguishing marker for distinguishing mesenchymal stem cells, the distinguishing marker being at least one of polypeptides encoded by genes having the base sequences identified with the accession numbers listed in Tables 1a to 1j.

(14) A method of judging whether a sample provider has been developed a disease related with mesenchymal stem cells or whether the sample provider has a possibility of developing the disease in the future, the method judging by treating a sample, which is separated *in vivo* from the sample provider, with any one or more of:

a method as set forth in any one of (1) to (5);

a microarray as set forth in (6);

an antibody as set forth in (7);

a kit as set forth in (8); and

a distinguishing marker as set forth in (12) or (13).

(15) A drug for regenerative medicine, the drug suppressing undifferentiating property of mesenchymal stem cells and comprising siRNA for a gene or a partial sequence thereof, the gene having any one of the base sequences identified with the accession numbers listed in Tables 1a to 1j.

[Effect of the Invention]

[0012] In the method of the present invention for distinguishing mesenchymal stem cells and the use thereof, the distinguishing marker is a gene whose expression pattern in undifferentiated mesenchymal stem cells is clearly different from expression pattern thereof in fibroblasts, osteoblasts, chondrocytes and adipose cells, etc. This makes it possible to distinguish and/or separate, e.g., undifferentiated mesenchymal stem cells contained in marrow from the connective tissue cells exactly accurately, and easily.

[0013] Thus, according to the present invention, it is possible to overcome the problems hindering the application of undifferentiated mesenchymal stem cells to the regenerative medicine, the mesenchymal stem cells being pluripotential and being capable of differentiating to bone, cartilages, fats, muscles, tendons/ligaments, nerves, etc. That is, according to the present invention, it is possible to overcome the problem in distinguishing undifferentiating mesenchymal stem cells from other cells such as fibroblasts and connective tissue cells. Thus, the present invention can make a great contribution to regenerative medicine using mesenchymal stem cells.

[0014] Moreover, mesenchymal stem cells used by the method of distinguishing the mesenchymal stem cells, and composition containing the same can be applied to a drug for regenerative medicine.

BRIEF DESCRIPTION OF DRAWINGS

[0015]

Fig. 1 a view schematically illustrating a flow of procedure of a present Example.

Fig. 2 is a view illustrating result of analysis to analyze a difference in expression of genes between mesenchymal stem cells (MSC) and other connective tissues by using a DNA microarray in a present Example.

BEST MODE FOR CARRYING OUT THE INVENTION

[0016] The present invention makes it possible to construct a method of effectively distinguishing and separating mesenchymal stem cells from other cell groups such as connective tissue cells (such as fibroblasts, osteoblasts, chondrocytes, adipose cells) etc. by using a DNA microarray to detect, as a distinguishing marker, a gene that is specifically expressed in undifferentiated stem cells. Use of the present invention makes it possible to perform a qualitative inspection of mesenchymal stem cells multiplied *in vitro* (on whether the mesenchymal stem cells have differentiation ability or not). This contributes to the practical application of the regenerative medicine using mesenchymal stem cells.

[0017] In the following, characteristic features of the present invention, that is, a method of distinguishing mesenchymal stem cells will be described firstly together with explanation on distinguishing/separating marker, microarray, and antibody to be used in the method. Finally, various applied technologies will be described herein such as distinguishing/ separating

method, cell-containing compositions (which further contain cell secreta (growth factor or the like) preferably), drugs for regenerative medicine, distinguishing/ separating kit, and the like.

[0018] In this DESCRIPTION, the term "polypeptide" is exchangeable with "peptide" or "protein". The polypeptide in the present invention may be a polypeptide isolated from a natural source, produced recombinantly, or synthesized chemically.

[0019] In this DESCRIPTION, the term "polynucleotide" is exchangeable with "gene", "nucleic acid", or "nucleic acid molecule", and intends to mean a polymer of nucleotides. Moreover, what is meant by the term "gene" encompass not only DNA but also RNA (e.g., mRNA). In this DESCRIPTION, the term "base sequence" is exchangeable with "gene sequence", "nucleic acid sequence" or "nucleotide sequence", and the "base sequence" is expressed as a sequence of deoxyribonucleotide (abbreviated as A, G, C, and T).

<1. Method of Distinguishing Mesenchymal Stem Cells>

[0020] A method according to the present invention for distinguishing mesenchymal stem cells comprises the step of distinguishing mesenchymal stem cells from the connective tissue cells by detecting a difference between expressions in mesenchymal stem cells and the connective tissue cells by using a distinguishing marker, which is at least one of genes having the base sequences identified with the accession numbers shown in Tables 1a to 1j above. The method according to the present invention is not particularly limited in terms of specific arrangements such as other steps, conditions, materials to use, devices to use, etc.

[0021] On Tables 1a to 1j, 139 genes are classified into sixteen classifications according to molecular functions of proteins encoded by the genes, referring to Gene Ontology (GO) of the European Bioinformatics Institute.

[0022] Classification 1 is a category for ATP-GTP binding proteins, and 8 kinds of genes with 8 accession numbers belong thereto. Moreover, Classification 2 is a category for binding proteins, and 10 kinds of genes with 10 accession numbers belong thereto. In this DESCRIPTION and Tables, "binding-1 ~ 10" means "DNA/metal ion/collagen binding-1~10". Classification 3 is a category for factors relating to cell growth factor or maintenance, and 11 kinds of genes with 11 accession numbers belong thereto.

[0023] Classification 4 is a category for cytokine, and 6 kinds of genes with 6 accession numbers belong thereto. Classification 5 is a category for cytoskeleton, and 9 kinds of genes with 9 accession numbers belong thereto. Classification 6 is a category for enzymes, and 3 kinds of genes with 3 accession numbers belong thereto.

[0024] Classification 7 is a category for extracellular matrix or cytoskeleton, and 5 kinds of genes with 5 accession numbers belong thereto. Classification 8 is a category for growth factors or receptors, and 7 kinds of genes with 7 accession numbers belong thereto.

[0025] Classification 9 is a category for membrane, and 12 kinds of genes with 12 accession numbers belong thereto. Classification 10 is a category for membrane binding proteins, and 4 kinds of genes with 4 accession numbers belong thereto.

[0026] Classification 11 is a category for factors relating to protein binding, and 10 kinds of genes with 10 accession numbers belong thereto. Classification 12 is a category for factors relating to protein modification, and 8 kinds of genes with 8 accession numbers belong thereto. Classification 13 is a category for factors relating to signal transduction, and 5 kinds of genes with 5 accession numbers belong thereto.

[0027] Classification 14 is a category for transcription factors, and 12 kinds of genes with 12 accession numbers belong thereto. Classification 15 is a category for factors relating to intercellular transport, and 13 kinds of genes with 13 accession numbers belong thereto.

[0028] Classification 16 is a category for other factors not belonging to any of the above classification, and 16 kinds of genes with 16 accession numbers belong thereto. The categories are classified according to open information disclosed in NCBI.

[0029] As described above, the gene groups listed on Tables 1a to 1j are classified in terms of the molecular functions of the proteins encoded by the genes. The use of these genes as distinguishing markers makes it possible to distinguish mesenchymal stem cells from the connective tissue cells by referring to the function or activity of the genes in mesenchymal stem cells and the connective tissue cells. More specifically, for example, if a factor relating to a particular extracellular matrix is expressed at a high expression level in mesenchymal stem cells, while the expression level of the factor is not so high in the connective tissue cells, then the use of a gene belonging to Classification 7 will make it possible to distinguish mesenchymal stem cells easily and exactly.

[0030] Moreover, it is advantageous that these genes, which can be used as the distinguishing markers, can be also utilized as markers of mesenchymal stem cells to distinguish them in terms of molecular function.

[0031] On Tables 1a to 1j, genes are listed in abbreviation in the column of "Gene symbol". general names and other information of the genes are listed in the column of "Gene title", and the accession numbers in Genbank are listed in the column of "Genbank number". For some genes (such as Transcript variant) that are given plural accession numbers, the scope of the present invention, needless to say, encompasses all genes represented with all the accession numbers.

5 [0032] Moreover, what is meant by the term "connective tissue" in this DESCRIPTION is all supporting and connective tissues encompassing cartilaginous tissue and osseous tissue. The supporting tissues collectively mean the connective tissue in a narrow sense, and specially differentiated connective tissue (cartilaginous tissue, osseous tissue, blood, and lymph). The term "connective tissue" may mean the supporting tissue in a broad sense. Ontogenically, the connective tissue is derived from "mesoblast (or from ectoderm in some cases)" and has functions of supporting an internal structures inside a body. Moreover the term "connective tissue cells" mean cell constructing the supporting and connective tissues. Example of immobilized cells encompass fibroblasts, reticular cells, adipose cells. Example of mobile cells encompass macrophages (histiocyte or macrophage), mast cells, plasma cells, lymphoid cells, granulocytes. Examples of immobilized cells constructing the cartilaginous tissue encompass chondrocytes. Examples of cells constructing osseous tissue encompass Osteoblasts and Osteocytes. It is preferable that the present invention be adopted to distinguish mesenchymal stem cells from fibroblasts, osteoblasts, chondrocytes, and adipose cells (which are collectively referred to as "connective tissue cells" hereinafter") among the various cells mentioned above.

10 [0033] Moreover, the gene groups listed in Tables 1a to 1j, which are used as "distinguishing markers" in the present invention, are genes that have been proved, by an analysis using DNA microarray to study expression profiles in undifferentiated mesenchymal stem cells, fibroblasts, osteoblasts, chondrocytes and adipose cells, that that they have an ability to show significant differences in expression levels between undifferentiated mesenchymal stem cells and other cell groups.

15 [0034] Referring to the difference in the expression level caused by the gene groups, it is possible to distinguish the undifferentiated mesenchymal stem cells from fibroblasts, osteoblasts, chondrocytes, and adipose cells easily, exactly, and accurately. The base sequence of the gene groups in Tables 1 and the amino acid sequence information of the proteins encoded by the gene groups have been publicly known. Especially, the base sequence information of the gene groups are available from the gene data base in the Genbank referring to the accession numbers listed in Tables 1a to 1j.

20 [0035] Moreover, among the genes listed in Tables 1a to 1j, these genes are preferable which satisfy the criterions as described in later-described Examples. For example, genes having high "Fold Average" and "Expression level" are preferably used solely or in combination. Furthermore, it is preferable to use such a gene as a marker that have "Fold Average" of 2 or more, and/or "Expression level" of 0.5 or more.

25 [0036] Moreover, the distinguishing marker is preferably at least one of the genes that belong to the classifications 6, 7, 8, 10, and 13 in Tables 1a to 1j.

30 [0037] The genes that belong to the classifications 6, 7, 8, 10, and 13 in Tables 1a to 1j show greatly different expression patterns especially between mesenchymal stem cells and the connective tissue cells. Most of the genes that belong to the classifications 6, 7, 8, 10, and 13 in Tables 1a to 1j show higher expression level in mesenchymal stem cells. Because of this, the gene that belong to the classifications 6, 7, 8, 10, and 13 in Tables 1a to 1j are preferably applicable as the distinguishing markers. Moreover, the use of such a gene that have a high expression level and show rather stable results with different individuals make it possible to distinguish mesenchymal stem cells exactly.

35 [0038] It is more preferable to use, in combination, one or more gene selected from each classification 6, 7, 8, 10, and 13 in Tables 1a to 1j, that is, to select at least one gene each from the classifications 6, 7, 8, 10, and 13 and to use the genes as the distinguishing marker in combination. By selecting at least one gene from the 5 classifications, it is possible to check the expression pattern for the gene(s) of each of the 5 classifications. This makes it possible to distinguish mesenchymal stem cells more exactly and more accurately.

40 [0039] Moreover, it is especially preferable that at least one gene selected from the genes listed in Table 2 be used as the distinguishing marker.

45 [0040] Table 2 lists 6 genes that are especially preferable among the 139 genes listed in Tables 1a to 1j. The 6 genes show especially greatly different expression patterns between mesenchymal stem cells and the connective tissue cells. Moreover, the 6 genes exhibit high expression levels. Because of these, the 6 genes are most preferably applicable as the distinguishing markers. Moreover, the use of such a small number of marker makes it possible to distinguish mesenchymal stem cells in a more user-friendly manner and with a lower cost.

50 [0041] Furthermore, it is possible to use, in combination, genes belonging to the same one of the 16 classification. For example by using, as the distinguishing marker, a combination of genes belonging to the classification relating to the transcription factor, it is possible to perform evaluation on protein synthesis specific to mesenchymal stem cells even at an early stage of the protein synthesis, or the like property. Moreover, by using a combination of genes belonging to the classification relating to the cell skeleton, it is possible to perform evaluation on protein production (such as production of keratins) etc. characteristic to mesenchymal stem cells, or the like property. Furthermore, by using a combination of genes belonging to the classification relating to growth factors, it is possible to perform evaluation on growth factor production etc. in the cells, or the like property. Moreover, by using a combination of genes belonging to the classification relating to extracellular matrix, it is possible to perform evaluation on adhesiveness of the cells, or the like property. Moreover, by using a combination of genes belonging to the classification relating to signal transduction, it is possible to perform evaluation on responsibility to extracellular stimulus, or the like property. Moreover, by using a combination of genes relating to the transportation, it is possible to evaluate a state of the intracellular transportation, or the like property.

[0042] As described above, the effects characteristic to the categories can be attained by using in combination the distinguishing markers classified in the categories respectively. Thus, such a combination of the distinguishing markers classified in the categories respectively is very useful and make it possible to distinguish mesenchymal stem cells more exactly and accurately.

[0043] Moreover, apart from the applications described above, it is possible to perform comprehensive analysis, which covers each characteristic of the classifications, by selecting at least one gene from each of 16 classifications (but may be not from the other classifications). In this case, it is sufficient for the distinguishing markers that they include at least one gene from each classification. Especially, the use of a maker with a high "Evaluation Level" described in Examples later, or the use of a greater number of markers will allow distinguishing or analyzing mesenchymal stem cells more exactly and accurately, thereby attaining a more reliable distinguishing method. Thus, the combination of the distinguishing markers is preferable to include the distinguishing markers having higher "Evaluation Levels", and to include as many the distinguishing markers as permitted.

[0044] Moreover, the detection of the difference in the expression levels of the distinguishing markers can be carried out by detecting the expression of the genes or the expression of he protein encoded by the genes. More specifically, the present invention can distinguish mesenchymal stem cells from the connective tissue cells by detecting the difference in the expression levels of the distinguishing marker genes as described above, which occurs between mesenchymal stem cells and the connective tissue cells. Thus, the present invention includes a distinguishing marker for mesenchymal stem cells, the distinguishing marker being one of the genes having the base sequences identified with the accession numbers listed in Tables 1a to 1j.

[0045] In the present invention, the detection of the expression of the gene groups acting as the distinguishing marker can be performed suitably by a conventionally known method that is applicable to detection of expression of known genes. For example, the detection of the gene groups of the distinguishing markers can be carried out by using a microarray, on which at least one of the followings (a) to (d) are immobilized, for distinguishing mesenchymal stem cells:

(a) at least one of genes having the base sequences identified with the accession numbers listed in Tables 1a to 1j;
 (b) an antisense chain of at least one of genes having the base sequences identified with the accession numbers listed in Tables 1a to 1j;

(c) a partial base sequence of (a) or (b); and

(d) a polynucleotide that is capable of hybridizing, under stringent conditions, with a polynucleotide having the base sequence described in any one of (a) to (c).

The microarray may be any type of conventionally known microarray such as the DNA microarray of Affymetrix US, a Stanford type DNA microarray, a DNA microarray on which oligonucleotides are directly synthesized chemically on a silica substrate by using fabricating technique, which is used in the semiconductor production. The microarray in the present invention is not particularly limited in terms of its specific size, shape, system, etc.

With the microarray for distinguishing mesenchymal stem cells, it is possible to perform comprehensive and systematic analysis on the expression of the gene groups of many distinguishing markers, and thus it is possible to distinguish mesenchymal stem cells from the connective tissue cells very easily, exactly, and accurately. As such, the microarray for distinguishing mesenchymal stem cells is highly useful. The present invention, therefore, includes the microarray for distinguishing mesenchymal stem cells.

In other words, the method according to the present invention for distinguishing mesenchymal stem cells is preferably arranged such that plural distinguishing markers are used as indicators. Especially, it is preferable to use a combination of plural kinds of distinguishing markers whose expression in mesenchymal stem cells is sufficiently different from that in other cell groups and whose expression level is high. For example, appropriate combinations of CHI3L1, FLG, KRTAP1-5, RGS4, HNT, SLC14A1, IFI30, ZNF423, LXN, whose Fold Average and Expression level are high are preferable.

Moreover, apart from the microarray for distinguishing mesenchymal stem cells, it is possible to use, for example, the northern blotting technique in order to detect the expression of the gene groups of the distinguishing markers according to the present invention. Moreover, in order to detect and distinguish the expression of the gene of the distinguishing marker according to the present invention, a detection probe can be used, which detects a distinguishing marker gene having a base sequence that hybridizes, under stringent conditions, with the whole or part of the DNA sequence of the gene of the distinguishing marker according to the present invention.

It is possible to carry out the detection of the expression of the genes in the mesenchymal stem cells and the connective tissue cells by using the detection probe. For example, a DNA probe of an appropriate length is prepared from a DNA sequence of a gene of a well-known distinguishing marker and labeled with, for example, fluorescence. This DNA probe is hybridized with the analyte, thereby to carry out the detection of mesenchymal stem cells. The detection probe may be a probe for detecting a distinguishing marker gene constituted with the whole or part of an antisense chain of a base sequence of a gene of a well-known marker.

The "stringent conditions for the hybridization of the DNA sequence of the marker gene" with the base sequence of

the present invention for preparation of the DNA probe are, for example, to carry out the hybridization at 42°C followed by washing treatment at 42°C with a buffer solution containing $1 \times \text{SSC}$ (0.15M NaCl, 0.015M sodium citrate) and 0.1% SDS (Sodium dodecyl sulfate), or more preferably to carry out the hybridization at 65°C followed by washing treatment at 65°C with a buffer solution containing $0.1 \times \text{SSC}$ and 0.1% SDS (Sodium dodecyl sulfate).
5 Other various factors than the temperature condition would influence the stringency of the hybridization. It is possible for a person skilled in the art to attain stringency equivalent to the exemplified stringency of the hybridization by combining the various factors.

The detection of the expression of the gene of the distinguishing marker in the analyte cells may be preceded by quantitative PCR or semi-quantitative PCR in order to amplify the genes of the analyte cells. The quantitative PCR or semi-quantitative PCR may be RT-PCR (reverse PCR). The quantitative PCR or semi-quantitative PCR is carried
10 out with a pair of sense primer and antisense primer for amplifying the marker gene of the present invention.

Moreover, the method according to the present invention for distinguishing mesenchymal stem cells can be carried out easily by the Invader (Registered Trademark) technique. For example, the method according to the present invention for distinguishing mesenchymal stem cells can be carried out in the following manner: A signal probe, which is designed to have (i) a sequence that hybridizes specifically with the sequence of the distinguishing marker, and (ii) a site cleaved by an enzyme, is reacted with total RNA (or cDNA) extracted from the analyte cells, Invader (Registered Trademark) Oligo, Cleavase (Registered Trademark) Enzyme, and FRET Probe at a predetermined temperature and for a predetermined period (for example, at 63°C for 2 hours). The following literatures may be referred to for concrete experimental methods and conditions to carry out the method appropriately. Literatures: (i)
15 T. J. Griffin et al., Proc Natl Acad Sci U S A 96, 6301-6 (1999), (ii) M. W. Kaiser et al., J Biol Chem 274, 21387-94 (1999), (iii) V. Lyamichev et al., Nat Biotechnol 17, 292-6 (1999), (iv) R. W. Kwiatkowski et al., Mol Diagn 4, 353-64 (1999), (v) J. G. Hall et al., Proc Natl Acad Sci U S A 97, 8272-7 (2000), (vi) M. Nagano et al., J Lipid Res 43, 1011-8 (2002), (vii) etc. The use of the invader technique would eliminate the need of gene amplification, and thus can be performed fast and at low costs. The use of a commercially-available invader kit makes it more easy to carry out
25 the present invention.

Moreover, the method according to the present invention for distinguishing stem cells may be carried out by in situ hybridization. For example, molecular hybrid of the sample of the analyte cells on a slide glass may be directly formed by using the distinguishing marker or a material labeled with a part of the sequence thereof may be used as a probe. More specifically, a thin specimen (paraffin segment, frozen segment, etc.) of the analyte cell is prepared
30 on a slide glass and hybridized with the labeled probe. Then, the specimen is exposed after the probe is washed away and a photographic emulsion is applied on the specimen in the same manner as in the northern hybridization technique. After development, the hybridized portion is identified from silver particle distribution. The following literatures may be referred to for concrete experimental methods and conditions to carry out the method appropriately. Literatures: (i) "in situ hybridization technique (July, 1995), edited by Toshiyuki FURUSHO and You IMURA, published by Kanehara & Co., Ltd., pages 932 to 937, and (ii) "Analysis of gene expression by in situ hybridization technique" "Gene Engineering Experiments (May, 1991), written by Shintaro NOMURA, published by Japan Radioisotope Association, pages 221 to 232., (iii) etc. There are two types of the *in situ* hybridization technique: one adopts auto radiography to detect a site at which a DNA probe labeled with a radio isotope (mainly ^3H) is located, and the other adopts fluorescent microscopy to detect fluorescent signal from the labeled DNA probe. Either technique
35 is applicable to the present invention.

In case where the detection of the expression of the gene of the distinguishing maker according to the present invention is carried out by detecting the protein encoded by the gene, distinguishing mesenchymal stem cells may be carried out by detecting the expression of the distinguishing marker protein in mesenchymal stem cells and connective tissue cells with an antibody prepared from the protein, which antibody binds with the protein specifically.
40 Therefore, distinguishing marker for distinguishing mesenchymal stem cells is included, which is any one of polypeptides encoded by the genes having the base sequences identified with the accession numbers listed in Tables 1a to 1j. Moreover, an antibody is included, which is inducible with a polypeptide described in (e) or (f) and bindable specifically with the polypeptide:

(e) a polypeptide encoded by any one of the genes having the base sequences identified with the accession numbers listed in Tables 1a to 1j; and
50

(f) a partial polypeptide of the polypeptide described in (e).

The antibody may be a polyclonal antibody or a monoclonal antibody. For example, by any standard method conventionally known in the art, the antibody may be prepared against an antigen that is a whole or partial sequence of the polypeptide encoded by the gene of the distinguishing marker of the present invention.
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[0046] For example, the monoclonal antibody may be prepared in any method. For example, the monoclonal antibody may be obtained from antibody-producing hybridoma prepared by fusing mouse splenetic lymphocytes and mouse-derived myelocytes, each of which are obtained from a mouse immune with the antigen. The hybridoma may be prepared

by any conventionally known method such as hybridoma technique (Kohler, G. and Milstein, C., Nature 256, 495-497 (1975)), trioma technique, human B-cell hybridoma technique (Monoclonal Antibodies and Cancer Therapy, Alan R Liss, Inc., 77-96(1985)).

5 [0047] The antigen is not particularly limited, provided that it is a polypeptide. The antigen may be an antigenic protein, which is formed by binding an antigen determinant substance with a carrier protein. More specifically, the antibody cannot be produced if the antigen is a hapten, which does not have an ability of inducing the antibody production etc. However, the antibody production can be induced by immunizing with antigenic protein prepared by covalent bonding the antigen with a carrier, which is a bio-macromolecule such as a heterogeneous protein. The carrier is not particularly limited and various proteins conventionally known in this field such as ovalbumin, γ globulin, hemocyanin, etc. may be the carrier. Moreover, the monoclonal antibody may be produced transgenically or by the like method.

10 [0048] Moreover, the preparation of the polyclonal antibody may be carried out by purifying an antibody component from a body fluid of an experimental animal inoculated and sensitized with the antibody. Moreover, the animal to be immunized may be a conventionally known experimental animal such as a mouse, rat, rabbit, monkey, hours, etc., and is not particularly limited. Moreover, the inoculation and sensitization with the antigen may be carried out with intervals or quantities which are adopted in a standard method known in this art.

15 [0049] Immunologic measuring methods for well-known antibodies may be adopted to detect the expression of the protein of the distinguishing marker in the analyte cells by using the antibody according to the present invention. Immunologic measuring methods may be a known immunologic measuring method such as RIA method, ELISA method, fluorescent antibody technique, etc. Moreover, besides the above methods, western blotting technique, enzyme immunoassay, observation of coagulation, precipitation, hemoclastic reaction caused by the antibody, morphological detecting methods such as tissue immunostaining, cell immunostaining may be adopted, if necessary.

20 [0050] In the present invention, the detection of the difference in the expression levels of one distinguishing marker may be performed to distinguish mesenchymal stem cells from the result thereof. In order to distinguish mesenchymal stem cells more exactly and more accurately, it is preferable that the differences of the expression levels of plural distinguishing markers be used as indicators. This is another reason why the use of the microarray for distinguishing mesenchymal stem cells is preferable in the case where the difference in the expression levels of one distinguishing marker is used as the indicator.

30 <2. Method of Distinguishing and Separating Mesenchymal Stem Cells>

[0051] The method according to the present invention for distinguishing and separating should include the step of separating mesenchymal stem cells identified by the method of distinguishing the mesenchymal stem cells as described in Item <1>, and is not particularly limited in terms of specific arrangements such as steps other than this step, conditions, materials to use, apparatuses to use, etc.

35 [0052] In the present invention, the separation of mesenchymal stem cells may be carried out by using a Fluorescence-Activated Cell Sorter (FACS), for example. More specifically, mesenchymal stem cells are labeled with the antibody according to the present invention by fluorescent antibody technique. Then, whether or not the polypeptide of the distinguishing marker of mesenchymal stem cells is expressed in the analyte cells is detected. Referring to the detection, mesenchymal stem cells are distinguished and separated. The labeling of undifferentiated mesenchymal stem cells by the fluorescent antibody technique can be done by direct fluorescent antibody technique, or indirect fluorescent antibody technique. In the direct fluorescent antibody technique, an antibody, which specifically binds with the polypeptide of the distinguishing marker according to the present invention, is labeled with fluorescent, and then binds with mesenchymal stem cells, in which the antigen is expressed, thereby to label mesenchymal stem cells. In the indirect fluorescent antibody technique, mesenchymal stem cells, in which the antibody is express, bind with an unlabelled specific antibody of the present invention. And then, a labeled secondary antibody (anti-immune globulin antibody) is bound thereto. The mesenchymal stem cells labeled in these manner can be examined and separated by flow cytometry. The separated sample may be collected via a filter and obverted via epifluorescent microscope for confirmation.

40 [0053] Moreover, apart from FACS, the separation can be done by a Magnetic Cell Sorting (MACS) system. MACS uses an antibody labeled with a magnetized microbeads instead of fluorescent labeling. The targeted cells are specifically labeled with the antibody labeled by the magnetized microbeads for MASC, and then applied to a separating column disposed to a strong permanent magneto. A strong magnetic field produced in the separating column holds the magnetically labeled cell in the separating column but lets the unlabeled cells pass through the separating column. The cells held in the separating column is eluted from the separating column by removing the separating column out of the strong magnetic field. Thereby, mesenchymal stem cells are separated.

45 [0054] Furthermore, the method of the present invention may include the step of concentrating the sample by using a membrane filter or condensation prior to the step of separating by FACS, MACS, or the like.

<3. Distinguishing/Separating Kit>

[0055] A kit according to the present invention for distinguishing/ separating mesenchymal stem cells should comprise any one of materials described respectively in (g) to (i), and is not particularly limited in terms of other materials, constituent components, etc.:

(g) the above-described microarray for distinguishing mesenchymal stem cells;

(h) the above-described antibody; and

(i) the probe for detecting whether the distinguishing marker gene for mesenchymal stem cells is expressed or not, the distinguishing marker gene comprising a polynucleotide, which, under stringent condition, hybridizes with a gene or a partial sequence thereof, the gene having a base sequence identified with the accession number listed in any one of Tables 1a to 1j.

[0056] The kit is for easily performing the method of distinguishing mesenchymal stem cells described in Item <1>, or the method of distinguishing/separating mesenchymal stem cells described in Item <2>. The kit can be easily commercialized by comprising any one of materials described respectively in (g) to (i).

[0057] Moreover, as described above, it is preferable for greater exactness and accuracy to perform the above methods with plural ones of the distinguishing markers listed in Tables 1a to 1j. Thus, it is preferable for the kit according to the present invention to comprising plural ones of the distinguishing markers. For example, as described in Item <1>, various combination of the genes may be selected and used as a distinguishing marker kit.

[0058] As described above, the combination of the distinguishing markers makes it possible to distinguish and separate mesenchymal stem cells more exactly and accurately compared with the single use of the distinguishing marker.

<4. Cell-containing compositions and Drugs of Regenerative medicine>

[0059] A cell-containing composition according to the present invention should comprise mesenchymal stem cells separated by the method of distinguishing and separating mesenchymal stem cell described in Item <2>, or mesenchymal stem cells thus obtained and then multiplied. The cell-containing composition according to the present invention is not particularly limited in terms of other arrangements such as compositional arrangement (buffer liquid, culture liquid, or the like), cell number, etc. Moreover, the cell-containing composition according to the present invention preferably contains a secreta (e.g., growth factor, or the like) secreted from cells contained in the cell-containing composition.

[0060] The cell-containing composition comprises undifferentiated mesenchymal stem cells capable of differentiating to bones, cartilages, fats, muscles, tendons/ligaments, nerves, etc. Thus, the cell-containing composition can be used as a drug (pharmaceutical composition) for regenerative medicine. That is, a drug according to the present invention for regenerative medicine is not limited particularly in terms of other specific arrangements, provided that it comprises the cell-containing composition. For example, the use of the drug may be such that the undifferentiated mesenchymal stem cells are differentiated to cells of a kind as suitable for the use, and then used. More specifically, this may be carried out in such a manner that the mesenchymal stem cells are differentiated to osteoblasts, chondrocytes and adipose cells, muscle cells, nerve cells, etc. by using a differentiation inducing material such as a cytokine or the like, and then the differentiated cells are administered to a patient to be treated with the regenerative medicine. Therefore, the present invention encompasses drugs for regenerative medicine containing a cell composition obtained by differentiation of the undifferentiated mesenchymal stem cells, apart from the drugs containing the undifferentiated mesenchymal stem cells.

[0061] Moreover, administration conditions of the drug for regenerative medicine in actual clinical applications may be determined as appropriate by animal experiments or the like performed as standard methods in this field. That is, the conditions suitable for prevention or therapeutic effects may be determined via animal experiments to study the administration conditions such as dosage, administration intervals, administration routes, etc. The drug for regenerative medicine can be utilized as a drug for "regenerative medicine by cell transplantation" which regenerates a tissue lost by a disease or impairment and resumes a function, which tissue cannot be regenerated by a conventional therapeutic method.

[0062] The drug for regenerative medicine is not limited to treatment of a particular disease, symptom, clinical profile, or the like, provided that the drug is used for the purpose of "regenerative medicine by cell transplantation". More specific examples of the drug for regenerative medicine include transplantation of marrow mesenchymal stem cells to a patient of lower limb ischemia (Buerger's disease), transplantation of marrow mesenchymal stem cells to a patient of a periodontal disease, transplantation of marrow mesenchymal stem cells to a patient of osteoarthritis, transportation of amniotic epithelium sheet to burn injured portion, transportation of amniotic stem cells to a patient of diabetes mellitus, and the other transplantation.

[0063] The drug for regenerative medicine may be used as a composition by mixed with a pharmaceutically allowable carrier. Examples of the carrier encompass sterilized water, physiological saline, buffers, plant oil, emulsifiers, suspending

agents, salts, stabilizers, preservatives, surfactants, release controllers, other proteins (BSA etc.), transfection reagents (encompassing lipofection reagents, liposome, and the like), and the like. Moreover, the following carriers are applicable in the present invention: extracellular matrixes such as glucose, lactose, gum Arabic, gelatin, mannitol, starch paste, magnesium trisilicate, talc, corn starch, keratin, colloid silica, potato starch, urea, hyaluronic acid, collagen, etc.; poly-

lactose, calcium phosphate carrier, etc.

[0064] The drug may have any form. For example, the drug may have forms of solution (injection-type), microcapsule, tablet, and the like. The drug may be administered systematically or locally. The local administration is preferable if the systematic administration is side effective or is not so effective as the local administration.

[0065] Moreover, the drug may be administered to a patient in any way and the administration may be, for example, surgical, percutaneous, transbronchial, muscular, interperitoneal, intravenous, intra-articular, subdermal, medullary, intracerebroventricular, or oral. The drug may be systematically administered or locally. The local administration to lesion section is preferable if the systematic administration is side effective. Dosage and the way of administration may be varied depending on weight, age, and symptom of the patient, therapeutic purpose, and tissue mobility of the active constituents of the drug, and the other factors. A person skilled in the art can arbitrarily select the dosage and the way of administration.

[0066] The therapeutic treatment targets human basically, but may target pet animals (pets) apart from human. Examples of the pet animals encompass non-human mammals such as mice, rats, rabbits, cats, dogs, monkeys, horses, sheep, cows, etc. and other spinal animals.

[0067] Moreover, the drug according to the present invention is preferably arranged such that the mesenchymal stem cells or cells differentiated from the mesenchymal stem cells, which are contained therein, be derived from the individual targeted by the therapeutic treatment. However, for the sake of mass production and the other factors, the drug according to the present invention may be arranged such that the mesenchymal stem cells or cells differentiated from the mesenchymal stem cells, which are contained therein, be not derived from the individual targeted by the therapeutic treatment (that is, allogeneic cell). In this arrangement, the immune reaction should be inhibited by a standard method such as use of an immune reaction inhibitor or the like.

<5. Other Use>

[0068] It has not been understood which part of the body mesenchymal stem cells are present *in vivo* (e.g., in marrow). However, the use of the antibody according to the present invention makes it possible to study which part of the body the mesenchymal stem cells are present. Therefore, the technique of the present invention can be applied to development of new medicines or the like. More specifically, if it is understood how the mesenchymal stem cells move or migrate to the lesion section *in vivo*, it is possible to develop a medicine to contain an active constituent for promoting movement or migration of the mesenchymal stem cell to the lesion.

[0069] By using, solely or in combination, a method according to the present invention for distinguishing mesenchymal stem cells, a microarray according to the present invention for distinguishing mesenchymal stem cells, an antibody according to the present invention, and a kit according to the present invention for distinguishing/separating mesenchymal stem cells, it is also possible to judge whether a mesenchymal stem cell-related disease has been developed or whether there is a possibility that such a mesenchymal stem cell-related disease will be developed. This judging method is applicable to both prevention and diagnosis of the diseases.

[0070] Applying the present invention to treating a sample separated from a living body is preferred to applying the present invention to treating a human body directly. The sample separated from the living body can be obtained from the human body by a standard method in this field. Examples of such a sample encompass cells (which encompass mesenchymal stem cells) obtained from marrow liquids, peripheral bloods, cord bloods, adipose tissues, periosteum, muscles, synovial membrane, oral cavity tissue. Especially, it is preferable that the biosample contain mesenchymal stem cells be obtained by any one of the methods disclosed in Patent Citations 1 to 3. It is preferable that the sample contain mesenchymal stem cells.

[0071] This judging method can be applied to judging whether an examined person has developed a disease or how much possibility of developing the disease in the future the examined person has, for example, by finding the gene expression profiles of the distinguishing marker of the mesenchymal stem cells in a healthy person and a patient of the disease in advance and comparing an expression profile of the mesenchymal stem cell in the examined person (patient) with the gene expression profiles of the healthy person and the patient of the disease to find which of the gene expression profiles of the healthy person and patient the expression profile of the examined person (patient) is similar. In this DESCRIPTION, the "healthy person" is a person who does not have the disease to be examined, and the "patient of the disease" is a person who has the disease. The method according to the present invention for judging whether a disease has been developed or not, may use the method for distinguishing mesenchymal stem cells or the like in other manners than the above arrangement, and may be appropriately modified to use a standard method in this field as of filing of the present application.

[0072] The "disease related with mesenchymal stem cells" encompasses any diseases which are caused (that is, "regeneration impairment syndromes) caused in relation to the mesenchymal stem cells such as conventionally known abnormality in mesenchymal stem cells or in differentiation from mesenchymal stem cells. For example, the disease may be a disease targeted by "regenerative medicine by cell transplantation" to regenerate a tissue lost by a disease or impairment and thereby to regain the function, a disease caused by a quantitative reduction in mesenchymal stem cells (abnormality in the number of cells or the like abnormality) or by a qualitative degradation in mesenchymal stem cells (abnormality in the differentiation ability or the like abnormality), that is, by shortage of supply of mesenchymal stem cells, and the like disease. Specific examples of the disease encompass lower limb ischemia (Buerger's disease), periodontal disease, osteoarthritis, intractable skin disease, diabetes, osteoporosis, ischemic heart disease, liver disease, kidney disease, neurodegenerative (Alzheimer disease etc.), and the like.

[0073] Osteoarthritis is an example of the disease caused by the shortage of the supply of mesenchymal stem cells. It is deduced that osteoarthritis is caused by quantitative abnormality in mesenchymal stem cell *in vivo* (more specifically, reduction in the number of the mesenchymal stem cells) due to various factors such as aging, life style, etc. Thus, it is expected that the use of the distinguishing method according to the present invention or the like makes it possible to grasp the quantitative change in mesenchymal stem cell *in vivo* so as to judge whether a disease has been developed or not and so as to prevent the development of the disease. That is, the quantitative change in mesenchymal stem cells can be detected by using the distinguishing method according to the present invention, the distinguishing marker, or the like. Thus, it is expected that the use of this technique makes it possible to diagnose whether or not there is a possibility of developing a disease that is caused by the shortage of the supply of mesenchymal stem cells. More specifically, for example, a biosample is obtained from the examined person (patient) on a regular basis (at intervals of a few months to few years) to be examined on the quantitative change in mesenchymal stem cells in the biosample by using the distinguishing method of the present invention or the like. The result of the examination of the examined person is compared with the results of examinations in quantitative changes in the mesenchymal stem cells in a healthy person and a patient of osteoarthritis. The examinations of the healthy person and the patient of the disease are performed in advance and in the same manner as the examination of the examined person. The comparison allows exact and accurate diagnosis of whether the examined person has developed osteoarthritis, or has a possibility of developing osteoarthritis in the future.

[0074] Moreover, the present invention encompasses drugs for regenerative medicine for suppressing undifferentiating property of mesenchymal stem cells, the drugs comprising siRNA corresponding to the genes having the base sequences identified with the accession numbers listed in Tables 1a to 1j, or to the partial sequences thereof. They are drugs for reducing the undifferentiating property of the mesenchymal stem cell by using RNAi. In other words, the drugs are drugs for regenerative medicine for suppressing the undifferentiating property of mesenchymal stem cell by using RNAi/siRNA by using the genes having the base sequences identified with the accession numbers listed in Tables 1a to 1j, or to the partial sequences thereof.

[0075] With the drug for regenerative medicine, it is possible to suppress the undifferentiating property of mesenchymal stem cells certainly and efficiently. Thus, the drug for regenerative medicine is highly beneficial for the regenerative medicine.

[0076] The embodiments of the present invention are described in further detail via the following Examples. Needless to say, the present invention is not limited to these Examples. The invention being thus described, it will be obvious that the same may be varied in many ways. Such variations are not to be regarded as a departure from the spirit and scope of the invention, and all such modifications as would be obvious to one skilled in the art are intended to be included within the scope of the following claims.

[Example]

[0077] In the present Examples, the following cells were examined in their gene expression profiles: three lines of human fibroblasts (hereinafter, may be referred to as "FB"), three lines of mesenchymal stem cells (hereinafter, may be referred to as "MSC"), three lines of osteoblasts (hereinafter, may be referred to as "OS"), three lines of chondrocytes (hereinafter, may be referred to as "CH"), three lines of adipose cells (hereinafter, may be referred to as "AD"). The osteoblasts, chondrocytes, and adipose cells were prepared by differentiation from the mesenchymal stem cells *in vitro*.

(0) Differentiation and Collection of Total RNA

[0078] Firstly, mesenchymal stem cells were differentiated to adipose cells, chondrocytes, or osteoblasts, and then total RNA was collected. More specifically, these differentiations were carried out as follows.

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(0-1) Differentiation to Adipose Cells and Collection of RNA

[0079] Media having the following compositions were used as basal medium, adipose differentiation inducing medium, and adipose differentiation maintenance medium.

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- Adipose Differentiation Inducing Medium
Basal Medium: DMEM (Sigma: D5796, high glucose = 4500mg/L)
Additives: 10% (V/V) FBS (Hyclone, Lot No.: ANC18139) Penicillin-Streptomycin (Sigma: P0781)
The followings were added freshly (to add the quantities in two weeks).
Insulin: 10 μ g/mL (10 mg/mL acetic acid aqueous solution stock) (Wako: 090-03446)
Dexamethason: 1 μ M (10mM EtOH stock) (Sigma: D4902)
Indomethacin: 200 μ M (2000 mM DMSO stock) (Wako: 097-02471)
3-isobutyl-1-methylxanthine: 500 μ M (1000mM DMSO stock) (Wako: 537-72353)

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- Adipose Differentiation Maintenance Medium
Basal Medium: DMEM (Sigma:#D-5796, high glucose=4500mg/L)
Addition: 10% (V/V) FBS (Hyclone, Lot No.: ANC 18139)
Penicillin-Streptomycin (Sigma: P0781)
The following was added freshly (to add the quantities in two weeks).
Insulin: 10 μ g/mL (10 mg/mL acetic acid aqueous solution stock) (Wako: 090-03446)

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[0080] After two weeks were past, L-glutamine: 2mM (200mM PBS stock) (Sigma: G3126) was added to the medium. After that, the addition thereof was repeated every two weeks.

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[0081] After MSC became confluent, the MSC was cultured for 11 days in total by repeating 2-day incubation in the adipose differentiation inducing medium and three-day incubation in the adipose differentiation maintenance medium via medium replacement. Then, total RNA was collected. The medium replacement is carried out by dropping a new medium gently to a surface of 10% residue of an old medium. All the additives were freshly added when the media were replaced.

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[0082] The RNA extraction after the adipose differentiation was carried out in the following manner. Firstly, the cells were prepared via 11-day adipose differentiation (in ϕ 100mm dish). Next, the medium was removed by suction, and the cells were washed with PBS twice. Then, the cell was homogenized with TRIzol (Registered Trademark) (4000 μ L/ ϕ 100mm dish) by using a 21G needle and 1ml syringe. After that, chloroform was added thereto in a 1/4 quantity thereof, the culture was stirred by Vortex, and then stood still for 20 minutes at room temperatures. Next, the culture was centrifuged at 14000 rpm for 20 minutes at room temperatures (Tomy, MCX-150). Then, a supernatant thereof was transferred into Eppendorf tube, in which 70% EtOH (prepared with RNAs free water) of a quantity equivalent to the supernatant was added thereafter. Then, 700 μ l of a sample thus prepared was applied into a RNeasy (registered trademark) Mini column, and vacuum was applied to the column (Qiagen, QIAvac 24). This was repeated until the whole sample was consumed (2 column/one ϕ 100mm dish). The above process was carried out according to the Manual attached to the RNeasy kit. Finally, RNA purification was carried out with a kit (#1906) produced by Ambion.

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(0-2) Differentiation to chondrocyte and Collection of RNA

[0083] The chondrocyte differentiation inducing medium had the following composition.

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- Chondrocyte Differentiation Inducing Medium
 α MEM (Sigma:#4526)
Penicillin Streptomycin: (Sigma: #P0781)
L-glutamine: 2mM (stock sol 200 mM PBS) (Sigma: #G3126)
Dexamethason: 10⁻⁷ M (stock sol 1 M EtOH) (Sigma: #D-1756)
Ascorbate 2-phosphate: 50 μ g/ml (stock sol 50 mg/ml MQ) (Sigma: #A-8960)
D-(+)-glucose: 4.5 g/l (stock sol 450 g/l) (Sigma: #G-8769)
Pyruvate: 100 μ g/ml (stock sol 100 mg/ml MQ) (Sigma: #28-4020-2)
ITS-plus: 1 % (V/V) (insulin 6.25 μ g/ml, transferrin 6.25 μ g/ml, selenous acid 6.25 μ g/ml, linoleic acid 5.33 μ g/ml, bovine serum albumin 1.25 mg/ml) (BD: #354352)
TGF- β 3: 10 ng/ml (stock sol 10 μ g/ml HCl 4 mM, HSA or BSA 1mg/ml) (Pepro Tec ECL Ltd #100-36)

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[0084] The chondrocyte differentiation inducing medium of the quantity was added in two weeks. Moreover, TGF- β 3 was not added initially: it was added freshly at medium replacement.

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[0085] Culturing in the chondrocyte differentiation was carried out by pellet incubation technique. More specifically, the culturing was carried out with the inoculation in a density of 2.5×10^5 cells/tube, and an initial quantity of the chondrocyte differentiation medium of 0.5ml per tube. After the inoculation, the medium was centrifuged ($500g \times 5min$). Then, from Day 0 on which the cells were inoculated, the medium was incubated for 28 days via medium replacement performed every 3 days. The first medium replacement reduced the quantity to 1ml per tube.

[0086] RNA extraction was carried out in the following manner. Firstly, the cells were prepared via 28-day chondrocyte differentiation (6 pellets or more). Then, the medium was removed by suction, and then 0.4ml of PBS was added in the pellets, and then sucked. After 0.2ml of TRIzol (Registered Trademark) (Invitrogen: 15596-018) was added to each tube, grinding extraction was performed with pellet pestle and silica powder. Then, it was further added in a quantity of 0.8ml/tube, and the extracted was transferred to tubes. Then, the extracted was treated with chloroform and ethanol. After that, it was treated with RNeasy kit. Thereafter, the process of the extraction was identical with that of the adipose differentiation.

(0-3) Differentiation to Osteoblast and Collection of RNA

[0087] The osteoblast differentiation inducing medium had the following composition.

- Basal Medium

- DMEM (Sigma D6046)
- FBS (Hyclone) (Bovine Fetal serum) of 10% Final Concentration
- Antibiotic: penicillin- streptomycin (Sigma:P0781)

- Osteoblast Differentiation Inducing Medium

- DMEM (Sigma D6046 containing glucose 1000mg/L)
- FBS (Hyclone) of 10% Final Concentration · Dexamethason (Sigma D-1756) of $10^{-7}M$ Final Concentration
- β -glycerophosphate (Tokyo Chemical Industry Co., Ltd. G-0195) of 1.0 mM Final Concentration
- Ascorbate 2-phosphate (Sigma: A-8960) of $50\mu g/ml$ Final Concentration added every two weeks
- L-glutamine of 2mM Final Concentration added every two weeks
- Antibiotic: penicillin- streptomycin (Sigma:P0781)

[0088] As a referential literature, referred to was "Osteogenic differentiation of purified culture-expanded human, mesenchymal stem cell in vitro." Jaiswal N. J. et al., Cell Biochem. 64, 295-312, 1997.

[0089] Firstly, a surface of a culture plate was soaked with 0.01% Collagen type 1 solution (functional peptide IFP9660) overnight. After the solution was removed therefrom, the plate was washed with PBS (phosphate buffered saline) twice. Next, the cells were inoculated on the basal medium for mesenchymal stem cells ($10000 \text{ cell}/\text{cm}^2$). After the cells were incubated to be confluent (in 2 to 3 days after the inoculation), the medium was replaced with the osteoblast differentiation inducing medium (Day 0). After 28-day incubation from Day 0 replacing the osteoblast differentiation inducing medium every 3 days, total RNA was collected. The collection of total RNA was carried out in the same manner as in the adipose cells.

[0090] An outline of the flow of the experiment after the collection of total RNA is illustrated in Fig. 1.

(1) cDNA/cRNA Synthesis

[0091] Firstly, double stranded cDNA was synthesized from the sample RNA using T7 oligo dT primer. Next, cRNA was synthesized from the double stranded cDNA by in vitro Transcription reaction. In the synthesis of cRNA, the sample was labeled by incorporating biotin-labeled ribonucleotide therein.

(2) Hybridization

[0092] Next, the biotin-labeled cRNA was fragmented and hybridized with GeneChip (Registered Trademark: Affymetrix) probe array.

(3) Fluorescent Labeling

[0093] After the array hybridized overnight was washed, streptavidin - phycoerythrin was added therein thereby labeling the sample with fluorescent.

(4) Scanning/Data Analysis

[0094] Finally, the fluorescent-labeled array was scanned to capture a non-photographic image, which was then analyzed by special analysis software so as to perform signal digitalization and expression analysis.

[0095] The steps (1) to (4) were done by analysis service provided from KURABO, using the DNA microarray "GeneChip (registered trademark)" produced by Affymetrix. See the homepage of KURABO at the following address: <http://www.bio.kurabo.co.jp/idensi/genechip/genechiptop.htm> The analysis service performs the analysis of a provided sample RNA with GeneChip (registered trademark). Because a person skilled in the art can understand the steps (2) to (4) by referring to the URL and KURABO's analysis service, the explanations on the steps (2) to (4) are omitted here.

[0096] In the present Example, the GeneChip (registered trademark) was Human Genome U 133 Plus 2.0 Arrays (HG-U 133 Plus 2.0). Moreover, the GeneChip analysis conditions of the analysis service in the present Example were as follows.

[0097] Biotin-labeled target was prepared initially with 2 μ g of total RNA. Its analysis protocol is described in One-cycle Target Labeling, GeneChip Expression Analysis Technial Manual, 701021 Rev.5, Section 2 Eukaryotic Sample and Array Processing, Chapter 1 Eukaryotic Target Preparation.

[0098] Analysis protocol of the hybridization/ scanning is described in GeneChip Expression Analysis Technial Manual, 701021 Rev.5, Section 2 Eukaryotic Sample and Array Processing, Chapter 2 Eukaryotic Target Hybridization. A hybridization oven used herein was Hybridization Oven 640 110V (Affymetrix 800138). A washing/staining apparatus used herein was Fluidics Station 450 (Affymetrix 00-0079). A scanner used herein was GeneChip Scanner 3000 (Affymetrix 00-0074). Software used herein was GeneChip Operating Software ver 1.1 (Affymetrix 690036).

[0099] Analysis protocol of analysis and digitalization of the scanned image is described in GeneChip Expression Analysis Technial Manual, 701021 Rev.5, Section 2 Eukaryotic Sample and Array Processing, Chapter 3 Washing, Staining, and Scanning. Software used herein was GeneChip Operating Software ver1.1. Algorism used herein was Statistical. Analysis parameters at creating a CIIP file were Scaling Factor; 1, Target Value; 500, Detection Call; Alpha1=0.05, Alpha2=0.065, and Tau=0.015.

[0100] The data of analysis and digitalization of the scanned image was obtained by the scanning/data analysis of (4) and processed by "GeneSpring" (Product Name, Trademark) so as to prepare a gene list or the like. See <http://www.silicongenetics.com/cgi/SiG.cgi/Products/GeneSpring/index.smf> for "GeneSpring", which is gene analysis software produced by Silicon Genetics. The software "GeneSpring" was used according to the manual attached therewith.

[0101] That is, gene expression profiles of various genes related to 54675 human genes (probes) were analyzed in the present Example. More specifically, RNAs were collected from cells of 15 lines and analyzed with the DNA microarray in terms of the expression levels for 54675 human genes (probes). The 15 lines were 3 lines of mesenchymal stem cells (MSC) having the ability of differentiating to various cells, 3 lines of the cells (OS) obtained from the bone differentiation of MSC, 3 lines of the cells (CH) obtained from the cartilage differentiation, 2 lines of the cells (AD) obtained from the adipose differentiation, and 3 lines of fibroblasts (FB) derived from skin and gingiva, which fibroblasts did not have the ability of differentiating to various cells.

[0102] The analysis results are illustrated in Fig. 2. Each curves represents one gene (probe) in Fig. 2 (that is, there are 54675 curves in Fig. 2) where the vertical axis represents the gene expression intensities and the horizontal axis represents cells, which are, from the left, AD (3 lines) obtained from the adipose differentiation, CH (3 lines) obtained from the cartilage differentiation, FB (3 lines) of skin and gingiva, stem cells MSC (3 lines), and OS (3 lines) from bone differentiation. It should be noted that the same kind of cells such as the left most 2 lines of AD obtained from adipose differentiation tend to show the same expression level, and thus tend to be plotted in parallel with each other.

[0103] Moreover, when Fig. 2 is shown in color, the curves are colored according to the expression in such a way that red represents genes expressed at high levels in MSC, blue represents genes expressed at low levels in MSC, and yellow represents genes expressed at medium levels in MSC. When Fig. 2 is shown in black and white, this information is not given.

[0104] The genes in red in 3 lines of MSC in the middle but on the right side of Fig. 2 but show low expression intensities in other cell types are applicable as undifferentiating markers specific to MSC. That is, genes having such expression profiles that "the expression level is high in MSC but low in the other cells" were selected and identified as the undifferentiating markers specific to MSC, the markers being capable of differentiating mesenchymal stem cells from bone, cartilage, adipose, and fibroblast. The selection of the distinguishing markers specific to MSC was carried out as follows.

[0105] Firstly, before the selection of the distinguishing markers specific to MSC, preprocess was carried out referring to flag information obtained from the analysis result of GeneChip (registered trademark). More specifically, genes indicated with flag information indicating expression of gene, that is, flag information "present call" or "margenal call" were selected. This was done because a gene with a low expression level in MSC would not allow to be detected exactly and accurately even if the expression thereof was different from that of the other genes.

[0106] Then, from among the genes satisfying the preprocess conditions, the distinguishing markers specific to MSC were selected. More specifically, this experiment examined and compared the expressions of various genes in the 5

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types of cells: MSC, OS (obtained from the bone differentiation from MSC), CH (obtained from the cartilage differentiation from MSC), AD (obtained from the adipose differentiation from MSC), and FB. In this way, five relative expression intensities in the 5 types of cells were obtained per gene. One of the criteria for the selection was whether a difference between the expression level in MSC and a lowest one of the expression levels of the four cells other than MSC was 2 or more.

[0107] In other words, the one of the criteria selected genes whose expression level in MSC was double or greater than that in AD, that in CH, that in FB, and that in OS. This is because the difference being at least double makes it possible to distinguish MSC from other cells exactly and accurately. That is, a gene whose expression level in MSC is double or greater than those in the other cells can be used as the marker practically.

[0108] The thus calculated difference between the expression in MSC and those in the other cells can be an indicator to concretely express how intensely the expression of a gene is expressed in MSC than in the other cells. Thus, "the difference of 2 or greater" was set as one of the criteria for the selection. That is, one purpose of the present invention is to find a distinguishing marker for selecting undifferentiated mesenchymal stem cells specifically. Thus, the marker should be expressed at a remarkably greater expression level in mesenchymal stem cells than in the other cells. Because of this, the criterion for the selection was set as such.

[0109] Another criterion was "the expression level of the gene in MSC is high". This is because a small absolute value of the expression level in mesenchymal stem cells would make it difficult to detect the gene exactly and accurately or would lead to large errors. That is, it was considered that the candidates of the distinguishing markers should have a large absolute expression level. Thus, the another criterion was set, which is "the gene has an expression level of 0.5 or greater in MSC".

[0110] One hundred thirty nine genes, which satisfied the criteria, were selected as the distinguishing markers of undifferentiated MSC. Tables 3a to 3e show the 139 distinguishing markers and the evaluation thereof on the criteria in the selection.

[Table 3a]

| Classification 1 | Gene symbol | Genbank number | Fold Average | Expression level |
|--------------------|-------------|----------------|--------------|------------------|
| ATP/GTP binding -1 | BRIP1 | NM_032043 | 4.7 | 0.2 |
| ATP/GTP binding -2 | PASK | NM_015148 | 9.4 | 0.3 |
| ATP/GTP binding -3 | RAC2 | NM_002872 | 13.6 | 1.0 |
| ATP/GTP binding -4 | KIF18A | NM_031217 | 4.8 | 0.4 |
| ATP/GTP binding -5 | NEK7 | NM_133494 | 2.9 | 34.2 |
| ATP/GTP binding -6 | ARL4C | NM_005737 | 3.7 | 8.6 |
| ATP/GTP binding -7 | EDEM1 | NM_014674 | 2.6 | 1.9 |
| ATP/GTP binding -8 | CAMK2D | NM_172127 | 2.7 | 4.2 |
| | | | | |
| Classification 2 | Gene symbol | Genbank number | Fold Average | Expression level |
| binding -1 | PDE5A | NM_001083 | 7.0 | 0.8 |
| binding -2 | RGS4 | NM_005613 | 25.8 | 9.7 |
| binding -3 | EGFL3 | NM_001409 | 7.1 | 0.7 |
| binding -4 | FHL2 | NM_001450 | 4.4 | 41.6 |
| binding -5 | HRB2 | NM_007043 | 4.4 | 7.6 |
| binding -6 | CAPZA1 | NM_006135 | 2.3 | 30.9 |
| binding -7 | PAPPA2 | NM_020318 | 4.8 | 0.3 |
| binding -8 | LOXL2 | NM_002318 | 10.8 | 4.0 |
| binding -9 | LOX | NM_002317 | 4.7 | 9.7 |
| binding -10 | ADAMTS5 | NM_007038 | 3.4 | 5.6 |

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(continued)

| Classification 2 | Gene symbol | Genbank number | Fold Average | Expression level |
|-----------------------------------|-------------|----------------|--------------|------------------|
| Classification 3 | Gene symbol | Genbank number | Fold Average | Expression level |
| cell growth and/or maintenance-1 | CCND1 | NM_053056 | 6.1 | 19.2 |
| cell growth and/or maintenance-2 | CDC25A | NM_001789 | 4.7 | 0.1 |
| cell growth and/or maintenance-3 | IER3 | NM_052815 | 6.8 | 8.5 |
| cell growth and/or maintenance-4 | BCL2 | NM_000633 | 5.0 | 0.3 |
| cell growth and/or maintenance-5 | NALP1 | NM_033004 | 6.3 | 5.6 |
| cell growth and/or maintenance-6 | PAK3 | NM_002578 | 12.8 | 0.3 |
| cell growth and/or maintenance-7 | PODXL | NM_001018111 | 6.8 | 0.7 |
| cell growth and/or maintenance-8 | CCL26 | NM_006072 | 7.7 | 0.4 |
| cell growth and/or maintenance-9 | FBLN1 | NM_006486 | 0.4 | 4.2 |
| cell growth and/or maintenance-10 | LAMA1 | NM_005559 | 4.5 | 0.8 |
| cell growth and/or maintenance-11 | NTNG1 | NM_014917 | 5.0 | 0.1 |

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[Table 3b]

| Classification 4 | Gene symbol | Genbank number | Fold Average | Expression level |
|------------------------|-------------|----------------|--------------|------------------|
| cytokine -1 | GDF15 | NM_004864 | 4.4 | 3.0 |
| cytokine -2 | IL6 | NM_000600 | 14.9 | 3.9 |
| cytokine -3 | CTGF | NM_001901 | 5.6 | 60.6 |
| cytokine -4 | VEGF | NM_001025366 | 4.5 | 24.4 |
| cytokine -5 | VEGFC | NM_005429 | 4.1 | 9.8 |
| cytokine -6 | HGF | NM_000601 | 6.5 | 0.7 |
| | | | | |
| Classification 5 | Gene symbol | Genbank number | Fold Average | Expression level |
| cytoskeleton-1 | KRT19 | NM_002276 | 130.0 | 1.7 |
| cytoskeleton-2 | KRTAP1-5 | NM_031957 | 29.8 | 14.5 |
| cytoskeleton-3 | KRTAP2-1 | BC012486 | 9.5 | 1.8 |
| cytoskeleton-4 | KRTHA4 | NM_021013 | 20.8 | 1.1 |
| cytoskeleton-5 | CKAP2 | NM_018204 | 4.8 | 0.1 |
| cytoskeleton-6 | KRTAP1-1 | NM_030967 | 38.1 | 2.5 |
| cytoskeleton-7 | KRT18 | NM_000224 | 30.2 | 2.1 |
| cytoskeleton-8 | KAP2.1B | AJ406929 | 18.7 | 0.3 |
| cytoskeleton-9 | SSH1 | NM_018984 | 3.0 | 6.7 |
| | | | | |
| Classification 6 | Gene symbol | Genbank number | Fold Average | Expression level |
| enzyme-1 | LXN | NM_020169 | 10.1 | 7.6 |
| enzyme-2 | IFI30 | NM_006332 | 11.0 | 5.5 |
| enzyme-3 | CPA4 | NM_016352 | 8.1 | 1.0 |
| | | | | |
| Classification 7 | Gene symbol | Genbank number | Fold Average | Expression level |
| extracellular matrix-1 | CHI3L1 | NM_001276 | 158.5 | 25.7 |
| extracellular matrix-2 | KRT23 | NM_015515 | 4.0 | 0.1 |
| extracellular matrix-3 | FLG | NM_002016 | 284.4 | 8.8 |
| extracellular matrix-4 | ADAMTS1 | NM_006988 | 7.2 | 6.9 |
| extracellular matrix-5 | FRMD5 | NM_001031729 | 23.8 | 2.1 |

[Table 3c]

| Classification 8 | Gene symbol | Genbank number | Fold Average | Expression level |
|-----------------------------|-------------|----------------|--------------|------------------|
| growth factor or receptor-1 | IGFBP1 | NM_000596 | 5.8 | 0.3 |
| growth factor or receptor-2 | CFI | NM_000204 | 28.7 | 1.7 |
| growth factor or receptor-3 | ESM1 | NM_007036 | 11.4 | 0.7 |
| growth factor or receptor-4 | F2RL1 | NM_005242 | 4.1 | 0.4 |
| growth factor or receptor-5 | MET | NM_000245 | 7.3 | 1.1 |
| growth factor or receptor-6 | HTR7 | NM_000872 | 3.7 | 0.2 |

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(continued)

| Classification 8 | Gene symbol | Genbank number | Fold Average | Expression level |
|-----------------------------|-------------|----------------|--------------|------------------|
| growth factor or receptor-7 | IGFBP3 | NM_001013398 | 3.4 | 90.7 |
| | | | | |
| Classification 9 | Gene symbol | Genbank number | Fold Average | Expression level |
| membrane -1 | ABHD2 | NM_007011 | 4.5 | 2.1 |
| membrane -2 | ITGA2 | NM_002203 | 7.7 | 2.2 |
| membrane -3 | LAMA3 | NM_198129 | 6.6 | 1.3 |
| membrane -4 | NETO2 | NM_018092 | 7.9 | 4.9 |
| membrane -5 | NTN4 | NM_021229 | 5.5 | 6.5 |
| membrane -6 | PTGER1 | NM_000955 | 5.2 | 0.5 |
| membrane -7 | EPHB2 | NM_017449 | 12.4 | 0.4 |
| membrane -8 | SFRP1 | NM_003012 | 0.4 | 0.6 |
| membrane -9 | CD33L3 | NM_213602 | 11.9 | 1.3 |
| membrane -10 | GLIPR1 | NM_006851 | 4.8 | 6.8 |
| membrane -11 | UGCG | NM_003358 | 4.2 | 14.2 |
| membrane -12 | ADORA1 | NM_000674 | 3.5 | 0.5 |

[Table 3d]

| Classification 10 | Gene symbol | Genbank number | Fold Average | Expression level |
|----------------------------|-------------|----------------|--------------|------------------|
| membrane binding protein-1 | ANXA10 | NM_007193 | 24.5 | 1.2 |
| membrane binding protein-2 | RARRES1 | NM_206963 | 7.2 | 0.5 |
| membrane binding protein-3 | HNT | NM_016522 | 13.1 | 16.0 |
| membrane binding protein-4 | CNTNAP3 | NM_033655 | 22.3 | 1.2 |
| Classification 11 | Gene symbol | Genbank number | Fold Average | Expression level |
| protein binding -1 | SYT1 | NM_005639 | 6.5 | 0.1 |
| protein binding -2 | MLF1 | NM_022443 | 4.6 | 0.1 |
| protein binding -3 | CDCP1 | NM_022842 | 17.4 | 0.9 |
| protein binding -4 | KIAA0746 | NM_015187 | 6.1 | 4.2 |
| protein binding -5 | PSCDBP | NM_004288 | 4.1 | 0.2 |
| protein binding -6 | SKI | NM_003036 | 3.0 | 2.8 |
| protein binding -7 | SNX25 | NM_031953 | 2.9 | 3.1 |
| protein binding -8 | CDH6 | NM_004932 | 4.5 | 0.7 |
| protein binding -9 | DCBLD2 | NM_080927 | 10.4 | 3.9 |
| protein binding -10 | ENG | NM_000118 | 3.2 | 8.7 |
| | | | | |
| Classification 12 | Gene symbol | Genbank number | Fold Average | Expression level |
| protein modification-1 | SH3RF1 | NM_020870 | 3.4 | 4.9 |

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(continued)

| Classification 12 | Gene symbol | Genbank number | Fold Average | Expression level |
|------------------------|-------------|----------------|--------------|------------------|
| protein modification-2 | SMURF2 | NM_022739 | 5.0 | 19.7 |
| protein modification-3 | TFPI2 | NM_006528 | 5.8 | 11.5 |
| protein modification-4 | ITGB3 | NM_000212 | 8.1 | 0.3 |
| protein modification-5 | MYPN | NM_032578 | 4.8 | 0.3 |
| protein modification-6 | LRP2BP | NM_018409 | 5.6 | 4.8 |
| protein modification-7 | HECW2 | NM_020760 | 5.2 | 3.1 |
| protein modification-8 | PKIA | NM_006823 | 4.3 | 0.5 |
| | | | | |
| Classification 13 | Gene symbol | Genbank number | Fold Average | Expression level |
| signal molecule-1 | LYPD1 | NM_144586 | 29.6 | 0.9 |
| signal molecule-2 | GATA6 | NM_005257 | 27.8 | 3.2 |
| signal molecule-3 | RAB27B | NM_004163 | 10.1 | 0.8 |
| signal molecule-4 | SOX11 | NM_003108 | 23.6 | 0.2 |
| signal molecule-5 | ARHGAP22 | NM_021226 | 9.1 | 3.3 |

[Table 3e]

| Classification 14 | Gene symbol | Genbank number | Fold Average | Expression level |
|-------------------|-------------|----------------|--------------|------------------|
| transcription-1 | ETV1 | NM_004956 | 6.9 | 3.6 |
| transcription-2 | ETV5 | NM_004454 | 3.4 | 2.1 |
| transcription-3 | FOXP1 | NM_032682 | 3.5 | 8.6 |
| transcription-4 | HMGA2 | NM_003483 | 6.2 | 4.4 |
| transcription-5 | KLF12 | NM_007249 | 5.2 | 0.4 |
| transcription-6 | PRDM16 | NM_022114 | 8.1 | 0.7 |
| transcription-7 | SIM2 | NM_009586 | 3.8 | 0.4 |
| transcription-8 | SUHW2 | NM_080764 | 4.6 | 0.1 |
| transcription-9 | ENO1 | NM_001428 | 3.7 | 0.3 |
| transcription-10 | MITF | NM_198159 | 0.7 | 0.6 |
| transcription-11 | TCF3 | NM_003200 | 3.2 | 0.2 |
| transcription-12 | SMYD3 | NM_022743 | 3.0 | 7.5 |
| | | | | |
| Classification 15 | Gene symbol | Genbank number | Fold Average | Expression level |
| transport-1 | ATP6V1G3 | NM_133262 | 3.9 | 0.3 |
| transport-2 | KCTD16 | NM_020768 | 5.8 | 0.4 |
| transport-3 | NUPL1 | NM_014089 | 4.0 | 0.9 |
| transport-4 | SLC14A1 | NM_015865 | 22.3 | 6.5 |
| transport-5 | SLC16A4 | NM_004696 | 5.6 | 5.1 |

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(continued)

| Classification 15 | Gene symbol | Genbank number | Fold Average | Expression level |
|-------------------|-------------|----------------|--------------|------------------|
| transport-6 | SLC4A4 | NM_003759 | 6.6 | 0.4 |
| transport-7 | SLC9A7 | NM_032591 | 7.3 | 0.6 |
| transport-8 | TRPC4 | NM_016179 | 27.0 | 0.3 |
| transport-9 | MCFD2 | NM_139279 | 3.7 | 10.0 |
| transport-10 | SLC26A4 | NM_000441 | 4.1 | 0.3 |
| transport-11 | MCOLN3 | NM_018298 | 3.1 | 0.6 |
| transport-12 | SLC25A37 | NM_016612 | 2.2 | 4.2 |
| transport-13 | SLC30A7 | NM_133496 | 2.7 | 3.5 |
| | | | | |
| Classification 16 | Gene symbol | Genbank number | Fold Average | Expression level |
| others -1 | FLJ38725 | NM_153218 | 7.7 | 1.8 |
| others -2 | KIAA1913 | NM_052913 | 7.2 | 20.2 |
| others -3 | PHLDB2 | NM_145753 | 4.3 | 0.7 |
| others -4 | PLCXD2 | NM_153268 | 7.2 | 0.3 |
| others -5 | SAMD3 | NM_001017373 | 5.3 | 0.6 |
| others -6 | ZNF423 | NM_015069 | 10.9 | 7.1 |
| others -7 | FLJ33996 | NM_175894.2 | 13.6 | 0.2 |
| others -8 | PLEKHK1 | NM_145307 | 5.0 | 0.1 |
| others -9 | PTOV1 | NM_017432 | 3.2 | 0.0 |
| others -10 | FAM40B | NM_020704 | 5.4 | 0.4 |
| others -11 | ABI3BP | NM_015429 | 4.7 | 21.0 |
| others -12 | NHS | NM_198270 | 4.4 | 0.4 |
| others -13 | DTL | NM_016448 | 4.1 | 0.8 |
| others -14 | C1GALT1 | NM_020156 | 3.8 | 2.9 |
| others -15 | CPNE8 | NM_153634 | 3.1 | 1.0 |
| others -16 | TMEM49 | NM_030938 | 1.2 | 10.1 |

[0111] In Tables 3a to 3e, the "Classification", "Gene symbol", "Genbank number" are same as in Tables 1a to 1j. The "Fold Average" indicates how high the expression of the gene was in comparison with the other cells. That is, the "Fold Average" is one of the criterions. In the present invention, a gene having "Fold Average" of 2 or more was judged as being preferable.

[0112] Moreover, the "Expression level" indicates how high the expression level was in MSC. This "Expression level" is one of the criterions. In the present invention, a gene having "Expression level" of 0.5 or more was judged as being preferable.

[0113] The "Fold Average" was calculated as follows. In the present Example, the relative expression levels in the 5 kinds of cells were obtained per gene. The expression level in MSC was compared with the other 4 expression levels. The "Fold Change" was a division of the expression level in MSC over another expression level. An average of the Fold changes of the cells was the "Fold Average". For example, if the expression level in MSC is 4.2, the expression level in OS is 0.3, the expression level in CH is 0.4, the expression level in AD is 1.5, and the expression level in FB is 1.3, then the "Fold Change" is $MSC/OS = 14.0$. The fold changes of each cells were obtained in the same manner and the average of the fold changes was calculated as "Fold Average".

[0114] The 139 genes listed in Tables 3a to 3d, which met the criterions, can be used as the distinguishing marker of the present invention. Those one of the genes which met the two criterions are especially preferable.

[0115] Therefore, the expression of each of these genes in MSC is different from the expression thereof in the other connective tissue cells (FB, OS, CH, AD). That is, the genes are expressed specifically only in MSC but so weakly in the other connective tissue cells that the other connective tissue cells can be distinguished from MSC. Thus, the use of the gene expression as the distinguishing marker makes it possible to distinguish MSC solely and specifically.

INDUSTRIAL APPLICABILITY

[0116] As described above, undifferentiated mesenchymal stem cells can be differentiated to bone, cartilages, fats, muscles, tendons/ligaments, nerves, etc. Undifferentiated mesenchymal stem are expected as transplantation cells for remedying impairment of these tissues in regenerative medicine. To be applied to regenerative medicine, it is necessary to exactly, accurately and easily check that the cells are mesenchymal stem cells and that the mesenchymal stem cells are pluripotential. The present invention is a technical solution to this technical problem, and thus can make a great contribution to practical application of the regenerative medicine. The present invention is not only academically remarkable but also applicable to a wide range of industries including health industries, pharmaceutical industries, and the like.

Claims

1. A method of distinguishing mesenchymal stem cells, comprising:

distinguishing the mesenchymal stem cells from connective tissue cells by detecting a difference between expression in the mesenchymal stem cells and expression in the connective tissue cells by using a distinguishing marker(s),

the distinguishing marker(s) being at least one of genes having the base sequences identified with accession numbers listed in Table 1a to 1j.

[Table 1a]

| Classification 1 | Gene symbol | Gene title | Genbank number |
|--------------------|-------------|---|----------------|
| ATP/GTP binding-1 | BRIP1 | BRCA1 interacting protein C-terminal helicase 1 | NM_032043 |
| ATP/GTP binding -2 | PASK | PAS domain containing serine/threonine kinase | NM_015148 |
| ATP/GTP binding -3 | RAC2 | ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) | NM_002872 |
| ATP/GTP binding -4 | KIF18A | kinesin family member 18A | NM_031217 |
| ATP/GTP binding -5 | NEK7 | NIMA (never in mitosis gene a)-related kinase 7 | NM_133494 |
| ATP/GTP binding -6 | ARL4C | ADP-ribosylation factor-like 4C | NM_005737 |
| ATP/GTP binding -7 | EDEM1 | ER degradation enhancer, mannosidase alpha-like 1 | NM_014674 |
| ATP/GTP binding -8 | CAMK2D | calcium/calmodulin-dependent protein kinase (CaM kinase) II delta | NM_172127 |
| Classification 2 | Gene symbol | Gene title | Genbank number |
| binding -1 | PDE5A | phosphodiesterase 5A, cGMP-specific | NM_001083 |
| binding -2 | RGS4 | regulator of G-protein signalling 4 | NM_005613 |
| binding -3 | EGFL3 | EGF-like-domain, multiple 3 | NM_001409 |
| binding -4 | FHL2 | four and a half LIM domains | NM_001450 |
| binding -5 | HRB2 | HIV-1 rev binding protein 2 | NM_007043 |
| binding -6 | CAPZA1 | capping protein (actin filament) muscle Z-line, alpha 1 | NM_006135 |
| binding -7 | PAPPA2 | pappalysin 2 | NM_020318 |
| binding -8 | LOXL2 | lysyl oxidase-like 2 | NM_002318 |
| binding -9 | LOX | lysyl oxidase | NM_002317 |

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(continued)

| Classification 2 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|---|----------------|
| binding -10 | ADAMTS5 | ADAM metallopeptidase with thrombospondin type 1 motif, 5 (aggrecanase-2) | NM_007038 |

[Table 1b]

| Classification 3 | Gene symbol | Gene title | Genbank number |
|-----------------------------------|-------------|---|----------------|
| cell growth and/or maintenance-1 | CCND1 | cyclin D1 (PRAD1: parathyroid adenomatosis 1) | NM_053056 |
| cell growth and/or maintenance-2 | CDC25A | cell division cycle 25A | NM_001789 |
| cell growth and/or maintenance-3 | IER3 | immediate early response 3 | NM_052815 |
| cell growth and/or maintenance-4 | BCL2 | B-cell CLL/lymphoma 2 | NM_000633 |
| cell growth and/or maintenance-5 | NALP1 | NACHT, leucine rich repeat and PYD containing 1 | NM_033004 |
| cell growth and/or maintenance-6 | PAK3 | p21 (CDKN1A)-activated kinase 3 | NM_002578 |
| cell growth and/or maintenance-7 | PODXL | podocalyxin-like | NM_001018 111 |
| cell growth and/or maintenance-8 | CCL26 | chemokine (C-C motif) ligand 26 | NM_006072 |
| cell growth and/or maintenance-9 | FBLN1 | fibulin 1 | NM_006486 |
| cell growth and/or maintenance-10 | LAMA1 | laminin, alpha 1 | NM_005559 |
| cell growth and/or maintenance-11 | NTNG1 | netrin G1 | NM_014917 |

[Table 1c]

| Classification 4 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| cytokine -1 | GDF15 | growth differentiation factor 15 | NM_004864 |
| cytokine -2 | IL6 | interleukin 6 (interferon, beta 2) | NM_000600 |
| cytokine -3 | CTGF | connective tissue growth factor | NM_001901 |
| cytokine -4 | VEGF | vascular endothelial growth factor | NM_001025 366 |
| cytokine -5 | VEGFC | vascular endothelial growth factor C | NM_005429 |
| cytokine -6 | HGF | hepatocyte growth factor (hepapoietin A; scatter | NM_000601 |
| Classification 5 | Gene symbol | Gene title | Genbank number |
| cytoskeleton-1 | KRT19 | keratin 19 | NM_002276 |
| cytoskeleton-2 | KRTAP1-5 | keratin associated protein 1- | NM_031957 |
| cytoskeleton-3 | KRTAP2-1 | keratin associated protein 2- | BC012486 |
| cytoskeleton-4 | KRTHA4 | keratin, hair, acidic, 4 | NM_021013 |
| cytoskeleton-5 | CKAP2 | cytoskeleton associated protein 2 | NM_018204 |
| cytoskeleton-6 | KRTAP1-1 | keratin associated protein 1- | NM_030967 |
| cytoskeleton-7 | KRT18 | keratin 18 | NM_000224 |
| cytoskeleton-8 | KAP2.1B | keratin associated protein 2.1B | AJ406929 |
| cytoskeleton-9 | SSH1 | slingshot homolog 1 (Drosophila) | NM_018984 |

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| Classification 5 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| Classification 6 | Gene symbol | Gene title | Genbank number |
| enzyme-1 | LXN | latexin | NM_020169 |
| enzyme-2 | IFI30 | interferon, gamma-inducible protein 30 | NM_006332 |
| enzyme-3 | CPA4 | carboxypeptidase A4 | NM_016352 |

[Table 1d]

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| Classification 7 | Gene symbol | Gene title | Genbank number |
|-----------------------------|-------------|--|----------------|
| extracellular matrix-1 | CHI3L1 | chitinase 3-like 1 (cartilage glycoprotein-39) | NM_001276 |
| extracellular matrix-2 | KRT23 | keratin 23 (histone deacetylase inducible) | NM_015515 |
| extracellular matrix-3 | FLG | filaggrin | NM_002016 |
| extracellular matrix-4 | ADAMTS1 | a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 | NM_006988 |
| extracellular matrix-5 | FRMD5 | FERM domain containing 5 | NM_001031 729 |
| Classification 8 | Gene symbol | Gene title | Genbank number |
| growth factor or receptor-1 | IGFBP1 | insulin-like growth factor binding protein 1 | NM_000596 |
| growth factor or receptor-2 | CFI | complement factor I | NM_000204 |
| growth factor or receptor-3 | ESM1 | endothelial cell-specific molecule 1 | NM_007036 |
| growth factor or receptor-4 | F2RL1 | coagulation factor II (thrombin) receptor-like 1 | NM_005242 |
| growth factor or receptor-5 | MET | met proto-oncogene (hepatocyte growth factor receptor) | NM_000245 |
| growth factor or receptor-6 | HTR7 | 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) | NM_000872 |
| growth factor or receptor-7 | IGFBP3 | insulin-like growth factor binding protein 3 | NM_001013 398 |

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[Table 1e]

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| Classification 9 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| membrane-1 | ABHD2 | abhydrolase domain containing 2 | NM_007011 |
| membrane -2 | ITGA2 | integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) | NM_002203 |
| membrane -3 | LAMA3 | laminin, alpha 3 | NM_198129 |
| membrane -4 | NETO2 | neuropilin (NRP) and tolloid (TLL)-like 2 | NM_018092 |
| membrane -5 | NTN4 | netrin 4 | NM_021229 |
| membrane -6 | PTGER1 | Prostaglandin E receptor 1 (subtype EP1), 42kDa | NM_000955 |
| membrane -7 | EPHB2 | EPH receptor B2 | NM_017449 |
| membrane -8 | SFRP1 | secreted frizzled-related protein 1 | NM_003012 |
| membrane -9 | CD33L3 | CD33 antigen-like 3 | NM_213602 |

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(continued)

| Classification 9 | Gene symbol | Gene title | Genbank number |
|----------------------------|-------------|---|----------------|
| membrane -10 | GLIPR1 | GLI pathogenesis-related 1 (glioma) | NM_006851 |
| membrane -11 | UGCG | UDP-glucose ceramide glucosyltransferase | NM_003358 |
| membrane -12 | ADORA1 | adenosine A1 receptor | NM_000674 |
| | | | |
| Classification 10 | Gene symbol | Gene title | Genbank number |
| membrane binding protein-1 | ANXA10 | annexin A10 | NM_007193 |
| membrane binding protein-2 | RARRES1 | retinoic acid receptor responder (tazarotene induced) 1 | NM_206963 |
| membrane binding protein-3 | HNT | neurotrimin | NM_016522 |
| membrane binding protein-4 | CNTNAP3 | contactin associated protein-like 3 | NM_033655 |

[Table 1f]

| Classification 11 | Gene symbol | Gene title | Genbank number |
|---------------------|-------------|--|----------------|
| protein binding-1 | SYT1 | synaptotagmin I | NM_005639 |
| protein binding -2 | MLF1 | myeloid leukemia factor 1 | NM_022443 |
| protein binding -3 | CDCP1 | CUB domain-containing protein 1 | NM_022842 |
| protein binding -4 | KLAA0746 | KIAA0746 protein | NM_015187 |
| protein binding -5 | PSCDBP | pleckstrin homology, Sec7 and coiled-coil domains, binding protein | NM_004288 |
| protein binding -6 | SKI | v-ski sarcoma viral oncogene homolog (avian) | NM_003036 |
| protein binding -7 | SNX25 | sorting nexin 25 | NM_031953 |
| protein binding -8 | CDH6 | cadherin 6, type 2, K-cadherin (fetal kidney) | NM_004932 |
| protein binding -9 | DCBLD2 | discoidin, CUB and LCCL domain containing 2 | NM_080927 |
| protein binding -10 | ENG | endoglin (Osler-Rendu-Weber syndrome 1) | NM_000118 |

[Table 1g]

| Classification 12 | Gene symbol | Gene title | Genbank number |
|------------------------|-------------|---|----------------|
| protein modification-1 | SH3RF1 | SH3 domain containing ring finger 1 | NM_020870 |
| protein modification-2 | SMURF2 | SMAD specific E3 ubiquitin protein ligase 2 | NM_022739 |
| protein modification-3 | TFPI2 | tissue factor pathway inhibitor 2 | NM_006528 |
| protein modification-4 | ITGB3 | integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) | NM_000212 |
| protein modification-5 | MYPN | myopalladin | NM_032578 |
| protein modification-6 | LRP2BP | LRP2 binding protein | NM_018409 |
| protein modification-7 | HECW2 | HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2 | NM_020760 |
| protein modification-8 | PKIA | protein kinase (cAMP-dependent, catalytic) inhibitor alpha | NM_006823 |
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| Classification 13 | Gene symbol | Gene title | Genbank number |
|----------------------|-------------|---------------------------------------|----------------|
| 5 signal molecule-1 | LYPD1 | LY6/PLAUR domain containing 1 | NM_144586 |
| signal molecule-2 | GATA6 | GATA binding protein 6 | NM_005257 |
| signal molecule-3 | RAB27B | RAB27B, member RAS oncogene family | NM_004163 |
| signal molecule-4 | SOX11 | SRY (sex determining region Y)-box 11 | NM_003108 |
| 10 signal molecule-5 | ARHGAP2 2 | Rho GTPase activating protein 22 | NM_021226 |

[Table 1h]

| Classification 14 | Gene symbol | Gene title | Genbank number |
|---------------------|-------------|--|----------------|
| 15 transcription-1 | ETV1 | ets variant gene 1 | NM_004956 |
| transcription-2 | ETV5 | ets variant gene 5 (ets-related molecule) | NM_004454 |
| 20 transcription-3 | FOXP1 | forkhead box P1 | NM_032682 |
| transcription-4 | HMGA2 | high mobility group AT-hook 2 | NM_003483 |
| transcription-5 | KLF12 | Kruppel-like factor 12 | NM_007249 |
| transcription-6 | PRDM16 | PR domain containing 16 | NM_022114 |
| 25 transcription-7 | SIM2 | single-minded homolog 2 (Drosophila) | NM_009586 |
| transcription-8 | SUHW2 | suppressor of hairy wing homolog 2 (Drosophila) | NM_080764 |
| transcription-9 | ENO1 | enolase 1 | NM_001428 |
| 30 transcription-10 | MITF | microphthalmia-associated transcription factor | NM_198159 |
| transcription-11 | TCF3 | transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) | NM_003200 |
| transcription-12 | SMYD3 | SET and MYND domain containing 3 | NM_022743 |

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[Table 1j]

| Classification 15 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| 40 transport-1 | ATP6V1G3 | ATPase, H ⁺ transporting, lysosomal 13kDa, V1 subunit G isoform 3 | NM_133262 |
| transport-2 | KCTD16 | potassium channel tetramerisation domain containing 16 | NM_020768 |
| transport-3 | NUPL1 | nucleoporin like 1 | NM_014089 |
| 45 transport-4 | SLC14A1 | solute carrier family 14 (urea transporter), member 1 (Kidd blood group) | NM_015865 |
| transport-5 | SLC16A4 | solute carrier family 16 (monocarboxylic acid transporters), member 4 | NM_004696 |
| 50 transport-6 | SLC4A4 | solute carrier family 4, sodium bicarbonate cotransporter, member 4 | NM_003759 |
| transport-7 | SLC9A7 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 7 | NM_032591 |
| 55 transport-8 | TRPC4 | transient receptor potential cation channel, subfamily C, member 4 | NM_016179 |
| transport-9 | MCFD2 | multiple coagulation factor deficiency 2 | NM_139279 |

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| Classification 15 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|---|----------------|
| transport-10 | SLC26A4 | solute carrier family 26, member 4 | NM_000441 |
| transport-11 | MCOLN3 | mucolipin 3 | NM_018298 |
| transport-12 | SLC25A37 | solute carrier family 25, member 37 | NM_016612 |
| transport-13 | SLC30A7 | solute carrier family 30 (zinc transporter), member 7 | NM_133496 |

[Table 1j]

| Classification 16 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| others -1 | FLJ38725 | hypothetical protein FLJ38725 | NM_153218 |
| others -2 | KIAA1913 | KIAA1913 | NM_052913 |
| others -3 | PHLDB2 | pleckstrin homology-like domain, family B, member 2 | NM_145753 |
| others -4 | PLCXD2 | phosphatidylinositol-specific phospholipase C, X domain containing 2 | NM_153268 |
| others -5 | SAMD3 | sterile alpha motif domain containing 3 | NM_001017.3 |
| others -6 | ZNF423 | zinc finger protein 423 | NM_015069 |
| others -7 | FLJ33996 | hypothetical protein FLJ33996 | NM_175894.2 |
| others -8 | PLEKHK1 | pleckstrin homology domain containing, family K member 1 | NM_145307 |
| others -9 | PTOV1 | prostate tumor overexpressed gene 1 | NM_017432 |
| others -10 | FAM40B | family with sequence similarity 40, member B | NM_020704 |
| others -11 | ABI3BP | ABI gene family, member 3 (NESH) binding protein | NM_015429 |
| others -12 | NHS | Nance-Horan syndrome (congenital cataracts and dental anomalies) | NM_198270 |
| others -13 | DTL | denticleless homolog (Drosophila) | NM_16448 |
| others -14 | C1GALT1 | core 1 synthase, glycoprotein-N- acetylgalactosamine 3-beta- | NM_020156 |
| others -15 | CPNE8 | copine VIII | NM_153634 |
| others -16 | TMEM49 | transmembrane protein 49 | NM_030938 |

2. The method as set forth in claim 1, wherein the distinguishing marker(s) is at least one of the genes listed the classifications 6, 7, 8, 10, and 13 in Tables 1a to 1j.
3. The method as set forth in claim 2, wherein the distinguishing markers are a combination of one or more genes from each of the classifications 6, 7, 8, 10, and 13 in Tables 1a to 1j.
4. The method as set forth in any one of claim 1 to 3, wherein the distinguishing marker is at least one of the genes listed in Table 2.

| Gene symbol | Gene title | Genbank number |
|-------------|--|----------------|
| CHI3L1 | chitinase 3-like 1 (cartilage glycoprotein-39) | NM_001276 |
| FLG | filaggrin | NM_002016 |
| CFI | complement factor I | NM_000204 |

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(continued)

| Gene symbol | Gene title | Genbank number |
|-------------|-------------------------------|----------------|
| ANXA10 | annexin A10 | NM_007193 |
| LYPDC1 | LY6/PLAUR domain containing 1 | NM_144586 |
| GATA6 | GATA binding protein 6 | NM_005257 |

5. The method as set forth in any one of claims 1 to 4, wherein the detection of the difference in the expressions of the distinguishing markers is carried out by detecting expression of the gene or expression of a protein encoded by the gene.

6. A microarray for distinguishing mesenchymal stem cells, the microarray comprising at least one of (a) to (d) immobilized thereon:

- (a) at least one of genes having the base sequences identified with the accession numbers listed in Tables 3a to 3j;
- (b) an antisense chain of at least one of genes having the base sequences identified with the accession numbers listed in Tables 3a to 3j;
- (c) a partial base sequence of (a) or (b); and
- (d) a polynucleotide that is capable of hybridizing, under stringent conditions, with a polynucleotide having the base sequence described in any one of (a) to (c).

[Table 3a]

| Classification 1 | Gene symbol | Gene title | Genbank number |
|--------------------|-------------|---|----------------|
| ATP/GTP binding -1 | BRIP1 | BRCA1 interacting protein C-terminal helicase 1 | NM_032043 |
| ATP/GTP binding -2 | PASK | PAS domain containing serine/threonine kinase | NM_015148 |
| ATP/GTP binding -3 | RAC2 | ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) | NM_002872 |
| ATP/GTP binding -4 | KIF18A | kinesin family member 18A | NM_031217 |
| ATP/GTP binding -5 | NEK7 | NIMA (never in mitosis gene a)-related kinase 7 | NM_133494 |
| ATP/GTP binding -6 | ARL4C | ADP-ribosylation factor-like | NM_005737 |
| ATP/GTP binding -7 | EDEM1 | ER degradation enhancer, mannosidase alpha-like 1 | NM_014674 |
| ATP/GTP binding -8 | CAMK2D | calcium/calmodulin-dependent protein kinase (CaM kinase) II delta | NM_172127 |
| Classification 2 | Gene symbol | Gene title | Genbank number |
| binding -1 | PDE5A | phosphodiesterase 5A, cGMP-specific | NM_001083 |
| binding -2 | RGS4 | regulator of G-protein signalling 4 | NM_005613 |
| binding -3 | EGFL3 | EGF-like-domain, multiple 3 | NM_001409 |
| binding -4 | FHL2 | four and a half LIM domains | NM_001450 2 |
| binding -5 | HRB2 | HIV-1 rev binding protein 2 | NM_007043 |
| binding -6 | CAPZA1 | capping protein (actin filament) muscle Z-line, alpha 1 | NM_006135 |
| binding -7 | PAPPA2 | pappalysin 2 | NM_020318 |
| binding -8 | LOXL2 | lysyl oxidase-like 2 | NM_002318 |
| binding -9 | LOX | lysyl oxidase | NM_002317 |
| binding -10 | ADAMTS5 | ADAM metalloproteinase with thrombospondin type 1 motif, 5 (aggrecanase-2) | NM_007038 |

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[Table 3b]

| Classification 3 | Gene symbol | Gene title | Genbank number |
|-----------------------------------|-------------|---|----------------|
| cell growth and/or maintenance-1 | CCND1 | cyclin D1 (PRAD1: parathyroid adenomatosis 1) | NM_053056 |
| cell growth and/or maintenance-2 | CDC25A | cell division cycle 25A | NM_001789 |
| cell growth and/or maintenance-3 | IER3 | immediate early response 3 | NM_052815 |
| cell growth and/or maintenance-4 | BCL2 | B-cell CLL/lymphoma 2 | NM_000633 |
| cell growth and/or maintenance-5 | NALP1 | NACHT, leucine rich repeat and PYD containing 1 | NM_033004 |
| cell growth and/or maintenance-6 | PAK3 | p21 (CDKN1A)-activated kinase 3 | NM_002578 |
| cell growth and/or maintenance-7 | PODXL | podocalyxin-like | NM_001018 111 |
| cell growth and/or maintenance-8 | CCL26 | chemokine (C-C motif) ligand 26 | NM_006072 |
| cell growth and/or maintenance-9 | FBLN1 | fibulin 1 | NM_006486 |
| cell growth and/or maintenance-10 | LAMA1 | laminin, alpha 1 | NM_005559 |
| cell growth and/or maintenance-11 | NTNG1 | netrin G1 | NM_014917 |

[Table 3c]

| Classification 4 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| cytokine -1 | GDF15 | growth differentiation factor | NM_004864 |
| cytokine -2 | IL6 | interleukin 6 (interferon, beta 2) | NM_000600 |
| cytokine -3 | CTGF | connective tissue growth factor | NM_001901 |
| cytokine -4 | VEGF | vascular endothelial growth factor | NM_001025 366 |
| cytokine -5 | VEGFC | vascular endothelial growth factor C | NM_005429 |
| cytokine -6 | HGF | hepatocyte growth factor (hepapoietin A; scatter | NM_000601 |
| Classification 5 | Gene symbol | Gene title | Genbank number |
| cytoskeleton-1 | KRT19 | keratin 19 | NM_002276 |
| cytoskeleton-2 | KRTAP1-5 | keratin associated protein 1- | NM_031957 |
| cytoskeleton-3 | KRTAP2-1 | keratin associated protein 2- | BC012486 |
| cytoskeleton-4 | KRTHA4 | keratin, hair, acidic, 4 | NM_021013 |
| cytoskeleton-5 | CKAP2 | cytoskeleton associated protein 2 | NM_018204 |
| cytoskeleton-6 | KRTAP1-1 | keratin associated protein 1- | NM_030967 |
| cytoskeleton-7 | KRT18 | keratin 18 | NM_000224 |
| cytoskeleton-8 | KAP2.1B | keratin associated protein 2.1B | AJ406929 |
| cytoskeleton-9 | SSH1 | slingshot homolog 1 (Drosophila) | NM_018984 |
| Classification 6 | Gene symbol | Gene title | Genbank number |
| enzyme-1 | LXN | latexin | NM_020169 |
| enzyme-2 | IFI30 | interferon, gamma-inducible protein 30 | NM_006332 |

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(continued)

| Classification 6 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|---------------------|----------------|
| enzyme-3 | CPA4 | carboxypeptidase A4 | NM_016352 |

[Table 3d]

| Classification 7 | Gene symbol | Gene title | Genbank number |
|-----------------------------|-------------|--|----------------|
| extracellular matrix-1 | CHI3L1 | chitinase 3-like 1 (cartilage glycoprotein-39) | NM_001276 |
| extracellular matrix-2 | KRT23 | keratin 23 (histone deacetylase inducible) | NM_015515 |
| extracellular matrix-3 | FLG | filaggrin | NM_002016 |
| extracellular matrix-4 | ADAMTS1 | a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 | NM_006988 |
| extracellular matrix-5 | FRMD5 | FERM domain containing 5 | NM_001031 729 |
| Classification 8 | Gene symbol | Gene title | Genbank number |
| growth factor or receptor-1 | IGFBP1 | insulin-like growth factor binding protein 1 | NM_000596 |
| growth factor or receptor-2 | CFI | complement factor I | NM_000204 |
| growth factor or receptor-3 | ESM1 | endothelial cell-specific molecule 1 | NM_007036 |
| growth factor or receptor-4 | F2RL1 | coagulation factor II (thrombin) receptor-like 1 | NM_005242 |
| growth factor or receptor-5 | MET | met proto-oncogene (hepatocyte growth factor receptor) | NM_000245 |
| growth factor or receptor-6 | HTR7 | 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) | NM_000872 |
| growth factor or receptor-7 | IGFBP3 | insulin-like growth factor binding protein 3 | NM_001013 398 |

[Table 3e]

| Classification 9 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| membrane -1 | ABHD2 | abhydrolase domain containing 2 | NM_007011 |
| membrane -2 | ITGA2 | integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) | NM_002203 |
| membrane -3 | LAMA3 | laminin, alpha 3 | NM_198129 |
| membrane -4 | NETO2 | neuropilin (NRP) and tolloid (TLL)-like 2 | NM_018092 |
| membrane -5 | NTN4 | netrin 4 | NM_021229 |
| membrane -6 | PTGER1 | prostaglandin E receptor 1 (subtype EP1), 42kDa | NM_000955 |
| membrane -7 | EPHB2 | EPH receptor B2 | NM_017449 |
| membrane -8 | SFRP1 | secreted frizzled-related protein 1 | NM_003012 |
| membrane -9 | CD33L3 | CD33 antigen-like 3 | NM_213602 |
| membrane -10 | GLIPR1 | GLI pathogenesis-related 1 (glioma) | NM_006851 |
| membrane -11 | UGCG | UDP-glucose ceramide glucosyltransferase | NM_003358 |
| membrane -12 | ADORA1 | adenosine A1 receptor | NM_000674 |

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(continued)

| Classification 10 I | Gene symbol | Gene title | Genbank number |
|----------------------------|-------------|---|----------------|
| membrane binding protein-1 | ANXA10 | annexin A10 | NM_007193 |
| membrane binding protein-2 | RARRES1 | retinoic acid receptor responder (tazarotene induced) 1 | NM_206963 |
| membrane binding protein-3 | HNT | neurotrimin | NM_016522 |
| membrane binding protein-4 | CNTNAP3 | contactin associated protein-like 3 | NM_033655 |

[Table 3f]

| Classification 11 | Gene symbol | Gene title | Genbank number |
|---------------------|-------------|--|----------------|
| protein binding -1 | SYT1 | synaptotagmin I | NM_005639 |
| protein binding -2 | MLF1 | myeloid leukemia factor 1 | NM_022443 |
| protein binding -3 | CDCP1 | CUB domain-containing protein 1 | NM_022842 |
| protein binding -4 | KIAA0746 | KIAA0746 protein | NM_015187 |
| protein binding -5 | PSCDBP | pleckstrin homology, Sec7 and coiled-coil domains, binding protein | NM_004288 |
| protein binding -6 | SKI | v-ski sarcoma viral oncogene homolog (avian) | NM_003036 |
| protein binding -7 | SNX25 | sorting nexin 25 | NM_031953 |
| protein binding -8 | CDH6 | cadherin 6, type 2, K-cadherin (fetal kidney) | NM_004932 |
| protein binding -9 | DCBLD2 | discoidin, CUB and LCCL domain containing 2 | NM_080927 |
| protein binding -10 | ENG | endoglin (Osler-Rendu-Weber syndrome 1) | NM_000118 |

[Table 3g]

| Classification 12 | Gene symbol | Gene title | Genbank number |
|------------------------|-------------|---|----------------|
| protein modification-1 | SH3RF1 | SH3 domain containing ring finger 1 | NM_020870 |
| protein modification-2 | SMURF2 | SMAD specific E3 ubiquitin protein ligase 2 | NM_022739 |
| protein modification-3 | TFPI2 | tissue factor pathway inhibitor 2 | NM_006528 |
| protein modification-4 | ITGB3 | integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) | NM_000212 |
| protein modification-5 | MYPN | myopalladin | NM_032578 |
| protein modification-6 | LRP2BP | LRP2 binding protein | NM_018409 |
| protein modification-7 | HECW2 | HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2 | NM_020760 |
| protein modification-8 | PKIA | protein kinase (cAMP-dependent, catalytic) inhibitor alpha | NM_006823 |
| Classification 13 | Gene symbol | Gene title | Genbank number |
| signal molecule-1 | LYPD1 | LY6/PLAUR domain containing 1 domain | NM_144586 |
| signal molecule-2 | GATA6 | GATA binding protein 6 | NM_005257 |
| signal molecule-3 | RAB27B | RAB27B, member RAS oncogene family | NM_004163 |

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(continued)

| Classification 13 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|---------------------------------------|----------------|
| signal molecule-4 | SOX11 | SRY (sex determining region Y)-box 11 | NM_003108 |
| signal molecule-5 | ARHGAP2 2 | Rho GTPase activating protein 22 | NM_021226 |

[Table 3h]

| Classification 14 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| transcription-1 | ETV1 | ets variant gene 1 | NM_004956 |
| transcription-2 | ETV5 | ets variant gene 5 (ets-related molecule) | NM_004454 |
| transcription-3 | FOXP1 | forkhead box P1 | NM_032682 |
| transcription-4 | HMGA2 | high mobility group AT-hook 2 | NM_003483 |
| transcription-5 | KLF12 | Kruppel-like factor 12 | NM_007249 |
| transcription-6 | PRDM16 | PR domain containing 16 | NM_022114 |
| transcription-7 | SIM2 | single-minded homolog 2 (Drosophila) | NM_009586 |
| transcription-8 | SUHW2 | suppressor of hairy wing homolog 2 (Drosophila) | NM_080764 |
| transcription-9 | ENO1 | enolase 1 | NM_001428 |
| transcription-10 | MITF | microphthalmia-associated transcription factor | NM_198159 |
| transcription-11 | TCF3 | transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) | NM_003200 |
| transcription-12 | SMYD3 | SET and MYND domain containing 3 | NM_022743 |

[Table 3i]

| Classification 15 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| transport-1 | ATP6V1G3 | ATPase, H ⁺ transporting, lysosomal 13kDa, V1 subunit G isoform 3 | NM_133262 |
| transport-2 | KCTD16 | potassium channel tetramerisation domain containing 16 | NM_020768 |
| transport-3 | NUPL1 | nucleoporin like 1 | NM_014089 |
| transport-4 | SLC14A1 | solute carrier family 14 (urea transporter), member 1 (Kidd blood group) | NM_015865 |
| transport-5 | SLC16A4 | solute carrier family 16 (monocarboxylic acid transporters), member 4 | NM_004696 |
| transport-6 | SLC4A4 | solute carrier family 4, sodium bicarbonate cotransporter, member 4 | NM_003759 |
| transport-7 | SLC9A7 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 7 | NM_032591 |
| transport-8 | TRPC4 | transient receptor potential cation channel, subfamily C, member 4 | NM_016179 |
| transport-9 | MCFD2 | multiple coagulation factor deficiency 2 | NM_139279 |
| transport-10 | SLC26A4 | solute carrier family 26, member 4 | NM_000441 |
| transport-11 | MCOLN3 | mucolipin 3 | NM_018298 |
| transport-12 | SLC25A37 | solute carrier family 25, member 37 | NM_016612 |

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(continued)

| Classification 15 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|---|----------------|
| transport-13 | SLC30A7 | solute carrier family 30 (zinc transporter), member 7 | NM_133496 |

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[Table 3j]

| Classification 16 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| others -1 | FLJ38725 | hypothetical protein FLJ38725 | NM_153218 |
| others -2 | KIAA1913 | KIAA1913 | NM_052913 |
| others -3 | PHLDB2 | pleckstrin homology-like domain, family B, member 2 | NM_145753 |
| others -4 | PLCXD2 | phosphatidylinositol-specific phospholipase C, X domain containing 2 | NM_153268 |
| others -5 | SAMD3 | sterile alpha motif domain containing 3 | NM_001017 373 |
| others -6 | ZNF423 | zinc finger protein 423 | NM_015069 |
| others -7 | FLJ33996 | hypothetical protein FLJ33996 | NM_175894.2 |
| others -8 | PLEKHK1 | pleckstrin homology domain containing, family K member 1 | NM_145307 |
| others -9 | PTOV1 | prostate tumor overexpressed gene 1 | NM_017432 |
| others -10 | FAM40B | family with sequence similarity 40, member B | NM_020704 |
| others -11 | ABI3BP | ABI gene family, member 3 (NESH) binding protein | NM_015429 |
| others -12 | NHS | Nance-Horan syndrome (congenital cataracts and dental anomalies) | NM_198270 |
| others -13 | DTL | denticleless homolog (Drosophila) | NM_016448 |
| others -14 | C1GALT1 | core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta- | NM_020156 |
| others -15 | CPNE8 | copine VIII | NM_153634 |
| others -16 | TMEM49 | transmembrane protein 49 | NM_030938 |

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7. An antibody, being inducible with a polypeptide described in (e) or (f), and bindable specifically with the polypeptide specifically:

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(e) a polypeptide encoded by any one of the genes having the base sequences identified with the accession numbers listed in Tables 4a to 4j; and

(f) a partial polypeptide of the polypeptide described in (e).

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[Table 4a]

| Classification 1 | Gene symbol | Gene title | Genbank number |
|--------------------|-------------|---|----------------|
| ATP/GTP binding -1 | BRIP1 | BRCA1 interacting protein C-terminal helicase 1 | NM_032043 |
| ATP/GTP binding -2 | PASK | PAS domain containing serine/threonine kinase | NM_015148 |
| ATP/GTP binding-3 | RAC2 | ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) | NM_002872 |
| ATP/GTP binding -4 | KIF18A | kinesin family member 18A | NM_031217 |
| ATP/GTP binding -5 | NEK7 | NIMA (never in mitosis gene a)-related kinase 7 | NM_133494 |
| ATP/GTP binding -6 | ARL4C | ADP-ribosylation factor-like 4C | NM_005737 |
| ATP/GTP binding -7 | EDEM1 | ER degradation enhancer, mannosidase alpha-like 1 | NM_014674 |

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(continued)

| Classification 1 | Gene symbol | Gene title | Genbank number |
|--------------------|-------------|--|----------------|
| ATP/GTP binding -8 | CAMK2D | calcium/calmodulin-dependent protein kinase (CaM kinase) II delta | NM_172127 |
| Classification 2 | Gene symbol | Gene title | Genbank number |
| binding -1 | PDE5A | phosphodiesterase 5A, cGMP-specific | NM_001083 |
| binding -2 | RGS4 | regulator of G-protein signalling 4 | NM_005613 |
| binding -3 | EGFL3 | EGF-like-domain, multiple 3 | NM_001409 |
| binding -4 | FHL2 | four and a half LIM domains 2 | NM_001450 |
| binding -5 | HRB2 | HIV-1 rev binding protein 2 | NM_007043 |
| binding -6 | CAPZA1 | capping protein (actin filament) muscle Z-line, alpha 1 | NM_006135 |
| binding -7 | PAPPA2 | pappalysin 2 | NM_020318 |
| binding -8 | LOXL2 | lysyl oxidase-like 2 | NM_002318 |
| binding -9 | LOX | lysyl oxidase | NM_002317 |
| binding -10 | ADAMTS5 | ADAM metalloproteinase with thrombospondin type 1 motif, 5 (aggrecanase-2) | NM_007038 |

[Table 4b]

| Classification 3 | Gene symbol | Gene title | Genbank number |
|-----------------------------------|-------------|---|----------------|
| cell growth and/or maintenance-1 | CCND1 | cyclin D1 (PRAD1: parathyroid adenomatosis 1) | NM_053056 |
| cell growth and/or maintenance-2 | CDC25A | cell division cycle 25A | NM_001789 |
| cell growth and/or maintenance-3 | IER3 | immediate early response 3 | NM_052815 |
| cell growth and/or maintenance-4 | BCL2 | B-cell CLL/lymphoma 2 | NM_000633 |
| cell growth and/or maintenance-5 | NALP1 | NACHT, leucine rich repeat and PYD containing 1 | NM_033004 |
| cell growth and/or maintenance-6 | PAK3 | p21 (CDKN1A)-activated kinase 3 | NM_002578 |
| cell growth and/or maintenance-7 | PODXL | podocalyxin-like | NM_001018 111 |
| cell growth and/or maintenance-8 | CCL26 | chemokine (C-C motif) ligand 26 | NM_006072 |
| cell growth and/or maintenance-9 | FBLN1 | fibulin 1 | NM_006486 |
| cell growth and/or maintenance-10 | LAMA1 | laminin, alpha 1 | NM_005559 |
| cell growth and/or maintenance-11 | NTNG1 | netrin G1 | NM_014917 |

[Table 4c]

| Classification 4 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--------------------------------------|----------------|
| cytokine -1 | GDF15 | growth 15 differentiation factor | NM_004864 |
| cytokine -2 | IL6 | interleukin 6 (interferon, beta 2) | NM_000600 |
| cytokine -3 | CTGF | connective tissue growth factor | NM_001901 |
| cytokine -4 | VEGF | vascular endothelial growth factor | NM_001025 366 |
| cytokine -5 | VEGFC | vascular endothelial growth factor C | NM_005429 |

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(continued)

| Classification 4 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| cytokine -6 | HGF | hepatocyte growth factor (hepapoietin A; scatter | NM_000601 |
| Classification 5 | Gene symbol | Gene title | Genbank number |
| cytoskeleton-1 | KRT19 | keratin 19 | NM_002276 |
| cytoskeleton-2 | KRTAP1-5 | keratin associated protein 1- | NM_031957 |
| cytoskeleton-3 | KRTAP2-1 | keratin associated protein 2- | BC012486 |
| cytoskeleton-4 | KRTHA4 | keratin, hair, acidic, 4 | NM_021013 |
| cytoskeleton-5 | CKAP2 | cytoskeleton associated protein 2 | NM_018204 |
| cytoskeleton-6 | KRTAP1-1 | keratin associated protein 1- | NM_030967 |
| cytoskeleton-7 | KRT18 | keratin 18 | NM_000224 |
| cytoskeleton-8 | KAP2.1B | keratin associated protein 2.1B | AJ406929 |
| cytoskeleton-9 | SSH1 | slingshot homolog 1 (Drosophila) | NM_018984 |
| Classification 6 | Gene symbol | Gene title | Genbank number |
| enzyme-1 | LXN | latexin | NM_020169 |
| enzyme-2 | IFI30 | interferon, gamma-inducible protein 30 | NM_006332 |
| enzyme-3 | CPA4 | carboxypeptidase A4 | NM_016352 |

[Table 4d]

| Classification 7 | Gene symbol | Gene title | Genbank number |
|-----------------------------|-------------|--|----------------|
| extracellular matrix-1 | CHI3L1 | chitinase 3-like 1 (cartilage glycoprotein-39) | NM_001276 |
| extracellular matrix-2 | KRT23 | keratin 23 (histone deacetylase inducible) | NM_015515 |
| extracellular matrix-3 | FLG | filaggrin | NM_002016 |
| extracellular matrix-4 | ADAMTS1 | a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type I motif, I | NM_006988 |
| extracellular matrix-5 | FRMD5 | FERM domain containing 5 | NM_001031 729 |
| Classification 8 | Gene symbol | Gene title | Genbank number |
| growth factor or receptor-1 | IGFBP1 | insulin-like growth factor binding protein 1 | NM_000596 |
| growth factor or receptor-2 | CFI | complement factor I | NM_000204 |
| growth factor or receptor-3 | ESM1 | endothelial cell-specific molecule 1 | NM_007036 |
| growth factor or receptor-4 | F2RL1 | coagulation factor II (thrombin) receptor-like 1 | NM_005242 |
| growth factor or receptor-5 | MET | met proto-oncogene (hepatocyte growth factor receptor) | NM_000245 |
| growth factor or receptor-6 | HTR7 | 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) | NM_000872 |
| growth factor or receptor-7 | IGFBP3 | insulin-like growth factor binding protein 3 | NM_001013 398 |

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[Table 4e]

| Classification 9 | Gene symbol | Gene title | Genbank number |
|------------------------------------|-------------|--|----------------|
| membrane -1 | ABHD2 | abhydrolase domain containing 2 | NM_007011 |
| membrane -2 | ITGA2 | integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) | NM_002203 |
| membrane -3 | LAMA3 | laminin, alpha 3 | NM_198129 |
| membrane -4 | NETO2 | neuropilin (NRP) and tolloid (TLL)-like 2 | NM_018092 |
| membrane -5 | NTN4 | netrin 4 | NM_021229 |
| membrane -6 | PTGER1 | prostaglandin E receptor 1 (subtype EP1), 42kDa | NM_000955 |
| membrane -7 | EPHB2 | EPH receptor B2 | NM_017449 |
| membrane -8 | SFRP1 | secreted frizzled-related protein 1 | NM_003012 |
| membrane -9 | CD33L3 | CD33 antigen-like 3 | NM_213602 |
| membrane -10 | GLIPR1 | GLI pathogenesis-related 1 (glioma) | NM_006851 |
| membrane -11 | UGCG | UDP-glucose ceramide glucosyltransferase | NM_003358 |
| membrane -12 | ADORA1 | adenosine A1 receptor | NM_000674 |
| | | | |
| Classification 10 | Gene symbol | Gene title | Genbank number |
| membrane binding protein-1 | ANXA10 | annexin A10 | NM_007193 |
| membrane binding protein-2 binding | RARRES1 | retinoic acid receptor responder (tazarotene induced) 1 | NM_206963 |
| membrane binding protein-3 | HNT | neurotrimin | NM_016522 |
| membrane binding protein-4 | CNTNAP3 | contactin associated protein-like 3 | NN_033655 |

[Table 4f]

| Classification 11 | Gene symbol | Gene title | Genbank number |
|---------------------|-------------|--|----------------|
| protein binding -1 | SYT1 | synaptotagmin I | NM_005639 |
| protein binding -2 | MLF1 | myeloid leukemia factor 1 | NM_022443 |
| protein binding -3 | CDCP1 | CUB domain-containing protein 1 | NM_022842 |
| protein binding -4 | KIAA0746 | KIAA0746 protein | NM_015187 |
| protein binding -5 | PSCDBP | pleckstrin homology, Sec7 and coiled-coil domains, binding protein | NM_004288 |
| protein binding -6 | SKI | v-ski sarcoma viral oncogene homolog (avian) | NM_003036 |
| protein binding -7 | SNX25 | sorting nexin 25 | NM_031953 |
| protein binding -8 | CDH6 | cadherin 6, type 2, K-cadherin (fetal kidney) | NM_004932 |
| protein binding -9 | DCBLD2 | discoidin, CUB and LCCL domain containing 2 | NM_080927 |
| protein binding -10 | ENG | endoglin (Osler-Rendu-Weber syndrome 1) | NM_000118 |

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[Table 4g]

| Classification 12 | Gene symbol | Gene title | Genbank number |
|------------------------|-------------|---|----------------|
| protein modification-1 | SH3RF1 | SH3 domain containing ring finger 1 | NM_020870 |
| protein modification-2 | SMURF2 | SMAD specific E3 ubiquitin protein ligase 2 | NM_022739 |
| protein modification-3 | TFPI2 | tissue factor pathway inhibitor 2 | NM_006528 |
| protein modification-4 | ITGB3 | integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) | NM_000212 |
| protein modification-5 | MYPN | myopalladin | NM_032578 |
| protein modification-6 | LRP2BP | LRP2 binding protein | NM_018409 |
| protein modification-7 | HECW2 | HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2 | NM_020760 |
| protein modification-8 | PKIA | protein kinase (cAMP-dependent, catalytic) inhibitor alpha | NM_006823 |
| | | | |
| Classification 13 | Gene symbol | Gene title | Genbank number |
| signal molecule-1 | LYPD1 | LY6/PLAUR domain containing 1 | NM_144586 |
| signal molecule-2 | GATA6 | GATA binding protein 6 | NM_005257 |
| signal molecule-3 | RAB27B | RAB27B, member RAS oncogene family | NM_004163 |
| signal molecule-4 | SOX11 | SRY (sex determining region Y)-box 11 | NM_003108 |
| signal molecule-5 | ARHGAP22 | Rho GTPase activating protein 22 | NM_021226 |

[Table 4h]

| Classification 14 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| transcription-1 | ETV1 | ets variant gene 1 | NM_004956 |
| transcription-2 | ETV5 | ets variant gene 5 (ets- related molecule) | NM_004454 |
| transcription-3 | FOXP1 | forkhead box P1 | NM_032682 |
| transcription-4 | HMGA2 | high mobility group AT-hook 2 | NM_003483 |
| transcription-5 | KLF12 | Kruppel-like factor 12 | NM_007249 |
| transcription-6 | PRDM16 | PR domain containing 16 | NM_022114 |
| transcription-7 | SIM2 | single-minded homolog 2 (Drosophila) | NM_009586 |
| transcription-8 | SUHW2 | suppressor of hairy wing homolog 2 (Drosophila) | NM_080764 |
| transcription-9 | ENO1 | enolase 1 | NM_001428 |
| transcription-10 | MITF | microphthalmia-associated transcription factor | NM_198159 |
| transcription-11 | TCF3 | transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) | NM_003200 |
| transcription-12 | SMYD3 | SET and MYND domain containing 3 | NM_022743 |

[Table 4i]

| Classification 15 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| transport-1 | ATP6V1G3 | ATPase, H ⁺ transporting, lysosomal 13kDa, VI subunit G isoform 3 | NM_133262 |

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| Classification 15 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| transport-2 | KCTD16 | potassium channel tetramerisation domain containing 16 | NM_020768 |
| transport-3 | NUPL1 | nucleoporin like 1 | NM_014089 |
| transport-4 | SLC14A1 | solute carrier family 14 (urea transporter), member 1 (Kidd blood group) | NM_015865 |
| transport-5 | SLC16A4 | solute carrier family 16 (monocarboxylic acid transporters), member 4 | NM_004696 |
| transport-6 | SLC4A4 | solute carrier family 4, sodium bicarbonate cotransporter, member 4 | NM_003759 |
| transport-7 | SLC9A7 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 7 | NM_032591 |
| transport-8 | TRPC4 | transient receptor potential cation channel, subfamily C, member 4 | NM_016179 |
| transport-9 | MCFD2 | multiple coagulation factor deficiency 2 | NM_139279 |
| transport-10 | SLC26A4 | solute carrier family 26, member 4 | NM_000441 |
| transport-11 | MCOLN3 | mucolipin 3 | NM_018298 |
| transport-12 | SLC25A37 | solute carrier family 25, member 37 | NM_016612 |
| transport-13 | SLC30A7 | solute carrier family 30 (zinc transporter), member 7 | NM_133496 |

[Table 4j]

| Classification 16 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| others -1 | FLJ38725 | hypothetical protein FLJ38725 | NM_153218 |
| others -2 | KIAA1913 | KIAA1913 | NM_052913 |
| others -3 | PHLDB2 | pleckstrin homology-like domain, family B, member 2 | NM_145753 |
| others -4 | PLCXD2 | phosphatidylinositol-specific phospholipase C, X domain containing 2 | NM_153268 |
| others -5 | SAMD3 | sterile alpha motif domain containing 3 | NM_001017 373 |
| others -6 | ZNF423 | zinc finger protein 423 | NM_015069 |
| others -7 | FLJ33996 | hypothetical protein FLJ33996 | NM_175894. 2 |
| others -8 | PLEKHK1 | pleckstrin homology domain containing, family K member 1 | NM_145307 |
| others -9 | PTOV1 | Prostate tumor overexpressed gene 1 | NM_017432 |
| others -10 | FAM40B | family with sequence similarity 40, member B | NM_020704 |
| others -11 | ABI3BP | ABI gene family, member 3 (NESH) binding protein | NM_015429 |
| others -12 | NHS | Nance-Horan syndrome (congenital cataracts and dental anomalies) | NM_198270 |
| others -13 | DTL | denticleless homolog (Drosophila) | NM_016448 |
| others -14 | C1GALT1 | core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta- | NM_020156 |
| others -15 | CPNE8 | copine VIII | NM_53634 |
| others -16 | TMEM49 | transmembrane protein 49 | NM_030938 |

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8. A kit for distinguishing and separating mesenchymal stem cells, comprising any one of (g) to (i):

(g) a microarray as set forth in claim 6;

(h) an antibody as set forth in claim 7; and

(i) a probe for detecting whether the distinguishing marker gene for mesenchymal stem cells is expressed or not, the distinguishing marker gene comprising a polynucleotide, which, under stringent condition, hybridizes with a gene or a partial sequence thereof, the gene having a base sequence identified with the accession number listed in any one of Tables 5a to 5j.

[Table 5a]

| Classification 1 | Gene symbol | Gene title number | Genbank |
|--------------------|-------------|---|----------------|
| ATP/GTP binding -1 | BRIP1 | BRCA1 interacting protein C-terminal helicase 1 | NM_032043 |
| ATP/GTP binding -2 | PASK | PAS domain containing serine/threonine kinase | NM_015148 |
| ATP/GTP binding -3 | RAC2 | ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) | NM_002872 |
| ATP/GTP binding -4 | KIF18A | kinesin family member 18A | NM_31217 |
| ATP/GTP binding -5 | NEK7 | NIMA (never in mitosis gene a)-related kinase 7 | NM_133494 |
| ATP/GTP binding -6 | ARL4C | ADP-ribosylation factor-like 4C | NM_005737 |
| ATP/GTP binding -7 | EDEM1 | ER degradation enhancer, mannosidase alpha-like 1 | NM_014674 |
| ATP/GTP binding -8 | CAMK2D | calcium/calmodulin-dependent protein kinase (CaM kinase) II delta | NM_172127 |
| Classification 2 | Gene symbol | Gene title | Genbank number |
| binding -1 | PDE5A | phosphodiesterase 5A, cGMP-specific | NM_001083 |
| binding -2 | RGS4 | regulator of G-protein signalling 4 | NM_005613 |
| binding -3 | EGFL3 | EGF-like-domain, multiple 3 | NM_01409 |
| binding -4 | FHL2 | four and a half LIM domains | NM_001450 2 |
| binding-5 | HRB2 | HIV-1 rev binding protein 2 | NM_07043 |
| binding -6 | CAPZA1 | capping protein (actin filament) muscle Z-line, alpha 1 | NM_006135 |
| binding -7 | PAPPA2 | pappalysin 2 | NM_020318 |
| binding -8 | LOXL2 | lysyloxidase-like2 | NM_002318 |
| binding -9 | LOX | lysyl oxidase | NM_002317 |
| binding -10 | ADAMTS5 | ADAM metallopeptidase with thrombospondin type 1 motif, 5 (aggrecanase-2) | NM_007038 |

[Table 5b]

| Classification 3 | Gene symbol | Gene title | Genbank number |
|----------------------------------|-------------|---|----------------|
| cell growth and/or maintenance-1 | CCND1 | cyclin D1 (PRAD1: parathyroid adenomatosis 1) | NM_053056 |
| cell growth and/or maintenance-2 | CDC25A | cell division cycle 25A | NM_001789 |
| cell growth and/or maintenance-3 | IER3 | immediate early response 3 | NM_052815 |
| cell growth and/or maintenance-4 | BCL2 | B-cell CLL/lymphoma 2 | NM_000633 |
| cell growth and/or maintenance-5 | NALP1 | NACHT, leucine rich repeat and PYD containing 1 | NM_033004 |
| cell growth and/or maintenance-6 | PAK3 | p21 (CDKN1A)-activated kinase 3 | NM_002578 |

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(continued)

| Classification 3 | Gene symbol | Gene title | Genbank number |
|-----------------------------------|-------------|---------------------------------|----------------|
| cell growth and/or maintenance-7 | PODXL | podocalyxin-like | NM_001018 111 |
| cell growth and/or maintenance-8 | CCL26 | chemokine (C-C motif) ligand 26 | NM_006072 |
| cell growth and/or maintenance-9 | FBLN1 | fibulin 1 | NM_006486 |
| cell growth and/or maintenance-10 | LAMA1 | laminin, alpha 1 | NM_005559 |
| cell growth and/or maintenance-11 | NTNG1 | netrin G1 | NM_014917 |

[Table 5c]

| Classification 4 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| cytokine -1 | GDF15 | growth differentiation factor | NM_004864 |
| cytokine -2 | IL6 | interleukin 6 (interferon, beta 2) | NM_000600 |
| cytokine -3 | CTGF | connective tissue growth factor | NM_001901 |
| cytokine -4 | VEGF | vascular endothelial growth factor | NM_001025 366 |
| cytokine -5 | VEGFC | vascular endothelial growth factor C | NM_005429 |
| cytokine-6 | HGF | hepatocyte growth factor (hepapoietin A; scatter | NM_000601 |
| Classification 5 | Gene symbol | Gene title | Genbank number |
| cytoskeleton-1 | KRT19 | keratin 19 | NM_002276 |
| cytoskeleton-2 | KRTAP1-5 | keratin associated protein 1- | NM_031957 |
| cytoskeleton-3 | KRTAP2-1 | keratin associated protein 2- | BC012486 |
| cytoskeleton-4 | KRTHA4 | keratin, hair, acidic, 4 | NM_021013 |
| cytoskeleton-5 | CKAP2 | cytoskeleton associated protein 2 | NM_018204 |
| cytoskeleton-6 | KRTAP1-1 | keratin associated protein 1- | NM_030967 |
| cytoskeleton-7 | KRT18 | keratin 18 | NM_000224 |
| cytoskeleton-8 | KAP2.1B | keratin associated protein 2.1B | AJ406929 |
| cytoskeleton-9 | SSH1 | slingshot homolog 1 (Drosophila) | NM_018984 |
| Classification 6 | Gene symbol | Gene title | Genbank number |
| enzyme-1 | LXN | latexin | NM_020169 |
| enzyme-2 | IFI30 | interferon, gamma-inducible protein 30 | NM_006332 |
| enzyme-3 | CPA4 | carboxypeptidase A4 | NM_016352 |

[Table 5d]

| Classification 7 | Gene symbol | Gene title | Genbank number |
|------------------------|-------------|--|----------------|
| extracellular matrix-1 | CHI3L1 | chitinase 3-like 1 (cartilage glycoprotein-39) | NM_001276 |
| extracellular matrix-2 | KRT23 | keratin 23 (histone deacetylase inducible) | NM_015515 |
| extracellular matrix-3 | FLG | filaggrin | NM_002016 |
| extracellular matrix-4 | ADAMTS1 | a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 | NM_006988 |
| extracellular matrix-5 | FRMD5 | FERM domain containing 5 | NM_001031 729 |

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(continued)

| Classification 8 | Gene symbol | Gene title | Genbank number |
|--------------------------------|-------------|--|----------------|
| 5 growth factor or receptor-1 | IGFBP1 | insulin-like growth factor binding protein 1 | NM_000596 |
| growth factor or receptor-2 | CFI | complement factor I | NM_000204 |
| growth factor or receptor-3 | ESM1 | endothelial cell-specific molecule 1 | NM_007036 |
| growth factor or receptor-4 | F2RL1 | coagulation factor II (thrombin) receptor-like 1 | NM_005242 |
| 10 growth factor or receptor-5 | MET | met proto-oncogene (hepatocyte growth factor receptor) | NM_000245 |
| growth factor or receptor-6 | HTR7 | 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) | NM_000872 |
| 15 growth factor or receptor-7 | IGFBP3 | insulin-like growth factor binding protein 3 | NM_001013 398 |

[Table 5e]

| Classification 9 | Gene symbol | Gene title | Genbank number |
|-------------------------------|-------------|--|----------------|
| 20 membrane -1 | ABHD2 | abhydrolase domain containing 2 | NM_007011 |
| membrane -2 | ITGA2 | integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) | NM_002203 |
| 25 membrane -3 | LAMA3 | laminin, alpha 3 | NM_198129 |
| membrane -4 | NETO2 | neuropilin (NRP) and tolloid (TLL)-like 2 | NM_018092 |
| membrane -5 | NTN4 | netrin 4 | NM_021229 |
| 30 membrane -6 | PTGER1 | prostaglandin E receptor 1 (subtype EP1), 42kDa | NM_000955 |
| membrane -7 | EPHB2 | EPH receptor B2 | NM_017449 |
| membrane -8 | SFRP1 | secreted frizzled-related protein 1 | NM_003012 |
| 35 membrane -9 | CD33L3 | CD33 antigen-like 3 | NM_213602 |
| membrane-10 | GLIPR1 | GLI pathogenesis-related 1 (glioma) | NM_006851 |
| membrane -11 | UGCG | UDP-glucose ceramide glucosyltransferase | NM_003358 |
| 40 membrane -12 | ADORA1 | adenosine A1 receptor | NM_00674 |
| | | | |
| Classification 10 | Gene symbol | Gene title | Genbank number |
| 45 membrane binding protein-1 | ANXA10 | annexin A10 | NM_007193 |
| membrane binding protein-2 | RARRES1 | retinoic acid receptor responder (tazarotene induced) 1 | NM_206963 |
| membrane binding protein-3 | HNT | neurotrimin | NM_016522 |
| 50 membrane binding protein-4 | CNTNAP3 | contactin associated protein-like 3 | NM_033655 |

[Table 5f]

| Classification 11 | Gene symbol | Gene title | Genbank number |
|-----------------------|-------------|---------------------------|----------------|
| 55 protein binding -1 | SYT1 | synaptotagmin I | NM_005639 |
| protein binding -2 | MLF1 | myeloid leukemia factor 1 | NM_022443 |

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(continued)

| Classification 11 | Gene symbol | Gene title | Genbank number |
|---------------------|-------------|--|----------------|
| protein binding-3 | CDCP1 | CUB domain-containing protein 1 | NM_022842 |
| protein binding -4 | KIAA0746 | KIAA0746 protein | NM_015187 |
| protein binding -5 | PSCDBP | pleckstrin homology, Sec7 and coiled-coil domains, binding protein | NM_004288 |
| protein binding -6 | SKI | v-ski sarcoma viral oncogene homolog (avian) | NM_003036 |
| protein binding -7 | SNX25 | sorting nexin 25 | NM_031953 |
| protein binding -8 | CDH6 | cadherin 6, type 2, K-cadherin (fetal kidney) | NM_004932 |
| protein binding -9 | DCBLD2 | discoidin, CUB and LCCL domain containing 2 | NM_080927 |
| protein binding -10 | ENG | endoglin (Osler-Rendu-Weber syndrome 1) | NM_000118 |

[Table 5g]

| Classification 12 | Gene symbol | Gene title | Genbank number |
|------------------------|-------------|---|----------------|
| protein modification-1 | SH3RF1 | SH3 domain containing ring finger 1 | NM_020870 |
| protein modification-2 | SMURF2 | SMAD specific E3 ubiquitin protein ligase 2 | NM_022739 |
| protein modification-3 | TFPI2 | tissue factor pathway inhibitor 2 | NM_006528 |
| protein modification-4 | ITGB3 | integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) | NM_000212 |
| protein modification-5 | MYPN | myopalladin | NM_032578 |
| protein modification-6 | LRP2BP | LRP2 binding protein | NM_018409 |
| protein modification-7 | HECW2 | HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2 | NM_020760 |
| protein modification-8 | PKIA | protein kinase (cAMP-dependent, catalytic) inhibitor alpha | NM_006823 |
| Classification 13 | Gene symbol | Gene title | Genbank number |
| signal molecule-1 | LYPD1 | LY6/PLAUR domain containing 1 | NM_144586 |
| signal molecule-2 | GATA6 | GATA binding protein 6 | NM_005257 |
| signal molecule-3 | RAB27B | RAB27B, member RAS oncogene family | NM_004163 |
| signal molecule-4 | SOX11 | SRY (sex determining region Y)-box 11 | NM_003108 |
| signal molecule-5 | ARHGAP2 2 | Rho GTPase activating protein 22 | NM_021226 |

[Table 5h]

| Classification 14 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|---|----------------|
| transcription-1 | ETV1 | ets variant gene 1 | NM_004956 |
| transcription-2 | ETV5 | ets variant gene 5 (ets-related molecule) | NM_004454 |
| transcription-3 | FOXP1 | forkhead box P1 | NM_032682 |
| transcription-4 | HMG2 | high mobility group AT-hook 2 | NM_003483 |
| transcription-5 | KLF12 | Kruppel-like factor 12 | NM_007249 |

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(continued)

| Classification 14 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| transcription-6 | PRDM16 | PR domain containing 16 | NM_022114 |
| transcription-7 | SIM2 | single-minded homolog 2 (Drosophila) | NM_009586 |
| transcription-8 | SUHW2 | suppressor of hairy wing homolog 2 (Drosophila) | NM_080764 |
| transcription-9 | ENO1 | enolase 1 | NM_001428 |
| transcription-10 | MITF | microphthalmia-associated transcription factor | NM_198159 |
| transcription-11 | TCF3 | transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) | NM_003200 |
| transcription-12 | SMYD3 | SET and MYND domain containing 3 | NM_022743 |

[Table 5i]

| Classification 15 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| transport-1 | ATP6V1G3 | ATPase, H ⁺ transporting, lysosomal 13kDa, V1 subunit G isoform 3 | NM_133262 |
| transport-2 | KCTD16 | potassium channel tetramerisation domain containing 16 | NM_020768 |
| transport-3 | NUPL1 | nucleoporin like 1 | NM_014089 |
| transport-4 | SLC14A1 | solute carrier family 14 (urea transporter), member 1 (Kidd blood group) | NM_015865 |
| transport-5 | SLC16A4 | solute carrier family 16 (monocarboxylic acid transporters), member 4 | NM_004696 |
| transport-6 | SLC4A4 | solute carrier family 4, sodium bicarbonate cotransporter, member 4 | NM_003759 |
| transport-7 | SLC9A7 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 7 | NM_032591 |
| transport-8 | . TRPC4 | transient receptor potential cation channel, subfamily C, member 4 | NM_016179 |
| transport-9 | MCFD2 | multiple coagulation factor deficiency 2 | NM_139279 |
| transport-10 | SLC26A4 | solute carrier family 26, member 4 | NM_000441 |
| transport-11 | MCOLN3 | mucolipin 3 | NM_018298 |
| transport-12 | SLC25A37 | solute carrier family 25, member 37 | NM_016612 |
| transport-13 | SLC30A7 | solute carrier family 30 (zinc transporter), member 7 | NM_133496 |

[Table 5j]

| Classification 16 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| others -1 | FLJ38725 | hypothetical protein FLJ38725 | NM_153218 |
| others -2 | KIAA1913 | KIAA1913 | NM_052913 |
| others -3 | PHLDB2 | pleckstrin homology-like domain, family B, member 2 | NM_145753 |
| others -4 | PLCXD2 | phosphatidylinositol-specific phospholipase C, X domain containing 2 | NM_153268 |
| others -5 | SAMD3 | sterile alpha motif domain containing 3 | NM_001017_373 |

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(continued)

| Classification 16 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| others -6 | ZNF423 | zinc finger protein 423 | NM_015069 |
| others -7 | FLJ33996 | hypothetical protein FLJ33996 | NM_175894 2 |
| others -8 | PLEKHK1 | pleckstrin homology domain containing, family K member 1 | NM_145307 |
| others -9 | PTOV1 | prostate tumor gene 1 overexpressed gene 1 | NM_017432 |
| others -10 | FAM40B | family with sequence similarity 40, member B | NM_020704 |
| others -11 | ABI3BP | ABI gene family, member 3 (NESH) binding protein | NM_015429 |
| others -12 | NHS | Nance-Horan syndrome (congenital cataracts and dental anomalies) | NM_198270 |
| others -13 | DTL | denticleless homolog (Drosophila) | NM_016448 |
| others -14 | C1GALT1 | core 1 synthase, glycoprotein-N- acetylgalactosamine 3- beta- | NM_020156 |
| others -15 | CPNE8 | copine VIII | NM_153634 |
| others -16 | TMEM49 | transmembrane protein 49 | NM_030938 |

9. A method for distinguishing and separating mesenchymal stem cells, the method comprising:

separating the mesenchymal stem cells distinguished by a method as set forth in any one of claims 1 to 5.

10. A cell-containing composition comprising:

mesenchymal stem cells separated by a method as set forth in claim 9; or
a multiplied culture of the mesenchymal stem cells.

11. A drug for regenerative medicine, comprising:

a cell-containing composition as set forth in claim 10.

12. A distinguishing marker for distinguishing mesenchymal stem cells, the distinguishing marker being at least one of genes having the base sequences identified with the accession numbers listed in Tables 6a to 6j.

[Table 6a]

| Classification 1 | Gene symbol | Gene title | Genbank number |
|--------------------|-------------|--|----------------|
| ATP/GTP binding -1 | BRIP1 | BRCA1 interacting protein C-terminal helicase 1 | NM_032043 |
| ATP/GTP binding -2 | PASK | PAS domain containing serine/threonine kinase | NM_015148 |
| ATP/GTP binding -3 | RAC2 | ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) | NM_002872 |
| ATP/GTP binding -4 | KIF18A | kinesin family member 18A | NM_031217 |
| ATP/GTP binding -5 | NEK7 | NIMA (never in mitosis gene a)-related kinase 7 | NM_133494 |
| ATP/GTP binding -6 | ARL4C | ADP-ribosylation factor-like | NM_005737 |
| ATP/GTP binding -7 | EDEM1 | ER degradation enhancer, mannosidase alpha-like 1 | NM_014674 |
| ATP/GTP binding -8 | CAMK2D | calcium/calmodulin-dependent protein kinase (CaM kinase) II delta | NM_172127 |

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(continued)

| Classification 2 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| binding -1 | PDE5A | phosphodiesterase 5A, cGMP-specific | NM_001083 |
| binding -2 | RGS4 | regulator of G-protein signalling 4 | NM_005613 |
| binding -3 | EGFL3 | EGF-like-domain, multiple 3 | NM_001409 |
| binding -4 | FHL2 | four and a half LIM domains | NM_001450 |
| binding -5 | HRB2 | HIV-1 rev binding protein 2 | NM_007043 |
| binding -6 | CAPZA1 | capping protein (actin filament) muscle Z-line, alpha 1 | NM_006135 |
| binding -7 | PAPPA2 | pappalysin 2 | NM_020318 |
| binding -8 | LOXL2 | lysyl oxidase-like 2 | NM_002318 |
| binding -9 | LOX | lysyl oxidase | NM_002317 |
| binding -10 | ADAMTS5 | ADAM metalloproteinase with thrombospondin type 1 motif, 5 (aggrecanase-2) | NM_007038 |

[Table 6b]

| Classification 3 | Gene symbol | Gene title | Genbank number |
|-----------------------------------|-------------|---|----------------|
| cell growth and/or maintenance-1 | CCND1 | cyclin D1 (PRAD1: parathyroid adenomatosis 1) | NM_053056 |
| cell growth and/or maintenance-2 | CDC25A | cell division cycle 25A | NM_001789 |
| cell growth and/or maintenance-3 | IER3 | immediate early response 3 | NM_052815 |
| cell growth and/or maintenance-4 | BCL2 | B-cell CLL/lymphoma 2 | NM_000633 |
| cell growth and/or maintenance-5 | NALP1 | NACHT, leucine rich repeat and PYD containing 1 | NM_033004 |
| cell growth and/or maintenance-6 | PAK3 | p21 (CDKN1A)-activated kinase 3 | NM_002578 |
| cell growth and/or maintenance-7 | PODXL | podocalyxin-like | NM_001018 111 |
| cell growth and/or maintenance-8 | CCL26 | chemokine (C-C motif) ligand 26 | NM_006072 |
| cell growth and/or maintenance-9 | FBLN1 | fibulin 1 | NM_006486 |
| cell growth and/or maintenance-10 | LAMA1 | laminin, alpha 1 | NM_005559 |
| cell growth and/or maintenance-11 | NTNG1 | netrin G1 | NM_014917 |

[Table 6c]

| Classification 4 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| cytokine -1 | GDF15 | growth differentiation factor 15 | NM_004864 |
| cytokine -2 | IL6 | interleukin 6 (interferon, beta 2) | NM_000600 |
| cytokine-3 | CTGF | connective tissue growth factor | NM_001901 |
| cytokine -4 | VEGF | vascular endothelial growth factor | NM_001025 366 |
| cytokine -5 | VEGFC | vascular endothelial growth factor C | NM_005429 |
| cytokine -6 | HGF | hepatocyte growth factor (hepapoietin A; scatter | NM_000601 |

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(continued)

| Classification 5 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| cytoskeleton-1 | KRT19 | keratin 19 | NM_002276 |
| cytoskeleton-2 | KRTAP1-5 | keratin associated protein 1- | NM_031957 |
| cytoskeleton-3 | KRTAP2-1 | keratin associated protein 2- | BC012486 |
| cytoskeleton-4 | KRTHA4 | keratin, hair, acidic, 4 | NM_021013 |
| cytoskeleton-5 | CKAP2 | cytoskeleton associated protein 2 | NM_018204 |
| cytoskeleton-6 | KRTAP1-1 | keratin associated protein 1- | NM_030967 |
| cytoskeleton-7 | KRT18 | keratin 18 | NM_000224 |
| cytoskeleton-8 | KAP2.1B | keratin associated protein 2.1B | AJ406929 |
| cytoskeleton-9 | SSH1 | slingshot homolog 1 (Drosophila) | NM_018984 |
| Classification 6 | Gene symbol | Gene title | Genbank number |
| enzyme-1 | LXN | latexin | NM_020169 |
| enzyme-2 | IFI30 | interferon, gamma-inducible protein 30 | NM_006332 |
| enzyme-3 | CPA4 | carboxypeptidase A4 | NM_016352 |

[Table 6d]

| Classification 7 | Gene symbol | Gene title | Genbank number |
|-----------------------------|-------------|--|----------------|
| extracellular matrix-1 | CHI3L1 | chitinase 3-like 1 (cartilage glycoprotein-39) | NM_001276 |
| extracellular matrix-2 | KRT23 | keratin 23 (histone deacetylase inducible) | NM_015515 |
| extracellular matrix-3 | FLG | filaggrin | NM_002016 |
| extracellular matrix-4 | ADAMTS1 | a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 | NM_006988 |
| extracellular matrix-5 | FRMD5 | FERM domain containing 5 | NM_001031 |
| Classification 8 | Gene symbol | Gene title | Genbank number |
| growth factor or receptor-1 | IGFBP1 | insulin-like growth factor binding protein 1 | NM_000596 |
| growth factor or receptor-2 | CFI | complement factor I | NM_000204 |
| growth factor or receptor-3 | ESM1 | endothelial cell-specific molecule 1 | NM_007036 |
| growth factor or receptor-4 | F2RL1 | coagulation factor II (thrombin) receptor-like 1 | NM_005242 |
| growth factor or receptor-5 | MET | met proto-oncogene (hepatocyte growth factor receptor) | NM_000245 |
| growth factor or receptor-6 | HTR7 | 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) | NM_000872 |
| growth factor or receptor-7 | IGFBP3 | insulin-like growth factor binding protein 3 | NM_001013 398 |

[Table 6e]

| Classification 9 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|---------------------------------|----------------|
| membrane -1 | ABHD2 | abhydrolase domain containing 2 | NM_007011 |

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(continued)

| Classification 9 | Gene symbol | Gene title | Genbank number |
|-------------------------------|-------------|--|----------------|
| 5 membrane -2 | ITGA2 | integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) | NM_002203 |
| membrane -3 | LAMA3 | laminin, alpha 3 | NM_198129 |
| membrane -4 | NETO2 | neuropilin (NRP) and tolloid (TLL)-like 2 | NM_018092 |
| 10 membrane -5 | NTN4 | netrin 4 | NM_021229 |
| membrane -6 | PTGER1 | prostaglandin E receptor 1 (subtype EP1), 42kDa | NM_000955 |
| membrane -7 | EPHB2 | EPH receptor B2 | NM_017449 |
| 15 membrane -8 | SFRP1 | secreted frizzled-related protein 1 | NM_003012 |
| membrane -9 | CD33L3 | CD33 antigen-like 3 | NM_213602 |
| membrane-10 | GLIPR1 | GLI pathogenesis-related 1 (glioma) | NM_006851 |
| 20 membrane -11 | UGCG | UDP-glucose ceramide glucosyltransferase | NM_003358 |
| membrane -12 | ADORA1 | adenosine A1 receptor | NM_000674 |
| | | | |
| Classification 10 | Gene symbol | Gene title | Genbank number |
| 25 membrane binding protein-1 | ANXA10 | annexin A10 | NM_007193 |
| membrane binding protein-2 | RARRES1 | retinoic acid receptor responder (tazarotene induced) 1 | NM_206963 |
| membrane binding protein-3 | HNT | neurotrimin | NM_016522 |
| 30 membrane binding protein-4 | CNTNAP3 | contactin associated protein-like 3 | NM_033655 |

[Table 6f]

| Classification 11 | Gene symbol | Gene title | Genbank number |
|------------------------|-------------|--|----------------|
| 35 protein binding -1 | SYT1 | synaptotagmin I | NM_005639 |
| protein binding -2 | MLF1 | myeloid leukemia factor 1 | NM_022443 |
| protein binding -3 | CDCP1 | CUB domain-containing protein 1 | NM_022842 |
| 40 protein binding -4 | KIAA0746 | KIAA0746 protein | NM_015187 |
| protein binding -5 | PSCDBP | pleckstrin homology, Sec7 and coiled-coil domains, binding protein | NM_004288 |
| 45 protein binding -6 | SKI | v-ski sarcoma viral oncogene homolog (avian) | NM_003036 |
| protein binding -7 | SNX25 | sorting nexin 25 | NM_031953 |
| protein binding -8 | CDH6 | cadherin 6, type 2, K-cadherin (fetal kidney) | NM_004932 |
| protein binding -9 | DCBLD2 | discoidin, CUB and LCCL domain containing 2 | NM_080927 |
| 50 protein binding -10 | ENG | endoglin (Osler-Rendu-Weber syndrome 1) | NM_000118 |

[Table 6g]

| Classification 12 | Gene symbol | Gene title | Genbank number |
|---------------------------|-------------|-------------------------------------|----------------|
| 55 protein modification-1 | SH3RF1 | SH3 domain containing ring finger 1 | NM_020870 |

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(continued)

| Classification 12 | Gene symbol | Gene title | Genbank number |
|------------------------|-------------|---|----------------|
| protein modification-2 | SMURF2 | SMAD specific E3 ubiquitin protein ligase 2 | NM_022739 |
| protein modification-3 | TFPI2 | tissue factor pathway inhibitor 2 | NM_006528 |
| protein modification-4 | ITGB3 | integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) | NM_000212 |
| protein modification-5 | MYPN | myopalladin | NM_032578 |
| protein modification-6 | LRP2BP | LRP2 binding protein | NM_018409 |
| protein modification-7 | HECW2 | HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2 | NM_020760 |
| protein modification-8 | PKIA | protein kinase (cAMP-dependent, catalytic) inhibitor alpha | NM_006823 |
| Classification 13 | Gene symbol | Gene title | Genbank number |
| signal molecule-1 | LYPD1 | LY6/PLAUR domain containing 1 | NM_144586 |
| signal molecule-2 | GATA6 | GATA binding protein 6 | NM_005257 |
| signal molecule-3 | RAB27B | RAB27B, member RAS oncogene family | NM_004163 |
| signal molecule-4 | SOX11 | SRY (sex determining region Y)-box 11 | NM_003108 |
| signal molecule-5 | ARHGAP2 2 | Rho GTPase activating protein 22 | NM_021226 |

[Table 6h]

| Classification 14 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| transcription-1 | ETV1 | ets variant gene 1 | NM_004956 |
| transcription-2 | ETV5 | ets variant gene 5 (ets-related molecule) | NM_004454 |
| transcription-3 | FOXP1 | forkhead box P1 | NM_032682 |
| transcription-4 | HMG2 | high mobility group AT-hook 2 | NM_003483 |
| transcription-5 | KLF12 | Kruppel-like factor 12 | NM_007249 |
| transcription-6 | PRDM16 | PR domain containing 16 | NM_022114 |
| transcription-7 | SIM2 | single-minded homolog 2 (Drosophila) | NM_009586 |
| transcription-8 | SUHW2 | suppressor of hairy wing homolog 2 (Drosophila) | NM_080764 |
| transcription-9 | ENO1 | enolase 1 | NM_001428 |
| transcription-10 | MITF | microphthalmia-associated | NM_198159 |
| transcription-11 | TCF3 | transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) | NM_003200 |
| transcription-12 | SMYD3 | SET and MYND domain containing 3 | NM_022743 |

[Table 6i]

| Classification 15 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| transport-1 | ATP6V1G3 | ATPase, H ⁺ transporting, lysosomal 13kDa, V1 subunit G isoform 3 | NM_133262 |
| transport-2 | KCTD16 | potassium channel tetramerisation domain containing 16 | NM_020768 |

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(continued)

| Classification 15 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| transport-3 | NUPL1 | nucleoporin like 1 | NM_014089 |
| transport-4 | SLC14A1 | solute carrier family 14 (urea transporter), member 1 (Kidd blood group) | NM_015865 |
| transport-5 | SLC16A4 | solute carrier family 16 (monocarboxylic acid transporters), member 4 | NM_004696 |
| transport-6 | SLC4A4 | solute carrier family 4, sodium bicarbonate cotransporter, member 4 | NM_003759 |
| transport-7 | SLC9A7 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 7 | NM_032591 |
| transport-8 | TRPC4 | transient receptor potential cation channel, subfamily C, member 4 | NM_016179 |
| transport-9 | MCFD2 | multiple coagulation factor deficiency 2 | NM_139279 |
| transport-10 | SLC26A4 | solute carrier family 26, member 4 | NM_000441 |
| transport-11 | MCOLN3 | mucolipin 3 | NM_018298 |
| transport-12 | SLC25A37 | solute carrier family 25, member 37 | NM_016612 |
| transport-13 | SLC30A7 | solute carrier family 30 (zinc transporter), member 7 | NM_133496 |

[Table 6j]

| Classification 16 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| others -1 | FLJ38725 | hypothetical protein FLJ38725 | NM_153218 |
| others -2 | KIAA1913 | KLAA1913 | NM_052913 |
| others -3 | PHLDB2 | pleckstrin homology-like NM_145753 domain, family B, member 2 | |
| others -4 | PLCXD2 | phosphatidylinositol-specific phospholipase C, X domain containing 2 | NM_153268 |
| others -5 | SAMD3 | sterile alpha motif domain containing 3 | NM_001017 373 |
| others -6 | ZNF423 | zinc finger protein 423 | NM_015069 |
| others -7 | FLJ33996 | hypothetical protein FLJ33996 | NM_175894. 2 |
| others -8 | PLEKHK1 | pleckstrin homology domain containing, family K member 1 | NM_145307 |
| others -9 | PTOV1 | prostate tumor overexpressed gene 1 | NM_017432 |
| others -10 | FAM40B | family with sequence similarity 40, member B | NM_020704 |
| others -11 | ABI3BP | ABI gene family, member 3 (NESH) binding protein | NM_015429 |
| others -12 | NHS | Nance-Horan syndrome (congenital cataracts and dental anomalies) | NM_198270 |
| others -13 | DTL | denticleless homolog (Drosophila) | NM_016448 |
| others -14 | C1GALT1 | core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta- | NM_020156 |
| others -15 | CPNE8 | copine VIII | NM_153634 |
| others -16 | TMEM49 | transmembrane protein 49 | NM_030938 |

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13. A distinguishing marker for distinguishing mesenchymal stem cells, the distinguishing marker being at least one of polypeptides encoded by genes having the base sequences identified with the accession numbers listed in Tables 7a to 7j.

[Table 7a]

| Classification 1 | Gene symbol | Gene title | Genbank number |
|--------------------|-------------|---|----------------|
| ATP/GTP binding -1 | BRIP1 | BRCA1 interacting protein C-terminal helicase 1 | NM_032043 |
| ATP/GTP binding -2 | PASK | PAS domain containing serine/threonine kinase | NM_015148 |
| ATP/GTP binding -3 | RAC2 | ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) | NM_002872 |
| ATP/GTP binding -4 | KIF18A | kinesin family member 18A | NM_031217 |
| ATP/GTP binding -5 | NEK7 | NIMA (never in mitosis gene a)-related kinase 7 | NM_133494 |
| ATP/GTP binding -6 | ARL4C | ADP-ribosylation factor-like | NM_005737 |
| ATP/GTP binding -7 | EDEM1 | ER degradation enhancer, mannosidase alpha-like 1 | NM_014674 |
| ATP/GTP binding -8 | CAMK2D | calcium/calmodulin-dependent protein kinase (CaM kinase) II delta | NM_172127 |
| Classification 2 | Gene symbol | Gene title | Genbank number |
| binding -1 | PDE5A | phosphodiesterase 5A, cGMP-specific | NM_001083 |
| binding -2 | RGS4 | regulator of G-protein signalling 4 | NM_005613 |
| binding -3 | EGFL3 | EGF-like-domain, multiple 3 | NM_001409 |
| binding -4 | FHL2 | four and a half LIM domains 2 | NM_001450 |
| binding -5 | HRB2 | HIV-1 rev binding protein 2 | NM_007043 |
| binding -6 | CAPZA1 | capping protein (actin filament) muscle Z-line, alpha 1 | NM_006135 |
| binding -7 | PAPPA2 | pappalysin 2 | NM_020318 |
| binding -8 | LOXL2 | lysyl oxidase-like 2 | NM_002318 |
| binding -9 | LOX | lysyl oxidase | NM_002317 |
| binding -10 | ADAMTS5 | ADAM metalloproteinase with thrombospondin type 1 motif, 5 (aggrecanase-2) | NM_007038 |

[Table 7b]

| Classification 3 | Gene symbol | Gene title | Genbank number |
|----------------------------------|-------------|---|----------------|
| cell growth and/or maintenance-1 | CCND1 | cyclin D1 (PRAD1: parathyroid adenomatosis 1) | NM_053056 |
| cell growth and/or maintenance-2 | CDC25A | cell division cycle 25A | NM_001789 |
| cell growth and/or maintenance-3 | IER3 | immediate early response 3 | NM_052815 |
| cell growth and/or maintenance-4 | BCL2 | B-cell CLL/lymphoma 2 | NM_000633 |
| cell growth and/or maintenance-5 | NALP1 | NACHT, leucine rich repeat and PYD containing 1 | NM_033004 |
| cell growth and/or maintenance-6 | PAK3 | p21 (CDKN1A)-activated kinase 3 | NM_002578 |
| cell growth and/or maintenance-7 | PODXL | podocalyxin-like | NM_001018 111 |
| cell growth and/or maintenance-8 | CCL26 | chemokine (C-C motif) ligand 26 | NM_006072 |
| cell growth and/or maintenance-9 | FBLN1 | fibulin 1 | NM_006486 |

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(continued)

| Classification 3 | Gene symbol | Gene title | Genbank number |
|-----------------------------------|-------------|------------------|----------------|
| cell growth and/or maintenance-10 | LAMA1 | laminin, alpha 1 | NM_005559 |
| cell growth and/or maintenance-11 | NTNG1 | netrin G1 | NM_014917 |

[Table 7c]

| Classification 4 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| cytokine -1 | GDF15 | growth 15 differentiation factor | NM_004864 |
| cytokine -2 | IL6 | interleukin 6 (interferon, beta 2) | NM_000600 |
| cytokine -3 | CTGF | connective tissue growth factor | NM_001901 |
| cytokine -4 | VEGF | vascular endothelial growth factor | NM_001025 366 |
| cytokine -5 | VEGFC | vascular endothelial growth factor C | NM_005429 |
| cytokine -6 | HGF | hepatocyte growth factor (hepapoietin A; scatter | NM_000601 |
| Classification 5 | Gene symbol | Gene title | Genbank number |
| cytoskeleton-1 | KRT19 | keratin 19 | NM_002276 |
| cytoskeleton-2 | KRTAP1-5 | keratin associated protein 1- | NM_031957 |
| cytoskeleton-3 | KRTAP2-1 | keratin associated protein 2- | BC012486 |
| cytoskeleton-4 | KRTHA4 | keratin, hair, acidic, 4 | NM_021013 |
| cytoskeleton-5 | CKAP2 | cytoskeleton associated protein 2 | NM_018204 |
| cytoskeleton-6 | KRTAP1-1 | keratin associated protein 1- | NM_030967 |
| cytoskeleton-7 | KRT18 | keratin 18 | NM_000224 |
| cytoskeleton-8 | KAP2.1B | keratin associated protein 2.1B | AJ406929 |
| cytoskeleton-9 | SSH1 | slingshot homolog 1 (Drosophila) | NM_018984 |
| Classification 6 | Gene symbol | Gene title | Genbank number |
| enzyme-1 | LXN | latexin | NM_020169 |
| enzyme-2 | IFI30 | interferon, gamma-inducible protein 30 | NM_006332 |
| enzyme-3 | CPA4 | carboxypeptidase A4 | NM_016352 |

[Table 7d]

| Classification 7 | Gene symbol | Gene title | Genbank number |
|-----------------------------|-------------|--|----------------|
| extracellular matrix-1 | CHI3L1 | chitinase 3-like 1 (cartilage glycoprotein-39) | NM_001276 |
| extracellular matrix-2 | KRT23 | keratin 23 (histone deacetylase inducible) | NM_015515 |
| extracellular matrix-3 | FLG | filaggrin | NM_002016 |
| extracellular matrix-4 | ADAMTS1 | a disintegrin-like and metalloprotease (reprolysin type) With thrombospondin type 1 motif, 1 | NM_006988 |
| extracellular matrix-5 | FRMD5 | FERM domain containing 5 | NM_001031 |
| Classification 8 | Gene symbol | Gene title | Genbank number |
| growth factor or receptor-1 | IGFBP1 | insulin-like growth factor binding protein 1 | NM_000596 |

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(continued)

| Classification 8 | Gene symbol | Gene title | Genbank number |
|-----------------------------|-------------|--|----------------|
| growth factor or receptor-2 | CFI | complement factor I | NM_000204 |
| growth factor or receptor-3 | ESM1 | endothelial cell-specific molecule 1 | NM_007036 |
| growth factor or receptor-4 | F2RL1 | coagulation factor II (thrombin) receptor-like 1 | NM_005242 |
| growth factor or receptor-5 | MET | met proto-oncogene (hepatocyte growth factor receptor) | NM_000245 |
| growth factor or receptor-6 | HTR7 | 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) | NM_000872 |
| growth factor or receptor-7 | IGFBP3 | insulin-like growth factor binding protein 3 | NM_001013 398 |

[Table 7e]

| Classification 9 | Gene symbol | Gene title | Genbank number |
|----------------------------|-------------|--|----------------|
| membrane -1 | ABHD2 | abhydrolase domain containing 2 | NM_007011 |
| membrane -2 | ITGA2 | integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) | NM_002203 |
| membrane -3 | LAMA3 | laminin, alpha 3 | NM_198129 |
| membrane -4 | NETO2 | neuropilin (NRP) and tolloid (TLL)-like 2 | NM_018092 |
| membrane -5 | NTN4 | netrin 4 | NM_021229 |
| membrane -6 | PTGER1 | prostaglandin E receptor 1 (subtype EP1), 42kDa | NM_000955 |
| membrane -7 | EPHB2 | EPH receptor B2 | NM_017449 |
| membrane -8 | SFRP1 | secreted frizzled-related protein 1 | NM_003012 |
| membrane -9 | CD33L3 | CD33 antigen-like 3 | NM_213602 |
| membrane -10 | GLIPR1 | GLI pathogenesis-related 1 NM_ (glioma) | 006851 |
| membrane -11 | UGCG | UDP-glucose ceramide glucosyltransferase | NM_003358 |
| membrane -12 | ADORA1 | adenosine A1 receptor | NM_000674 |
| Classification 10 | Gene symbol | Gene title | Genbank number |
| membrane binding protein-1 | ANXA10 | annexin A10 | NM_007193 |
| membrane binding protein-2 | RARRES1 | retinoic acid receptor responder (tazarotene induced) 1 | NM_206963 |
| membrane binding protein-3 | HNT | neurotrimin | NM_016522 |
| membrane binding protein-4 | CNTNAP3 | contactin associated protein-like 3 | NM_033655 |

[Table 7f]

| Classification 11 | Gene symbol | Gene title | Genbank number |
|--------------------|-------------|---------------------------------|----------------|
| protein binding -1 | SYT1 | synaptotagmin I | NM_005639 |
| protein binding -2 | MLF1 | myeloid leukemia factor 1 | NM_022443 |
| protein binding -3 | CDCP1 | CUB domain-containing protein 1 | NM_022842 |

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(continued)

| Classification 11 | Gene symbol | Gene title | Genbank number |
|---------------------|-------------|--|----------------|
| protein binding -4 | KIAA0746 | KIAA0746 protein | NM_015187 |
| protein binding -5 | PSCDBP | pleckstrin homology, Sec7 and coiled-coil domains, binding protein | NM_004288 |
| protein binding -6 | SKI | v-ski sarcoma viral oncogene homolog (avian) | NM_003036 |
| protein binding -7 | SNX25 | sorting nexin 25 | NM_031953 |
| protein binding -8 | CDH6 | cadherin 6, type 2, K-cadherin (fetal kidney) | NM_004932 |
| protein binding-9 | DCBLD2 | discoidin, CUB and LCCL domain containing 2 | NM_080927 |
| protein binding -10 | ENG | endoglin (Osler-Rendu-Weber syndrome 1) | NM_000118 |

[Table 7g]

| Classification 12 | Gene symbol | Gene title | Genbank number |
|------------------------|-------------|---|----------------|
| protein modification-1 | SH3RF1 | SH3 domain containing ring finger 1 | NM_020870 |
| protein modification-2 | SMURF2 | SMAD specific E3 ubiquitin protein ligase 2 | NM_022739 |
| protein modification-3 | TFPI2 | tissue factor pathway inhibitor 2 | NM_006528 |
| protein modification-4 | ITGB3 | integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) | NM_000212 |
| protein modification-5 | MYPN | myopalladin | NM_032578 |
| protein modification-6 | LRP2BP | LRP2 binding protein | NM_018409 |
| protein modification-7 | HECW2 | HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2 | NM_020760 |
| protein modification-8 | PKIA | protein kinase (cAMP-dependent, catalytic) inhibitor alpha | NM_006823 |

| Classification 13 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|---------------------------------------|----------------|
| signal molecule-1 | LYPD1 | LY6/PLAUR domain containing 1 | NM_144586 |
| signal molecule-2 | GATA6 | GATA binding protein 6 | NM_005257 |
| signal molecule-3 | RAB27B | RAB27B, member RAS oncogene family | NM_004163 |
| signal molecule-4 | SOX11 | SRY (sex determining region Y)-box 11 | NM_003108 |
| signal molecule-5 | ARHGAP2 2 | Rho GTPase activating protein 22 | NM_021226 |

[Table 7h]

| Classification 14 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|---|----------------|
| transcription-1 | ETV1 | ets variant gene 1 | NM_004956 |
| transcription-2 | ETV5 | ets variant gene 5 (ets-related molecule) | NM_004454 |
| transcription-3 | FOXP1 | forkhead box P1 | NM_032682 |
| transcription-4 | HMGA2 | high mobility group AT-hook 2 | NM_003483 |
| transcription-5 | KLF12 | Kruppel-like factor 12 | NM_007249 |
| transcription-6 | PRDM16 | PR domain containing 16 | NM_022114 |

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(continued)

| Classification 14 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| transcription-7 | SIM2 | single-minded homolog 2 (Drosophila) | NM_009586 |
| transcription-8 | SUHW2 | suppressor of hairy wing homolog 2 (Drosophila) | NM_080764 |
| transcription-9 | ENO1 | enolase 1 | NM_001428 |
| transcription-10 | MITF | microphthalmia-associated transcription factor | NM_198159 |
| transcription-11 | TCF3 | transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) | NM_003200 |
| transcription-12 | SMYD3 | SET and MYND domain containing 3 | NM_022743 |

[Table 7i]

| Classification 15 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| transport-1 | ATP6V1G3 | ATPase, H ⁺ transporting, lysosomal 13kDa, V1 subunit G isoform 3 | NM_133262 |
| transport-2 | KCTD16 | potassium channel tetramerisation domain containing 16 | NM_020768 |
| transport-3 | NUPL1 | nucleoporin like 1 | NM_014089 |
| transport-4 | SLC14A1 | solute carrier family 14 (urea transporter), member 1 (Kidd blood group) | NM_015865 |
| transport-5 | SLC16A4 | solute carrier family 16 (monocarboxylic acid transporters), member 4 | NM_004696 |
| transport-6 | SLC4A4 | solute carrier family 4, sodium bicarbonate cotransporter, member 4 | NM_003759 |
| transport-7 | SLC9A7 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 7 | NM_032591 |
| transport-8 | TRPC4 | transient receptor potential cation channel, subfamily C, member 4 | NM_016179 |
| transport-9 | MCFD2 | multiple coagulation factor deficiency 2 | NM_139279 |
| transport-10 | SLC26A4 | solute carrier family 26, member 4 | NM_000441 |
| transport-11 | MCOLN3 | mucolipin 3 | NM_018298 |
| transport-12 | SLC25A37 | solute carrier family 25, member 37 | NM_016612 |
| transport-13 | SLC30A7 | solute carrier family 30 (zinc transporter), member 7 | NM_133496 |

[Table 7j]

| Classification 16 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| others -1 | FLJ38725 | hypothetical protein FLJ38725 | NM_153218 |
| others -2 | KIAA1913 | KIAA1913 | NM_052913 |
| others -3 | PHLDB2 | pleckstrin homology-like domain, family B, member 2 | NM_145753 |
| others -4 | PLCXD2 | phosphatidylinositol-specific phospholipase C, X domain containing 2 | NM_153268 |
| others 5 | SAMD3 | sterile alpha motif domain containing 3 | NM_001017_373 |
| others -6 | ZNF423 | zinc finger protein 423 | NM_015069 |

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(continued)

| Classification 16 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| others -7 | FLJ33996 | hypothetical protein FLJ33996 | NM_175894.2 |
| others -8 | PLEKHK1 | pleckstrin homology domain containing, family K member 1 | NM_145307 |
| others -9 | PTOV1 | prostate tumor overexpressed gene 1 | NM_017432 |
| others -10 | FAM40B | family with sequence similarity 40, member B | NM_020704 |
| others -11 | ABI3BP | ABI gene family, member 3 (NESH) binding protein | NM_015429 |
| others -12 | NHS | Nance-Horan syndrome (congenital cataracts and dental anomalies) | NM_198270 |
| others -13 | DTL | denticleless homolog (Drosophila) | NM_016448 |
| others -14 | C1GALT1 | core 1 synthase, glycoprotein-N- acetylgalactosamine 3- beta- | NM_020156 |
| others -15 | CPNE8 | copine VIII | NM_153634 |
| others -16 | TMEM49 | transmembrane protein 49 | NM_030938 |

14. A method of judging whether a sample provider has been developed a disease related with mesenchymal stem cells or whether the sample provider has a possibility of developing the disease in the future, the method judging by treating a sample, which is separated *in vivo* from the sample provider, with any one or more of:

- a method as set forth in any one of claims 1 to 5;
- a microarray as set forth in claim 6;
- an antibody as set forth in claim 7;
- a kit as set forth in claim 8; and
- a distinguishing marker as set forth in claim 12 or 13.

15. A drug for regenerative medicine, the drug suppressing undifferentiating property of mesenchymal stem cells and comprising siRNA for a gene or a partial sequence thereof, the gene having any one of the base sequences identified with the accession numbers listed in Tables 8a to 8j.

[Table 8a]

| Classification 1 | Gene symbol | Gene title | Genbank number |
|--------------------|-------------|---|----------------|
| ATP/GTP binding -1 | BRIP1 | BRCA1 interacting protein C-terminal helicase 1 | NM_032043 |
| ATP/GTP binding -2 | PASK | PAS domain containing serine/threonine kinase | NM_015148 |
| ATP/GTP binding -3 | RAC2 | ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) | NM_002872 |
| ATP/GTP binding -4 | KIF18A | kinesin family member 18A | NM_031217 |
| ATP/GTP binding -5 | NEK7 | NIMA (never in mitosis gene a)-related kinase 7 | NM_133494 |
| ATP/GTP binding -6 | ARL4C | ADP-ribosylation factor-like 4C | NM_005737 |
| ATP/GTP binding -7 | EDEM1 | ER degradation enhancer, mannosidase alpha-like 1 | NM_014674 |
| ATP/GTP binding -8 | CAMK2D | calcium/calmodulin-dependent protein kinase (CaM kinase) II delta | NM_172127 |
| Classification 2 | Gene symbol | Gene title | Genbank number |
| binding -1 | PDE5A | phosphodiesterase 5A, cGMP-specific | NM_001083 |
| binding -2 | RGS4 | regulator of G-protein signalling 4 | NM_005613 |
| binding -3 | EGFL3 | EGF-like-domain, multiple 3 | NM_001409 |

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(continued)

| Classification 2 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| binding -4 | FHL2 | four and a half LIM domains 2 | NM_001450 |
| binding -5 | HRB2 | HIV-1 rev binding protein 2 | NM_007043 |
| binding -6 | CAPZA1 | capping protein (actin filament) muscle Z-line, alpha 1 | NM_006135 |
| binding -7 | PAPPA2 | pappalysin 2 | NM_020318 |
| binding -8 | LOXL2 | lysyl oxidase-like 2 | NM_002318 |
| binding -9 | LOX | lysyl oxidase | NM_002317 |
| binding -10 | ADAMTS5 | ADAM metalloproteinase with thrombospondin type 1 motif, 5 (aggrecanase-2) | NM_007038 |

[Table 8b]

| Classification 3 | Gene symbol | Gene title | Genbank number |
|-----------------------------------|-------------|---|----------------|
| cell growth and/or maintenance-1 | CCND1 | cyclin D1 (PRAD1: parathyroid adenomatosis 1) | NM_053056 |
| cell growth and/or maintenance-2 | CDC25A | cell division cycle 25A | NM_001789 |
| cell growth and/or maintenance-3 | IER3 | immediate early response 3 | NM_052815 |
| cell growth and/or maintenance-4 | BCL2 | B-cell CLL/lymphoma 2 | NM_000633 |
| cell growth and/or maintenance-5 | NALP1 | NACHT, leucine rich repeat and PYD containing 1 | NM_033004 |
| cell growth and/or maintenance-6 | PAK3 | p21 (CDKN1A)-activated kinase 3 | NM_002578 |
| cell growth and/or maintenance-7 | PODXL | podocalyxin-like | NM_001018 111 |
| cell growth and/or maintenance-8 | CCL26 | chemokine (C-C motif) ligand 26 | NM_006072 |
| cell growth and/or maintenance-9 | FBLN1 | fibulin 1 | NM_006486 |
| cell growth and/or maintenance-10 | LAMA1 | laminin, alpha 1 | NM_005559 |
| cell growth and/or maintenance-11 | NTNG1 | netrin G1 | NM_014917 |

[Table 8c]

| Classification 4 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| cytokine -1 | GDF15 | growth differentiation factor | NM_004864 |
| cytokine-2 | IL6 | interleukin 6 (interferon, beta 2) | NM_000600 |
| cytokine -3 | CTGF | connective tissue growth factor | NM_001901 |
| cytokine -4 | VEGF | vascular endothelial growth factor | NM_001025 366 |
| cytokine -5 | VEGFC | vascular endothelial growth factor C | NM_005429 |
| cytokine -6 | HGF | hepatocyte growth factor (hepapoietin A; scatter | NM_000601 |
| Classification 5 | Gene symbol | Gene title | Genbank number |
| cytoskeleton-1 | KRT19 | keratin 19 | NM_002276 |
| cytoskeleton-2 | KRTAP1-5 | keratin associated protein 1- | NM_031957 |
| cytoskeleton-3 | KRTAP2-1 | keratin associated protein 2- | BC012486 |

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(continued)

| Classification 5 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| cytoskeleton-4 | KRTHA4 | keratin, hair, acidic, 4 | NM_021013 |
| cytoskeleton-5 | CKAP2 | cytoskeleton associated protein 2 | NM_018204 |
| cytoskeleton-6 | KRTAP1-1 | keratin associated protein 1- | NM_030967 |
| cytoskeleton-7 | KRT18 | keratin 18 | NM_000224 |
| cytoskeleton-8 | KAP2.1B | keratin associated protein 2.1B | AJ406929 |
| cytoskeleton-9 | SSH1 | slingshot homolog 1 (Drosophila) | NM_018984 |
| | | | |
| Classification 6 | Gene symbol | Gene title | Genbank number |
| enzyme-1 | LXN | latexin | NM_020169 |
| enzyme-2 | IFI30 | interferon, gamma-inducible protein 30 | NM_006332 |
| enzyme-3 | CPA4 | carboxypeptidase A4 | NM_016352 |

[Table 8d]

| Classification 7 | Gene symbol | Gene title | Genbank number |
|-----------------------------|-------------|--|----------------|
| extracellular matrix-1 | CHI3L1 | chitinase 3-like 1 (cartilage glycoprotein-39) | NM_001276 |
| extracellular matrix-2 | KRT23 | keratin 23 (histone deacetylase inducible) | NM_015515 |
| extracellular matrix-3 | FLG | filaggrin | NM_002016 |
| extracellular matrix-4 | ADAMTS1 | a disintegrin-like and metalloprotease (reprolysin type) With thrombospondin type 1 motif, 1 | NM_006988 |
| extracellular matrix-5 | FRMD5 | FERM domain containing 5 | NM_001031 |
| Classification 8 | Gene symbol | Gene title | Genbank number |
| growth factor or receptor-1 | IGFBP1 | insulin-like growth factor binding protein 1 | NM_000596 |
| growth factor or receptor-2 | CFI | complement factor I | NM_000204 |
| growth factor or receptor-3 | ESM1 | endothelial cell-specific molecule 1 | NM_007036 |
| growth factor or receptor-4 | F2RL1 | coagulation factor II (thrombin) receptor-like 1 | NM_005242 |
| growth factor or receptor-5 | MET | met proto-oncogene (hepatocyte growth factor receptor) | NM_000245 |
| growth factor or receptor-6 | HTR7 | 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) | NM_000872 |
| growth factor or receptor-7 | IGFBP3 | insulin-like growth factor binding protein 3 | NM_001013 398 |

[Table 8e]

| Classification 9 | Gene symbol | Gene title | Genbank number |
|------------------|-------------|--|----------------|
| membrane -1 | ABHD2 | abhydrolase domain containing 2 | NM_007011 |
| membrane -2 | ITGA2 | integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) | NM_002203 |
| membrane -3 | LAMA3 | laminin, alpha 3 | NM_198129 |
| membrane-4 | NETO2 | neuropilin (NRP) and tolloid (TLL)-like 2 | NM_018092 |

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(continued)

| Classification 9 | Gene symbol | Gene title | Genbank number |
|----------------------------|-------------|---|----------------|
| membrane -5 | NTN4 | netrin 4 | NM_021229 |
| membrane -6 | PTGER1 | prostaglandin E receptor 1 (subtype EP1), 42kDa | NM_000955 |
| membrane -7 | EPHB2 | EPH receptor B2 | NM_017449 |
| membrane -8 | SFRP1 | secreted frizzled-related protein 1 | NM_003012 |
| membrane -9 | CD33L3 | CD33 antigen-like 3 | NM_213602 |
| membrane -10 | GLIPR1 | GLI pathogenesis-related 1 (glioma) | NM_006851 |
| membrane -11 | UGCG | UDP-glucose ceramide glucosyltransferase | NM_003358 |
| membrane -12 | ADORA1 | adenosine A1 receptor | NM_000674 |
| | | | |
| Classification 10 | Gene symbol | Gene title | Genbank number |
| membrane binding protein-1 | ANYA10 | annexin A10 | NM_007193 |
| membrane binding protein-2 | RARRES1 | retinoic acid receptor responder (tazarotene induced) 1 | NM_206963 |
| membrane binding protein-3 | HNT | neurotrimin | NM_016522 |
| membrane binding protein-4 | CNTNAP3 | contactin associated protein-like 3 | NM_033655 |

[Table 8f]

| Classification 11 | Gene symbol | Gene title | Genbank number |
|---------------------|------------------------------|--|----------------|
| protein binding -1 | SYT1 | synaptotagmin I | NM_005639 |
| protein binding -2 | MLF1 | myeloid leukemia factor 1 | NM_022443 |
| protein binding -3 | CDCP1 | CUB domain-containing protein 1 | NM_022842 |
| protein binding -4 | KIAA0746 | KIAA0746 protein | NM_015187 |
| protein binding -5 | PSCDBP | pleckstrin homology, Sec7 and coiled-coil domains, binding protein | NM_004288 |
| protein binding -6 | SKI | v-ski sarcoma viral oncogene homolog (avian) | NM_003036 |
| protein binding -7 | SNX25 | sorting nexin 25 | NM_031953 |
| protein binding -8 | CDH6 cadherin (fetal kidney) | cadherin 6, type 2, K- | NM_004932 |
| protein binding -9 | DCBLD2 | discoidin, CUB and LCCL domain containing 2 | NM_080927 |
| protein binding -10 | ENG | endoglin (Osler-Rendu-Weber syndrome 1) | NM_000118 |

[Table 8g]

| Classification 12 | Gene symbol | Gene title | Genbank number |
|------------------------|-------------|---|----------------|
| protein modification-1 | SH3RF1 | SH3 domain containing ring finger 1 | NM_020870 |
| protein modification-2 | SMURF2 | SMAD specific E3 ubiquitin protein ligase 2 | NM_022739 |
| protein modification-3 | TFPI2 | tissue factor pathway inhibitor 2 | NM_006528 |

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(continued)

| Classification 12 | Gene symbol | Gene title | Genbank number |
|------------------------|-------------|---|----------------|
| protein modification-4 | ITGB3 | integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) | NM_000212 |
| protein modification-5 | MYPN | myopalladin | NM_032578 |
| protein modification-6 | LRP2BP | LRP2 binding protein | NM_018409 |
| protein modification-7 | HECW2 | HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2 | NM_020760 |
| protein modification-8 | PKIA | protein kinase (cAMP-dependent, catalytic) inhibitor alpha | NM_006823 |
| Classification 13 | Gene symbol | Gene title | Genbank number |
| signal molecule-1 | LYPD1 | LY6/PLAUR domain containing 1 | NM_144586 |
| signal molecule-2 | GATA6 | GATA binding protein 6 | NM_005257 |
| signal molecule-3 | RAB27B | RAB27B, member RAS oncogene family | NM_004163 |
| signal molecule-4 | SOX11 | SRY (sex determining region Y)-box 11 | NM_003108 |
| signal molecule-5 | ARHGAP2 2 | Rho GTPase activating protein 22 | NM_021226 |

[Table 8h]

| Classification 14 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| transcription-1 | ETV1 | ets variant gene 1 | NM_004956 |
| transcription-2 | ETV5 | ets variant gene 5 (ets-related molecule) | NM_004454 |
| transcription-3 | FOXP1 | forkhead box P1 | NM_032682 |
| transcription-4 | HMGA2 | high mobility group AT-hook 2 | NM_003483 |
| transcription-5 | KLF12 | Kruppel-like factor 12 | NM_007249 |
| transcription-6 | PRDM16 | PR domain containing 16 | NM_022114 |
| transcription-7 | SIM2 | single-minded homolog 2 (Drosophila) | NM_009586 |
| transcription-8 | SUHW2 | suppressor of hairy wing homolog 2 (Drosophila) | NM_080764 |
| transcription-9 | ENO1 | enolase 1 | NM_001428 |
| transcription-10 | MITF | microphthalmia-associated transcription factor transcription factor | NM_198159 |
| transcription-11 | TCF3 | transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) | NM_003200 |
| transcription-12 | SMYD3 | SET and MYND domain containing 3 | NM_022743 |

[Table 8i]

| Classification 15 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| transport-1 | ATP6V1G3 | ATPase, H ⁺ transporting, lysosomal 13kDa, V1 subunit G isoform 3 | NM_133262 |
| transport-2 | KCTD16 | potassium channel tetramerisation domain containing 16 | NM_020768 |
| transport-3 | NUPL1 | nucleoporin like 1 | NM_014089 |

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(continued)

| Classification 15 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| transport-4 | SLC14A1 | solute carrier family 14 (urea transporter), member 1 (Kidd blood group) | NM_015865 |
| transport-5 | SLC16A4 | solute carrier family 16 (monocarboxylic acid transporters), member 4 | NM_004696 |
| transport-6 | SLC4A4 | solute carrier family 4, sodium bicarbonate cotransporter, member 4 | NM_003759 |
| transport-7 | SLC9A7 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 7 | NM_032591 |
| transport-8 | TRPC4 | transient receptor potential cation channel, subfamily C, member 4 | NM_016179 |
| transport-9 | MCFD2 | multiple coagulation factor deficiency 2 | NM_139279 |
| transport-10 | SLC26A4 | solute carrier family 26, member 4 | NM_000441 |
| transport-11 | MCOLN3 | mucolipin 3 | NM_018298 |
| transport-12 | SLC25A37 | solute carrier family 25, member 37 | NM_016612 |
| transport-13 | SLC30A7 | solute carrier family 30 (zinc transporter), member 7 | NM_133496 |

[Table 8j]

| Classification 16 | Gene symbol | Gene title | Genbank number |
|-------------------|-------------|--|----------------|
| others -1 | FLJ38725 | hypothetical protein FLJ38725 | NM_153218 |
| others -2 | KIAA1913 | KIAA1913 | NM_052913 |
| others -3 | PHLDB2 | pleckstrin homology-like domain, family B, member 2 | NM_145753 |
| others -4 | PLCXD2 | phosphatidylinositol-specific phospholipase C, X domain containing 2 | NM_153268 |
| others -5 | SAMD3 | sterile alpha motif domain containing 3 | NM_001017.373 |
| others -6 | ZNF423 | zinc finger protein 423 | NM_015069 |
| others -7 | FLJ33996 | hypothetical protein FLJ33996 | NM_175894.2 |
| others -8 | PLEKHK1 | pleckstrin homology domain containing, family K member 1 | NM_145307 |
| others -9 | PTOV1 | prostate tumor overexpressed gene 1 | NM_017432 |
| others -10 | FAM40B | family with sequence similarity 40, member B | NM_020704 |
| others -11 | ABI3BP | ABI gene family, member 3 (NESH) binding protein | NM_015429 |
| others -12 | NHS | Nance-Horan syndrome (congenital cataracts and dental anomalies) | NM_198270 |
| others -13 | DTL | denticleless homolog (Drosophila) | NM_016448 |
| others -14 | C1GALT1 | core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta- | NM_020156 |
| others -15 | CPNE8 | copine VIII | NM_153634 |
| others -16 | TMEM49 | transmembrane protein 49 | NM_030938 |

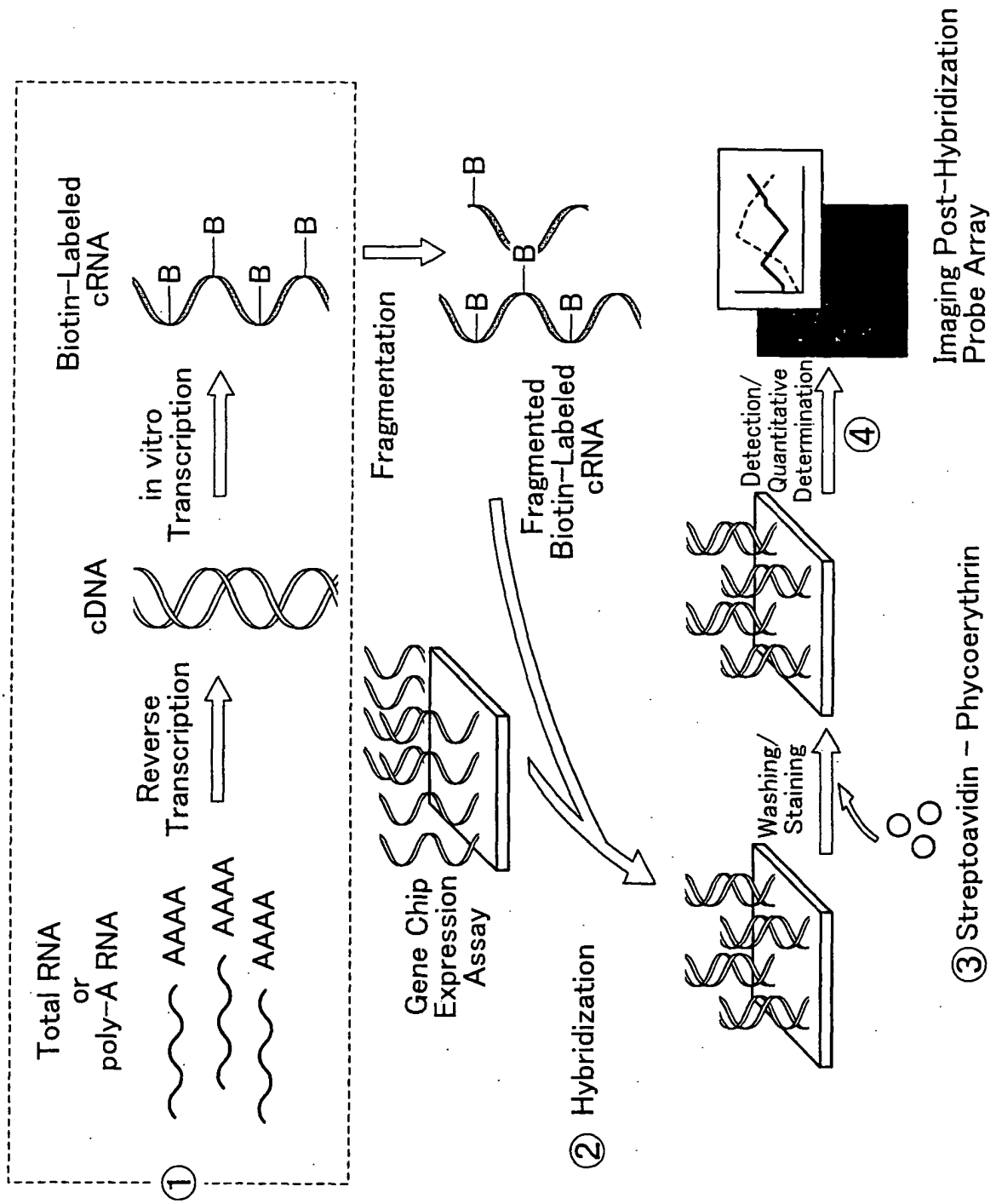
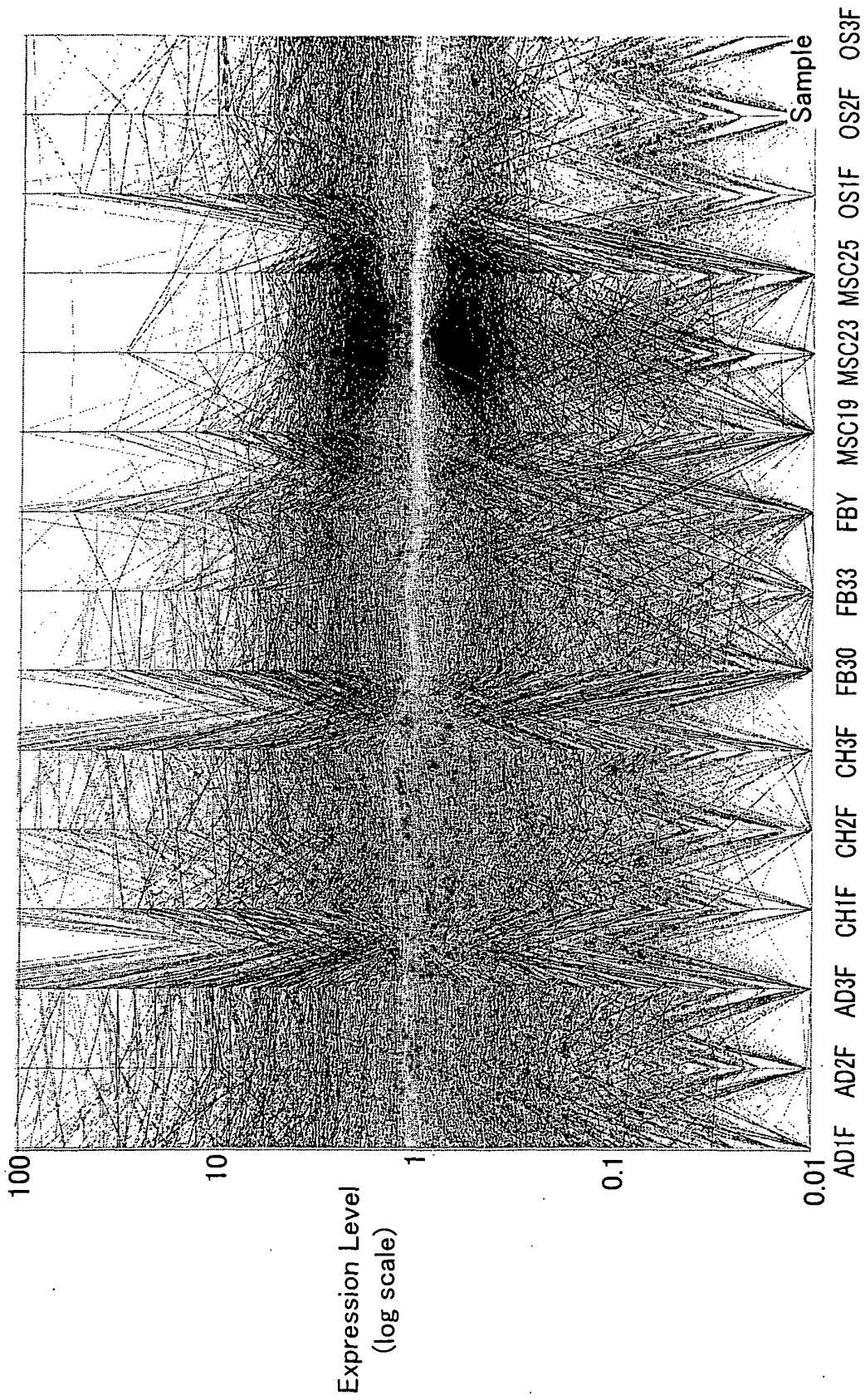


FIG. 2



INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP2006/306658

| | | |
|--|--|--|
| A. CLASSIFICATION OF SUBJECT MATTER C12N15/00(2006.01), C07K16/18(2006.01), C07K16/22(2006.01), C07K16/24(2006.01), C07K16/28(2006.01), C07K16/40(2006.01), C07K16/44(2006.01), C12M1/00(2006.01), C12N5/06(2006.01), C12N15/09(2006.01), 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) C12N15/00-15/90, C12N1/00-7/08, C07K16/00-16/48, C12M1/00, C12Q1/00-1/70, G01N33/53(2006.01), G01N37/00(2006.01), A61L27/00, C07K14/00-14/825, C12N9/00-9/99 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Jitsuyo Shinan Koho 1922-1996 Jitsuyo Shinan Toroku Koho 1996-2006 Kokai Jitsuyo Shinan Koho 1971-2006 Toroku Jitsuyo Shinan Koho 1994-2006 Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) BIOSIS/MEDLINE/WPIDS (STN), JMEDPlus (JDream2), JSTPlus (JDream2), GenBank/EMBL/DDBJ/GeneSeq | | |
| C. DOCUMENTS CONSIDERED TO BE RELEVANT | | |
| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
| X/Y | JP 2004-290189 A (Japan Science and Technology Agency, Yukio KATO, Two Cells Co., Ltd.), 21 October, 2004 (21.10.04), & WO 2004/081174 A2 | 1, 5-9, 12, 13/ 2-4, 10, 11, 15 |
| Y | CONNOR, J.R. et al., "Human cartilage glycoprotein 39 (HC gp-39) mRNA expression in adult and fetal, chondrocytes, osteoblasts and osteocytes by in-situ hybridization.", Osteoarthritis and Cartilage (2000), Vol.8, pages 87 to 95 | 2-4 |
| Y | Akira IGARASHI et al., "Saisei Iryo ni Okeru Ishokuyo Kanyokei Kansaibo no Kentei no Juyosei to Kentei Hoho no Kento", Saisei Iryo, 10 February, 2005 (10.02.05), Vol.4, special extra issue, page 115 | 10, 11, 15 |
| <input type="checkbox"/> Further documents are listed in the continuation of Box C. | | <input type="checkbox"/> See patent family annex. |
| * Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier application or patent but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed | | "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family |
| Date of the actual completion of the international search 13 June, 2006 (13.06.06) | | Date of mailing of the international search report 27 June, 2006 (27.06.06) |
| Name and mailing address of the ISA/ Japanese Patent Office | | Authorized officer |
| Facsimile No. | | Telephone No. |

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

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP2006/306658

Continuation of A. CLASSIFICATION OF SUBJECT MATTER
(International Patent Classification (IPC))

C12Q1/04(2006.01), *C12Q1/68*(2006.01), *G01N33/53*(2006.01), *G01N37/00*
(2006.01), *A61L27/00*(2006.01), *C07K14/47*(2006.01), *C07K14/475*
(2006.01), *C07K14/52*(2006.01), *C07K14/54*(2006.01), *C07K14/705*
(2006.01), *C07K14/81*(2006.01), *C12N9/10*(2006.01), *C12N9/12*(2006.01),
C12N9/50(2006.01)

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

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP2006/306658

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.: 14
because they relate to subject matter not required to be searched by this Authority, namely:
The invention of claim 14 relates to a method for the determination of the development or the risk of development of a disease associated with a mesenchymal stem cell in a subject by utilizing the inventions of claims 1 to 8, 12
(continued to extra sheet)
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:

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 an additional fee, this Authority did not invite payment of any additional fee.
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.:

- Remark on Protest**
- the The additional search fees were accompanied by the applicant's protest and, where applicable, 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.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP2006/306658

Continuation of Box No.II-1 of continuation of first sheet (2)

and 13 on a sample isolated from a living body (i.e., the subject; a supplier of the sample). However, reviewing the description, this invention appears to be directed to a human disease and relates to a method for determination of a disease in a supplier of an isolated sample, this invention is recognized to be a method for diagnosis of a human. Thus, the invention of claim 14 relates to a subject matter which this international searching authority is not required, under the provisions of PCT Article 17(2)(a)(i) and PCT Rule 39.1(v), to search.

REFERENCES CITED IN THE DESCRIPTION

This list of references cited by the applicant is for the reader's convenience only. It does not form part of the European patent document. Even though great care has been taken in compiling the references, errors or omissions cannot be excluded and the EPO disclaims all liability in this regard.

Patent documents cited in the description

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Non-patent literature cited in the description

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- Section 2 Eukaryotic Sample and Array Processing. GeneChip Expression Analysis Technial Manual [0098] [0099]

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|----------------|---|---------|------------|
| 专利名称(译) | 使用分子标记区分间充质干细胞的方法及其用途 | | |
| 公开(公告)号 | EP1870455A1 | 公开(公告)日 | 2007-12-26 |
| 申请号 | EP2006730606 | 申请日 | 2006-03-30 |
| [标]申请(专利权)人(译) | 智再如股份有限公司 | | |
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| IPC分类号 | C12N15/00 C07K16/18 C07K16/22 C07K16/24 C07K16/28 C07K16/40 C07K16/44 C12M1/00 C12N5/06 C12N15/09 C12Q1/04 C12Q1/68 G01N33/53 G01N37/00 A61L27/00 C07K14/47 C07K14/475 C07K14/52 C07K14/54 C07K14/705 C07K14/81 C12N5/077 C12N5/0775 C12Q1/6881 | | |
| CPC分类号 | C12Q1/6881 C12Q2600/158 G01N33/56966 G01N33/6845 | | |
| 优先权 | 2005104563 2005-03-31 JP | | |
| 其他公开文献 | EP1870455A4 | | |
| 外部链接 | Espacenet | | |

摘要(译)

本发明公开了一种区分间充质干细胞的方法，该方法包括使用选自具有表1中所示的登录号所示的核苷酸序列的基因的至少一种基因作为区分标记，检测区分标记之间的区别标记的差异。间充质干细胞和结缔组织细胞，以区分间充质干细胞和结缔组织细胞。该方法能够以良好的准确度区分未分化的间充质干细胞与其他结缔组织细胞如成纤维细胞，成骨细胞，软骨细胞和脂肪细胞。通过该方法给出的间充质干细胞或包含间充质干的组合物可以用作再生医学中使用的治疗剂。