What is claimed:

1. Use of an effective amount of a population of stem cells in the manufacture of a composition for a method of ameliorating aging effect or correcting the proteomic and other defects associated with aging in a subject, the population of stem cells is to be administered to the subject, wherein:~~A method, wherein~~:

   (i) the population of stem cells ~~the method is a method for~~ maintains~~ing~~ or increase~~s~~~~ing~~ the ratio of the number of stem cells to the number of differentiated cells in a tissue of a subject over time, ~~comprising administering to the subject an effective amount of a population of stem cells,~~ wherein the ratio is maintained or increased over time as compared to the ratio of the number of stem cells to the number of differentiated cells in a tissue of a control subject over time;

   (ii) the population of stem cells ~~the method is a method of~~ maintains~~ing~~ or increase~~s~~~~ing~~ the number of stem cells in a tissue of a subject over time, ~~comprising administering to the subject an effective amount of a population of stem cells~~, wherein the number of stem cells in the tissue of the subject is maintained or increased over time as compared to the number of stem cells in the same tissue of a control subject;

   (iii) the population of stem cells ~~the method is a method of~~ alters~~ing~~ the phenotype of an aging stem cell resident in a tissue of a subject, ~~comprising administering to the subject an effective amount of a population of stem cells,~~ wherein the amount of the population of stem cells is effective to alter the environmental niche of the aging stem cell such that the phenotype of the aging stem cell is altered as compared to the phenotype of the aging stem cell resident in the tissue of a control subject;

   (iv) the population of stem cells ~~the method is a method of~~ alters~~ing~~ the proteome of an aging cell in a tissue of a subject, ~~comprising administering to the subject an effective amount of a population of stem cells,~~ wherein the amount of the population of stem cells is effective to alter the proteome of the aging cell, wherein the altered proteome comprises one or more biomarkers found in a younger cell in the tissue of a control subject; or

(v) the population of stem cells ~~the method is a method of~~ alters~~ing~~ the transcriptome of an aging cell in a tissue of a subject, ~~comprising administering to the subject an effective amount of a population of stem cells,~~ wherein the amount of the population of stem cells is effective to alter the transcriptome of the aging cell, wherein the altered transcriptome comprises one or more transcripts found in a younger cell in the tissue of a control subject.

2. An in vitro method of:

(i) maintaining or increasing the number of endogenous stem cell in a tissue obtained from a subject over time, comprising administering to the tissue an effective amount of a population of stem cells, wherein the number of endogenous stem cells in the tissue is maintained or increased over time as compared to the number of endogenous stem cells in the same tissue of a control subject over time; or

(ii) altering the gene expression profile of an aging cell in a tissue of a subject, comprising administering to the tissue obtained from a subject an effective amount of a population of stem cells, wherein the amount is effective to alter gene expression profile comprises one or more genes found in a younger cell in the tissue of a control subject, wherein the gene is as provided in any one of Table 5 to 9.

~~2.~~ 3. The ~~method~~use of claim 1 or the method of claim 2, wherein:

(i) the tissue is selected from the group consisting of muscle, brain, heart, kidney, liver, bone marrow, and skin; or

(ii) the aging cell is a somatic cell;

wherein optionally the aging cell is selected from the group consisting of a muscle cell, a brain cell, a heart cell, a liver cell, a kidney cell, a bone marrow cell, and a skin cell; and

wherein optionally the muscle cell is a skeletal muscle cell or a striate muscle cell.

~~3.~~ 4. The ~~method~~use of any one of claims 1 or 3, or the method of any one of claims 2 to 3 ~~to 2~~, wherein the control subject is the same subject before administration of the population of stem cells or a subject that has not received the population of stem cells.

~~4.~~ 5. The ~~method~~use of any one of claims 1 or 3, or the method of claim of any one of claims ~~1~~2 to 3, wherein:

(i) the population of stem cells is to be administered systemically, locally to the tissue, parenterally, intravenously, intramuscularly, subcutaneously, subdermally, intracompartmentally, by continuous drip, or as a bolus;

(ii) the population of stem cells is prepared to be administered in an injectable liquid suspension or other biocompatible medium;

(iii) the population of stem cells is to be administered using a catheter, a controlled-release system, or an implantable substrate or matrix;

(iv) the population of stem cells is to be administered at a dose of between $1x10^5$ cells and $1x10^9$ cells, between $1x10^5$ cells and $1x10^7$ cells, or between $1x10^6$ cells and $1x10^7$ cells;

(v) the population of stem cells is to be administered as a single dose or multiple doses;

(vi) the population of stem cells is the first administration to the subject;

(vii) the population of stem cells is to be administered when the subject is 10-15 years of age, 15-20 years of age, 20-25 years of age, 25-30 years of age, 30-35 years of age, 35-40 years of age, 40-45 years of age, 45-50 years of age, 50-55 years of age, 55-60 years of age, 60-65 years of age, 65-70 years of age, 70-75 years of age, 75-80 years of age, 80-85 years of age, 85-90 years of age, 90-95 years of age, 95-100 years of age, or over 100 years of age; or

(viii) the population of stem cells is to be serially administered over the lifetime of the subject.

~~5.~~ 6. The ~~method~~use of any one of claims 1, or 3-5, or the method of any one of claims 2-5 ~~1 to 4~~, wherein the population of stem cells:

(i) comprises a population of stem cells selected from the group consisting of: embryonic stem cells, adult stem cells, and induced pluripotent stem cells;

(ii) consists essentially of a population of stem cells selected from the group consisting of: embryonic stem cells, adult stem cells, and induced pluripotent stem cells; or

(iii) consists of a population of stem cells selected from the group consisting of: embryonic stem cells, adult stem cells, and induced pluripotent stem cells.

~~6.~~ 7. The ~~method~~use of any one of claims 1, or 3-6 or the method of any claims of 2-6 ~~1 to 5~~, wherein the population of stem cells:

(i) comprises a population of stem cells selected from the group consisting of: bone marrow mesenchymal stem cells, amniotic membrane-derived mesenchymal stem cells, adipose tissue-derived mesenchymal stem cells, stem cells from human exfoliated deciduous teeth, skeletal muscle-derived stem cells, blood stem cells, skin stem cells, cord blood stem cells, limbal stem cells, hematopoietic stem cells, neural stem cells, heart-derived stem cells, intestinal stem cells, endothelial stem cells, epithelial stem cells, olfactory adult stem cells, neural crest stem cells, testicular stem cells, placental derived stem cells, and amniotic fluid-derived stem cells;

(ii) consists essentially of a population of stem cells selected from the group consisting of: bone marrow mesenchymal stem cells, amniotic membrane-derived mesenchymal stem cells, adipose tissue-derived mesenchymal stem cells, stem cells from human exfoliated deciduous teeth, skeletal muscle-derived stem cells, blood stem cells, skin stem cells, cord blood stem cells, limbal stem cells, hematopoietic stem cells, neural stem cells, heart-derived stem cells, intestinal stem cells, endothelial stem cells, epithelial stem cells, olfactory adult stem cells, neural crest stem cells, testicular stem cells, placental derived stem cells, and amniotic fluid-derived stem cells; or

(iii) consists of a population of stem cells selected from the group consisting of: bone marrow mesenchymal stem cells, amniotic membrane-derived mesenchymal stem cells, adipose tissue-derived mesenchymal stem cells, stem

cells from human exfoliated deciduous teeth, skeletal muscle-derived stem cells, blood stem cells, skin stem cells, cord blood stem cells, limbal stem cells, hematopoietic stem cells, neural stem cells, heart-derived stem cells, intestinal stem cells, endothelial stem cells, epithelial stem cells, olfactory adult stem cells, neural crest stem cells, testicular stem cells, placental derived stem cells, and amniotic fluid-derived stem cells;

wherein optionally the population of stem cells does not comprise one or more stem cells selected from the group consisting of: bone marrow mesenchymal stem cells, amniotic membrane-derived mesenchymal stem cells, adipose tissue-derived mesenchymal stem cells, stem cells from human exfoliated deciduous teeth, skeletal muscle-derived stem cells, blood stem cells, skin stem cells, cord blood stem cells, limbal stem cells, hematopoietic stem cells, neural stem cells, heart-derived stem cells, intestinal stem cells, endothelial stem cells, epithelial stem cells, olfactory adult stem cells, neural crest stem cells, testicular stem cells, placental derived stem cells, and amniotic fluid-derived stem cells.

~~7.~~ 8. The ~~method~~use of any one of claims 1, or 3-7 or the method of any one of claims 2-7 ~~to 6~~, wherein the population of stem cells (i) comprises placental-derived stem cells (PDSC), (ii) consists essentially of PDSC, or (iii) consists of PDSC.

~~8.~~ 9. The ~~method~~use of any one of claims 1, or 3-8 or the method of any one of claims 2-8 ~~to 7~~, wherein:

(i) the population of stem cells has previously been cryopreserved;

(ii) the population of stem cells has been passaged at least three times;

(iii) the population of stem cells has been passaged no more than ten times;

(iv) the population of stem cells are cells from a placental stem cell bank;

(v) the stem cells are embryonic-like stem cells;

(vi) the stem cells are pluripotent or multipotent stem cells;

(vii) the population of stem cells comprises cells obtained from a placenta that has been drained of cord blood; or

(viii) the population of stem cells comprises cells obtained from a placenta that has been perfused to remove residual blood.

~~9.~~ 10. The ~~method~~use of any one of claims 1, or 3-9, or the method of any one of claims 2-9 ~~to 8~~, wherein:

(i) the population of stem cells is autologous to the subject;

(ii) the population of stem cells is allogeneic to the subject;

(iii) the population of stem cells is syngeneic to the subject;

wherein optionally the population of stem cells is a homogeneous cell population or a mixed cell population;

(iv) the population of stem cells is an enriched stem cells population;

(v) the population of stem cells comprises PSC-100 cells;

wherein optionally the population of stem cells is an enriched population of PSC-100 cells; or

(vi) the population of stem cells is obtained from multiple donors;

wherein optionally the population of stem cells is obtained from multiple donors without use of HLA typing.

~~10.~~ 11. The ~~method~~use of any one of claims 1, or 3-10, or the method of any claims of 2-10 ~~to 9~~, wherein:

(i) the population of stem cells comprises cells that are $CD34^-$, $CD10^+$, $SH2^+$, and $CD90^+$ placental multipotent cells;

(ii) the population of stem cells comprises cells that are $CD34^-$, $CD38^-$, $CD45^-$, $CD10^+$, $CD29^+$, $CD44^+$, $CD54^+$, $CD90^+$, $SH2^+$, $SH3^+$, $SH4^+$ and $OCT\text{-}4^+$;

(iii) the population of stem cells comprises cells that are $CD34^-$, $CD10^+$, $CD105^+$, and $CD200^+$;

(iv) the population of stem cells comprises cells that are $CD73^+$;

(v) the population of stem cells comprises cells that are $CD73^+$ and $CD105^+$;

(vi) the population of stem cells comprises cells that are $CD200^+$;

(vii) the population of stem cells comprises cells that are $CD34^-$, $CD38^-$, $CD45^-$, $OCT\text{-}4^+$, and $CD200^+$;

(viii) the population of stem cells comprises cells that are $CD34^-$, $CD38^-$, $CD45^-$, $CD73^+$, $OCT\text{-}4^+$, and $CD200^+$;

(ix) the population of stem cells comprises cells that are $OCT\text{-}4^+$;

(x) the population of stem cells comprises cells that are $CD73^+$, $CD105^+$, and $OCT\text{-}4^+$;

(xi) the population of stem cells comprises cells that are $CD73^+$, $CD105^+$, and $CD200^+$;

(xii) the population of stem cells comprises cells that are $CD200^+$ and $OCT\text{-}4^+$;

(xiii) the population of stem cells comprises cells that are $CD73^+$, $CD105^+$, and $HLA\text{-}G^+$;

(xiv) the population of stem cells comprises cells that are $CD73^+$, $CD105^+$, $CD200^+$, and $HLA\text{-}G^+$;

(xv) the population of stem cells comprises cells that are $CD34^-$, $CD38^-$, $CD45^-$, and $HLA\text{-}G^+$; or

(xvi) the population of stem cells comprises cells that are $CD34^-$; $CD38^-$; $CD45^-$; $CD34^-$ and $CD38^-$; $CD34^-$ and $CD45^-$; $CD38^-$ and $CD45^-$; or $CD34^-$, $CD38^-$ and $CD45^-$.

~~11.~~ 12. The ~~method~~use of any one of claims 1, or 3 to11, or the method of any one of claims 2-11 ~~to 10~~, wherein ~~the method further comprises~~

(i) ~~determining~~ the number of stem cells and/or differentiated cells in the tissue is determined before administration of the population of stem cells to the subject, and

(ii) ~~determining~~ the number of stem cells and/or differentiated cells in the tissue is to be determined after administration of the population of stem cells to the subject;

wherein optionally

(A) ~~the method~~ the population of stem cells increases the number of stem cells in the tissue after administration as compared to before administration of the population of stem cells; or

(B) the subject has an increased number of stem cells as compared to a subject that has not received an administration of population of stem cells;

and wherein optionally

(1) the increase in the number of stem cells persists over time;

(2) the increase in the number of stem cells is the result of an expansion of stem cells resident in the tissue or the result of an expansion of the stem cells in the tissue; or

(3) the increase in the number of stem cells results in the remodeling, renewal, renovation, rejuvenation, repair and/or restoration of the tissue of the subject;

and wherein the number of stem cells is assessed by stem cell colony forming units.

~~12.~~ 13. The ~~method~~use of any one of claims 1, or 3-12, ~~to 11~~ or the method of any one of claims 2 to 12, wherein the ~~method further comprises contacting~~ the population of stem cells is to be contacted with

(i) young stem cells, young progenitor cells, or young precursor cells; or

(ii) one or more additional factors isolated from young stem cells, young progenitor cells, or young precursor cells;

wherein optionally the one or more additional factors are selected from the group consisting of cytokines, hormones, promoters, repressors, proteins,

nucleic acids, viruses, immunogens, angiogenic factors, growth factors, anti-apoptotic factors, and anti-oxidative factors.

~~13.~~ 14. The ~~method~~use of any one of claims 1, or 3-13, or the method of any one of claims 2-13 ~~to 12~~, wherein the method further comprises culturing and/or expanding the population of stem cells prior to administration to the subject, wherein

(i) the culturing and/or expanding is *in vitro* or *in situ*;

(ii) the population of stem cells is cultured and/or expanded in an extracorporeal device; or

(iii) the population of stem cells is cultured and/or expanded in the presence of

(A) young stem cells, young progenitor cells, or young precursor cells; or

(B) additional factors isolated from young stem cells, young progenitor cells, or young precursor cells;

wherein optionally the one or more additional factors are selected from the group consisting of cytokines, hormones, promoters, repressors, proteins, nucleic acids, viruses, immunogens, angiogenic factors, growth factors, anti-apoptotic factors, and anti-oxidative factors.

~~14.~~ 15. The ~~method~~use of any one of claims 1, or 3-14, or the method of any one of claims 3-14 ~~to 13~~, wherein ~~the method further comprises~~

(i) ~~characterizing~~ the genome of the stem cells is characterized~~, wherein the genomic characterization is conducted~~

(A) prior to administration of the population of stem cells ~~to the subject~~;

(B) after administration of the population of stem cells ~~to the subject~~; or

(C) prior to administration of the population of stem cells ~~to the subject~~, and after administration of the population of stem cells ~~to the subject~~;

(ii) ~~characterizing~~ the proteome of the stem cells is characterized~~, wherein the proteome characterization is conducted~~

(A) prior to administration of the population of stem cells ~~to the subject~~;

(B) after administration of the population of stem cells ~~to the subject~~; or

(C) prior to administration of the population of stem cells ~~to the subject~~, and after administration of the population of stem cells ~~to the subject~~;

(iii) ~~characterizing~~ the genome of the stem cells and/or differentiated cells in the tissue is characterized~~, wherein the genomic characterization is conducted~~

(A) prior to administration of the population of stem cells ~~to the subject~~;

(B) after administration of the population of stem cells ~~to the subject~~; or

(C) prior to administration of the population of stem cells ~~to the subject~~, and after administration of the population of stem cells ~~to the subject~~; or

(iv) ~~characterizing~~ the proteome of the stem cells and/or differentiated cells in the tissue is characterized~~, wherein the proteome characterization is conducted~~

(A) prior to administration of the population of stem cells ~~to the subject~~;

(B) after administration of the population of stem cells ~~to the subject~~; or

(C) prior to administration of the population of stem cells ~~to the subject~~, and after administration of the population of stem cells ~~to the subject~~;

~~15.~~ 16. The ~~method~~use of any one of claims 1 or 3-15, or the method of any one of claims 3-15 ~~to 14~~, wherein the one or more biomarkers are proteins expressed in a skeletal muscle cell, a striated muscle cell, a brain cell, a heart cell, a kidney cell, a liver cell, a bone marrow cell, or a skin cell.

~~16.~~ 17. The ~~method~~ use of any one of claims 1 or 3-16, or the method of any one of claims 3-16 ~~to 15~~, wherein the one or more biomarkers are selected from the group consisting of

(i) myosin light chain 3 (MLCF3), myosin light polypeptide 2 (slow), myosin light chain 1 (MLC1F), myosin binding protein C (MYBPC1), myosin binding protein H, alpha actin (fragment), actin (skeletal muscle), actin alpha (cardiac),

troponin T class Ia alpha-1, troponin T class IIa beta-1, troponin T beta/alpha, capZ beta, desmin, gelsolin (cytosolic), beta-tubulin, p23, triosephosphate isomerase 1, glycosylase I, glyoxalase I, enolase 3 (beta muscle), glycerol 3-P dehydrogenase, isocitrate dehydrogenase 3 (NAD+), cytochrome c oxidase (polypeptide Va), creatine kinase (muscle form), Cu/Zn superoxide dismutase, ferritin heavy chain (H-ferritin), aldehyde dehydrogenase (mitochondrial), glutathione transferase (omega 1), heat shock 20 kDa protein (Hsp20), heat shock 27 kDa protein (Hsp27), disulfide isomerase ER60 (ERp57), 14-3-3 protein, guanine deaminase (guanase), Rho-GDI (alpha), phosphohistidine phosphatase, mRNA capping enzyme, similar to apobec2 protein, galectin 1, albumin, vitamin D binding protein prepeptide, protein kinase C interacting protein-1, RIKEN cDNA 1700012G19, myosin heavy chain 2 (MYH2), troponin T type 1 (TNNT1), ryanodine receptor 1 (skeletal) (RYR1), calsequestrin 1 (fast-twitch, skeletal muscle) (CASQ1), junctophilin 1 (JPH1), adenosine monosphosphate deaminase (AMPD1), phosphorylase glycogen muscle (PYGM), and enolase 3 (beta, muscle) (ENO3);

(ii) MLCF3, myosin light polypeptide 2 (slow), MLC1F, myosin binding protein C, myosin binding protein H, alpha actin (fragment), actin (skeletal muscle), actin alpha (cardiac), troponin T class IIa beta-1, troponin T beta/alpha, capZ beta, triosephosphate isomerase 1, glycosylase I, glyoxalase I, enolase 3 (beta muscle), glycerol 3-P dehydrogenase, isocitrate dehydrogenase 3 (NAD+), cytochrome c oxidase (polypeptide Va), creatine kinase (muscle form), Cu/Zn superoxide dismutase, phosphohistidine phosphatase, protein kinase C interacting protein-1, and RIKEN cDNA 1700012G19, wherein a decrease in expression in the one or more biomarkers is indicative of aging;

(iii) troponin T class Ia alpha-1, troponin T class IIa beta-1, desmin, gelsolin (cytosolic), beta-tubulin, p23, ferritin heavy chain (H-ferritin), aldehyde dehydrogenase (mitochondrial), glutathione transferase (omega 1), Hsp20, Hsp20, disulfide isomerase ER60 (ERp57), 14-3-3 protein, guanine deaminase (guanase), Rho-GDI (alpha), mRNA capping enzyme, similar to apobec2 protein, galectin 1, albumin, vitamin D binding protein prepeptide, wherein an increase in expression in the one or more biomarkers is indicative of aging;

(iv) myristoylated alanine-rich C-kinase substrate, alpha-internexin, isoform B of methyl-CpG-binding protein 2, histone H1.4, isoform 1 of serum albumin,

guanine nucleotide-binding protein (G(1)/G(S)/G(T) subunit beta-1, adenylate kinase 1, fructose-biphosphate aldolase A, tenascin-R, isoform 2 of clusterin, synaptic transmission, cation transport, isoform 1 of myeline proteolipid protein, neuromodulin, dihydropyrimidinase-related protein 2, dihydropteridine reductase, matrin-3, alpha-enolase, isoform 1 of gelsolin, APP isoform of APP714 of amyloid beta A4 protein (fragment), annexin A6, isoform tau-E of microtubule-associated protein tau, MAP1A 331 kDa protein, neuroblast differentiation-associated protein AH NAK, cell cycle exit and neuronal differentiation protein 1, glyceraldehyde-3-phosphate dehydrogenase, HIST1H1D, isoform KGA of glutaminase kidney isoform, superoxide dismutase (Mn) (SOD2), isoform 1 of myelin basic protein (MBP), and vimentin (VIM);

(v) amyloid beta (A4) precursor protein (APP), myristoylated alanine-rich protein kinase C substrate (MARCKS), internexin neuronal intermediate filament protein alpha (INA), methyl CpG binding protein (MECP), histone cluster 1 H1e (HIST1H1E), albumin (ALB), guanine nucleotide binding protein (G protein) beta polypeptide (GNB1), adenylate kinase 1 (AK1), aldose A fructose-biphosphate (ALDOA), tenascin R (TNR), clusterin (CLU), synapsin 1 (SYN1), ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac musle (ATP5A1), proteolipid protein 1 (PLP1), growth associated protein 43 (GAP43), dihydropyrimidinase-like 2 (DPYSL2), quinoid dihydropteridine reductase (QDPR), matrin 3 (MATR3), enolase 1 (alpha) (ENO1), gelsolin (GSN), annexin A6 (ANXA6), microtubule associated protein tau (MAPT), microtuble-associated protein 1A (MAP1A), AHNAK nucleoprotein, cell cycle exit and neuronal differentiation 1 (CEND1), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), histone cluster 1, H1d (HIST1H1D), glutaminase (GLS), superoxide dismutase (SOD2), MBP, VIM, ELAV-like protein 3 (ELAVL3), neurogranin (NRGN), receptor expression enhancing protein 2 (REEP2), glutamate decarboxylase 1 (GAD1), protocadherin alpha-1 (PCDHA1), glial fibrillary acidic protein (GFAP), S100 calcium binding protein (S100B), family with sequence similarity 19 (chemokine (C-C- motif)-like), member A1 (FAM19A1), aquaporin 4 (AQP4), c-type lectin domain family 2, member L (CLEC2L),

neurofilament triplet L protein (NF-L), peroxiredoxin (EC 1.11.1.), aconitate hydratase (EC 4.2.1.3), enolase 2 (EC 4.2.1.11), and T-complex protein 1;

(vi) amyloid beta (A4) precursor protein (APP), marcks, internexin neuronal intermediate filament protein alpha (INA), methyl CpG binding protein (MECP), histone cluster 1 H1e (HIST1H1E), albumin (ALB), guanine nucleotide binding protein (G protein) beta polypeptide (GNB1), adenylate kinase 1 (AK1), aldose A fructose-biphosphate (ALDOA), tenascin R (TNR) and clusterin (CLU);

(vii) proteolipid protein 1 (PLP1), growth associated protein 43 (GAP43), dihydropyrimidinase-like 2 (DPYSL2), quinoid dihydropteridine reductase (QDPR), matrin 3 (MATR3), enolase 1 (alpha) (ENO1), and gelsolin (GSN);

(viii) microtubule associated protein tau (MAPT), microtuble-associated protein 1A (MAP1A), AHNAK nucleoprotein, cell cycle exit and neuronal differentiation 1 (CEND1) and glyceraldehyde-3-phosphate dehydrogenase (GAPDH);

(ix) neurofilament triplet L protein (NF-L), peroxiredoxin (EC 1.11.1.), aconitate hydratase (EC 4.2.1.3), enolase 2 (EC 4.2.1.11), and T-complex protein 1;

(x) myosin, heavy chain 6, cardiac muscle, alpha (MYH6), actin, alpha, cardiac muscle 1 (ACTC1), troponin I type 3 (cardiac) (TNNI3), natriuretic peptide A (NPPA), A kinase (PRKA) anchor protein 6 (AKAP6), nestin (NES), ATPase, Na+,K+ transporting, alpha 3 polypeptide (ATP1A3), cadherin 2, type 1, N-cadherin (neuronal) (CDH2), plakophilin 2 (PKP2), ATP synthase subunit d (Atp5h), ATP synthase subunit o (Atp5o), ATP synthase subunit delta (Atp5d), ATP synthase subunit alpha (Atp5a1), ATP synthase subunit beta (Atp5b), cytochrome c (Cycs), mito, pyruvate dehydgrenase E1 component subunit beta (Pdhb), phosphoglycerate kinase 1 (Pgk1), heat shock protein 70 (Hspa9), 60 kDa heat shock protein (Hspd1), desmin (Desm), troponin T2 (Tnnt2), tropomyosin alpha 1 (Tpm1), voltage dependent anion channel-1 (Vdac1), and elongation factor 2 (Eef2);

(xi) ATP synthase subunit d (Atp5h), ATP synthase subunit o (Atp5o), ATP synthase subunit delta (Atp5d), ATP synthase subunit alpha (Atp5a1), ATP synthase subunit beta (Atp5b), cytochrome c (Cycs), mito, pyruvate dehydgrenase E1 component subunit beta (Pdhb), phosphoglycerate kinase 1 (Pgk1), heat shock protein 70 (Hspa9), 60 kDa heat shock protein (Hspd1),

desmin (Desm), troponin T2 (Tnnt2), tropomyosin alpha 1 (Tpm1), voltage dependent anion channel-1 (Vdac1), and elongation factor 2 (Eef2); wherein optionally the biomarker is elongation factor 2 (Eef2) and an increase in the expression of Eef2 is indicative of aging;

(xii) ATP synthase subunit alpha (Atp5a1), ATP synthase subunit beta (Atp5b), cytochrome c (Cycs), mito, pyruvate dehydgrenase E1 component subunit beta (Pdhb), phosphoglycerate kinase 1 (Pgk1), heat shock protein 70 (Hspa9), desmin (Desm), troponin T2 (Tnnt2), tropomyosin alpha 1 (Tpm1), voltage dependent anion channel-1 (Vdac1), wherein a decrease in the expression of the one or more biomarkers is indicative of aging;

(xiii) podocin (NPHS2), nephrin (NPHS1), kin of IRRE like (NEPH1 or KIRREL), podocalyxin-like (PODXL), fibroblast growth factor 1 (FGF1), crumbs family member 2 (CRB2), solute carrier family 22 (organic anion transporter), member 8 (SLC22A8), solute carrier family 22 (organic anion transporter), member 13 (SLC22A13), aminocarboxymuconate semialdehyde decarboxylase (ACMSD), agmatine ureohydrolase (agmatinase) (AGMAT), betaine-homocysteine S-methyltransferase (BHMT), chromosome 11 open reading frame 54 (C11orf54), cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), dihycropyrimidinase (DPYS), gamma-glutamyltransferase 1 (GGT1), 4-hydroxyphenylpyruvate dioxygenase (HPD), heat-responsive protein 12 (HRSP12), low density lipoprotein receptor-related protein 2 (LRP2), pyruvate kinase, liver and RBC (PKLR), X-prolyl aminopeptidase (aminopeptidase P)2, membrane-bound (XPNPEP2), uromodulin (UMOD), calbindin (CALB1), solute carrier family 12 (sodium/potassium/chloride transporter), member 1 (SLC12A1), solute carrier family 12 (sodium/chloride transporter), member 3 (SLC12A3), calcium-sensing receptor (CASR), aquaporin (AQP2),ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2 (ATP6V0D2), parvalbumin (PVALB), transmembrane protein 213 (TMEM213), transferrin, isocitrate dehydrogenase 1 (IDH), 3-hydroxyisobutyrate dehydrogenase, afenopin, heat shock protein (HSP) 9A, ATP synthase, ornithine aminotransferase, glutamate dehydrogenase, phosphoglycerate mutase, catalase, and glutathione (GSH);

(xiv) transferrin, isocitrate dehydrogenase 1 (IDH), and 3-hydroxyisobutyrate dehydrogenase, wherein an increase in the expression of the one or more biomarkers is indicative of an aging;

(xv) afenopin, phosphoglycerate mutase, and glutathione (GSH), wherein a decrease in the expression of the one or more biomarkers is indicative of aging;

(xvi) apolipoprotein B (APOB), apolipoprotein A-I (APOA1), fibrinogen gamma chain (FGG), complement component 2 (C2), kininogen 1 (KNG1), fibrinogen alpha chain (FGA), hydroxyacid oxidase (glycolate oxidase) 1 (HAO1), retinol dehydrogenase 16 (all-trans) (RDH16), aldolase B, fructose-bisphosphate (ALDOB), bile acid CoA: amino acid N-acyltransferase (glycine N-choloyltransferase) (BAAT), aldo-keto reductase family 1, member C4 (AKR1C4), solute carrier family 27 (fatty acid transporter), member 5 (SLC27A5), epoxide hydrolase, 3-ketoacyl-CoA thiolase A, sarcosine oxidase, and 2,4-dienoyl reductase;

(xvii) epoxide hydroxylase, 3-ketoacyl-CoA thiolase A, sarcosine oxidase, and 2,4-dienoyl reductase, wherein an increase in expression of the one or more biomarkers is indicative of aging;

(xviii) defensin, alpha 1 (DEFA1), defensin, alpha 1B (DEFA1B), defensin, alpha 3 (DEFA3), defensin, alpha 4 (DEFA4), cathepsin G (CTSG), myeloperoxidase (MPO), hemoglobin, beta (HBB), hemoglobin, alpha 1 (HBA1), hemoglobin, alpha 2 (HBA2), S100 calcium binding protein 12 (S100A12), chromosome 19 open reading frame 59 (C19orf59), pyruvate dehydrogenase (lipoamide) beta, fatty acid-binding protein 5, galectin-3, c-synuclein, heterobiomarkerous nuclear ribonucleoprotein A1, myosin light chain, regulatory B (Mrlcb), transgelin, similar to purine-nucleoside phosphorylase (punA), heterobiomarkerous nuclear ribonucleoprotein A2/B1 isoform A2 (Hnrpa2b1), Huntingtin interacting protein K (HYPK), beta-actin FE-3 (Actg1), caldesmon 1 (Cald1, calponin-1 (Cnn1), E-FABP (C-FABP) (Fabp5), capping protein (actin filament), gelsolin-like (CAPG), similar to coactosin-like 1 (Cotl1), calponin-1 (calponin H1, smooth muscle; basic calponin) (Cnn1), vinculin (VCL), VIM, beta-tropomyosin (TPM2), transgelin 2 (Tagln2), tropomyosin 1, alpha isoform c (TPM1), calponin 3, acidic (CNN3), calponin 2 isoform a (Calponin 2), F-actin capping protein beta subunit (Capzb), alpha-globulin

(Hba1), alpha-actin (aa 40-375) (Acta2), smooth muscle protein SM22 homolog-bovine (fragments) (Tagln2), thioredoxin 2 (Txn1), peroxideroxin 2 (Prdx2), peroxiderodoxin 5 precursor (Prdx5), and Cu-Zn superoxide dismutase A5 (GSTA5);

(xix) fatty acid-binding protein 5, galectin-3, c-synuclein, heterobiomarkerous nuclear ribonucleoprotein A1, myosin light chain, regulatory B, peroxiredoxin 5 precursor, and transgelin;

(xx) beta-actin FE-3 (Actg1), caldesmon 1 (Cald1, calponin-1 (Cnn1), E-FABP (C-FABP) (Fabp5), galectin-3 (LGALS3), gamma synuclein (Sncg), heterobiomarkerous nuclear ribonucleoprotein A1 isoform a (HNRPA1), heterobiomarkerous nuclear ribonucleoprotein A2/B1 isoform A2 (Hnrpa2b1), Huntingtin interacting protein K (HYPK), myosin light chain, regulatory B (Mrlcb), peroxiredoxin 5 precursor (Prdx5), similar to purine-nucleoside phosphorylase (punA), pyruvate dehydrogenase (lipoamide) beta (PDHB), and transgelin (Tagln);

(xxi) transgelin (Tagln), capping protein (actin filament), gelsolin-like (CAPG), caldesmon 1 (Cald1), beta-actin FE-3 (Actg1), similar to coactosin-like 1 (Cotl1), calphonin-1 (calphonin H1, smooth muscle; basic calponin) (Cnn1), vinculin (VCL), VIM, beta-tropomyosin (TPM2), myosin light chain, regulatory B (Mrlcb), transgelin 2 (Tagln2), tropomyosin 1, alpha isoform c (TPM1), calponin 3, acidid (CNN3), calponin 2 isoform a (Calponin 2), F-actin capping protein beta subunit (Capzb), alpha-globulin (Hba1), alpha-actin (aa 40-375) (Acta2), smooth muscle protein SM22 homolog-bovine (fragments) (Tagln2), thioredoxin 2 (Txn1), peroxideroxin 2 (Prdx2), peroxiderodoxin 5 precursor (Prdx5), and Cu-Zn superoxide dismutase A5 (GSTA5);

(xxii) collagen, type XVII, alplha 1 (COL17A1), tumor protein p73 (TP73), keratin 10 (KRT10), caspase 14, apoptosis-related cysteine peptidase (CASP14), filaggrin (FLG), keratinocyte proline-rich protein (KPRP), corneodesmosin (CDSN), kallikrein-related peptidase 5 (KLK5), melan-A (MLANA), dopachrome tautomerase (DCT), tyrosinase (TYR), CD1a molecule (CD1A), CD207 molecule, langerin, (CD207), annexin A6 (ANXA6), glutaminyl-tRNA synthetase (QARS), cation-independent mannose-6-phosphate (IGF2R), twinfilin-2 (TWF2), 40S ribosomal protein S5 (RPS5), putative pre-mRNA-

splicing factor ATP-dependent RNA helicase DHX15 (DHX15), 26S proteasome non-ATPase regulatory subunit 1 (PSMD1), 40S ribosomal protein S29 (RPS29), synaptopodin-2 (SYNPO2), T-complex protein 1 subunit zeta (CCT6A), annexin 5 (ANXA5), tRNA-splicing ligase RtcB homolog (C22orf28), serine/arginine-rich splicing factor 9 (SRSF9), myosin light polypeptide 6 (MYL6), protein phosphatase 1 regulatory subunit 7 (PPP1R7), UPF0568 protein C14orf166 (C14orf166), 26 proteasome non-ATPase regulatory subunit 14 (PSMD14), serine hydroxymethyltransferase, mitochondrial (SHMT2), heat shock 70 kDa protein 1A/1B (HSPA1A), ATP-dependent RNA helicase DDX1 (DDX1), calmodulin (CALM1), AP-2 complex subunit alpha-2 (AP2A2), Rho guanine nucleotide exchange factor 2 (ARHGEF2), annexin A4 (ANXA4), erythrocyte band 7 integral membrane protein (STOM), ATP-dependent RNA helicase DDX3X (DDX3X), calpain small subunit 1 (CAPNS1), NAD(P)H dehydrogenase [quinone] 1 (NQO1), Protein S100-A16 (S100A16), clathrin light chain B (CLTB), brain acid soluble protein 1 (BASP1), DnaJ homolog subfamily C member 3 (DNAJC3), AP-2 complex subunit alpha-1 (AP2A1), 40S ribosomal protein (RPS6), glycyl-tRNA synthetase (GARS), EH domain-containing protein 2 (EHD2), oligoribonuclease, mitochondrial (REXO2), thrombospondin-1 (THBS1), glycylpeptide N-tetradecanoyltransferase 1 (NMT1), adenylyl cyclase-associated protein 1 (CAP1), heat shock-related 70 kDa protein 2 (HSPA2), histone H2A type 1-A (HIST1H2AA), and T-complex protein 1 subunit alpha (TCP1);

(xxiii) mitochondrially encoded cytochrome c oxidase II (MTCO2), NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (NDUFA5), NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 (NDUFA9), NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10 (NDUFA10) and NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase) (NDUFS6), wherein a decrease in expression of the one or more biomarkers is indicative of aging;

(xxiv) annexin A6 (ANXA6), glutaminyl-tRNA synthetase (QARS), cation-independent mannose-6-phosphate (IGF2R), twinfilin-2 (TWF2), 40S ribosomal protein S5 (RPS5), putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 (DHX15), 26S proteasome non-ATPase

regulatory subunit 1 (PSMD1), 40S ribosomal protein S29 (RPS29), synaptopodin-2 (SYNPO2), T-complex protein 1 subunit zeta (CCT6A), annexin 5 (ANXA5), tRNA-splicing ligase RtcB homolog (C22orf28), serine/arginine-rich splicing factor 9 (SRSF9), myosin light polypeptide 6 (MYL6), protein phosphatase 1 regulatory subunit 7 (PPP1R7), UPF0568 protein C14orf166 (C14orf166), 26 proteasome non-ATPase regulatory subunit 14 (PSMD14), serine hydroxymethyltransferase, mitochondrial (SHMT2), heat shock 70 kDa protein 1A/1B (HSPA1A), ATP-dependent RNA helicase DDX1 (DDX1), calmodulin (CALM1), AP-2 complex subunit alpha-2 (AP2A2), Rho guanine nucleotide exchange factor 2 (ARHGEF2), annexin A4 (ANXA4), erythrocyte band 7 integral membrane protein (STOM), ATP-dependent RNA helicase DDX3X (DDX3X), calpain small subunit 1 (CAPNS1), NAD(P)H dehydrogenase [quinone] 1 (NQO1), Protein S100-A16 (S100A16), clathrin light chain B (CLTB), brain acid soluble protein 1 (BASP1), DnaJ homolog subfamily C member 3 (DNAJC3), AP-2 complex subunit alpha-1 (AP2A1), 40S ribosomal protein (RPS6), glycyl-tRNA synthetase (GARS), EH domain-containing protein 2 (EHD2), oligoribonuclease, mitochondrial (REXO2), thrombospondin-1 (THBS1), glycylpeptide N-tetradecanoyltransferase 1 (NMT1), adenylyl cyclase-associated protein 1 (CAP1), heat shock-related 70 kDa protein 2 (HSPA2), histone H2A type 1-A (HIST1H2AA), and T-complex protein 1 subunit alpha (TCP1);

(xxv) annexin A6 (ANXA6), glutaminyl-tRNA synthetase (QARS), cation-independent mannose-6-phosphate (IGF2R), putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 (DHX15), 40S ribosomal protein S29 (RPS29), synaptopodin-2 (SYNPO2), annexin 5 (ANXA5), serine/arginine-rich splicing factor 9 (SRSF9), myosin light polypeptide 6 (MYL6), heat shock 70 kDa protein 1A/1B (HSPA1A), calmodulin (CALM1), annexin A4 (ANXA4), erythrocyte band 7 integral membrane protein (STOM), NAD(P)H dehydrogenase [quinone] 1 (NQO1), clathrin light chain B (CLTB), brain acid soluble protein 1 (BASP1), 40S ribosomal protein (RPS6), EH domain-containing protein 2 (EHD2), thrombospondin-1 (THBS1), heat shock-related 70 kDa protein 2 (HSPA2), wherein an increase in expression of the one or more biomarkers is indicative of aging;

(xxvi) twinfilin-2 (TWF2), 40S ribosomal protein S5 (RPS5), 26S proteasome non-ATPase regulatory subunit 1 (PSMD1), T-complex protein 1 subunit zeta (CCT6A), tRNA-splicing ligase RtcB homolog (C22orf28), protein phosphatase 1 regulatory subunit 7 (PPP1R7), UPF0568 protein C14orf166 (C14orf166), 26 proteasome non-ATPase regulatory subunit 14 (PSMD14), serine hydroxymethyltransferase , mitochondrial (SHMT2), ATP-dependent RNA helicase DDX1 (DDX1), AP-2 complex subunit alpha-2 (AP2A2), Rho guanine nucleotide exchange factor 2 (ARHGEF2), ATP-dependent RNA helicase DDX3X (DDX3X), calpain small subunit 1 (CAPNS1), Protein S100-A16 (S100A16), DnaJ homolog subfamily C member 3 (DNAJC3), AP-2 complex subunit alpha-1 (AP2A1), glycyl-tRNA synthetase (GARS), oligoribonuclease, mitochondrial (REXO2), glycylpeptide N-tetradecanoyltransferase 1 (NMT1), adenylyl cyclase-associated protein 1 (CAP1), histone H2A type 1-A (HIST1H2AA), and T-complex protein 1 subunit alpha (TCP1), wherein a decrease in the expression of the one or more biomarkers is indicative of aging; or

(xxv) Abcg1, Abra, Actn3, Alas2, Alox15, Angptl4, Apod, Apold1, Arc, Arhgap24, Arl4c, Arntl, Arrdc2, Asb5, Atf3, Bag2, Bcl11a, Bcl6, Bdh1, Bdnf, Best3, Bhlhe40, Calhm1, Calml3, Car12, Ccl5, Cd74, Cdc42se1, Chac1, Chst5, Ciart, Cidec, Cish, Cited4, Ckap4, Cldn2, Clic6, Cpt1a, Csrnp1, Cxcl13, Dbp, Dnajb5, Dynll1, Dyrk2, Edn1, Egr1, Egr3, Elfn1, Emb, Enah, Fam107b, Fam110a, Fam134b, Fam167a, Fam46a, Fasn, Fgfr3, Fhl2, Fos, Fosb, Frk, Fst, Gdf15, Gem, Gngt1, Gnl3, Hba1, Hba2, Hbb, Hbb-b1, Hbegf, Hmox1, Hpdl, Hspa1b, Id4, Il2rb, Irs1, Irs2, Junb, Jund, Kbtbd8, Kcnk5, Kctd7, Kirrel2, Ky, Lamc2, Lipg, LOC689064, Lonrf3, Lrrc38, Lrrc52, Lrrn2, Lsr, Maff, Mchr1, Mfrp, Mllt11, Mns1, Mogat1, Mphosph6, Mpz, Muc20, Mybpc2, Myf6, Myh1, Myh2, Myh4, Myocd, Nedd9, Nfil3, Nkg7, Nr1d1, Nr4a2, Nr4a3, Ntf4, Nuak1, Parp16, Pdc, Pde7a, Pfkfb2, Pfkfb3, Pgam1, Phlda1, Pik3ip1, Plk3, Postn, Ppargc1a, Ppp1r14c, Pragmin, Prf1, Ptpn14, Pvalb, Rab23, Rab30, Rbm20, Rcan1, Rell1, Rfx1, RGD1307461, RGD1309676, RGD1359290, RGD1564428, Rhpn2, Rn45s, Rnd1, Rp1, Rrad, RT1-Ba, RT1-Bb, RT1-Da, RT1-Db1, Rtn4rl1, Scd1, Sdc4, Sec14l5, Siglec5, Sik1, Slc18a2, Slc2a5, Slc30a4, Slc4a1, Slc4a5, Slpi, Smad7, Snhg4, Spag8, Stc1, Sv2c, Terf2ip, Thrsp, Tmc8, Tmem171, Tmx4, Tnfrsf12a,

Tnni2, Ttc30b, Txnip, Txnip, Ucp3, Unc5b, Zfp112, Zfp13, Zfp385b, Zfp474, Zfyve28, Zic1 and Zmynd10.

~~17.~~ 18. The ~~method~~use of any one of claims 1, or 3-17, or the method of any one of claims 3-17 ~~to 16~~, wherein

(i) the increase in expression of the one or more biomarkers is gender specific;

(ii) the biomarker is ATP synthase and the expression of the ATP synthase in up-regulated in aging males;

(iii) the biomarker is catalase and the expression of the catalase is down-regulated in aging males;

(iv) the biomarker is ATP synthase and the expression of ATP synthase is down-regulated in aging females;

(v) the biomarker is ornithine aminotransferase and the expression of the ornithine aminotransferase is up-regulated in aging females; or

(vi) the biomarker is glutamate dehydrogenase and the expression of the glutamate dehydrogenase is down-regulated in aging females.

~~18.~~ 19. The ~~method~~use of any one of claims 1 to ~~17~~18, wherein the one or more transcripts are

(i) identified using a transcript array analysis;

(ii) expressed in the skeletal muscle, the brain, the heart, the kidney, the liver, the bone marrow, or the skin; or

(iii) selected from the group consisting of:

(A) myosin light chain 3 (MLCF3), myosin light polypeptide 2 (slow), myosin light chain 1 (MLC1F), myosin binding protein C (MYBPC1), myosin binding protein H, alpha actin (fragment), actin (skeletal muscle), actin alpha (cardiac), troponin T class Ia alpha-1, troponin T class IIa beta-1, troponin T beta/alpha, capZ beta, desmin, gelsolin (cytosolic), beta-tubulin, p23, triosephosphate isomerase 1, glycosylase I, glyoxalase I, enolase 3 (beta muscle), glycerol 3-P dehydrogenase, isocitrate dehydrogenase 3 (NAD+), cytochrome c oxidase (polypeptide Va), creatine kinase (muscle form), Cu/Zn superoxide dismutase, ferritin heavy chain (H-ferritin), aldehyde dehydrogenase (mitochondrial), glutathione transferase (omega 1), heat shock 20 kDa protein (Hsp20), heat shock 27 kDa protein (Hsp27), disulfide

isomerase ER60 (ERp57), 14-3-3 protein, guanine deaminase (guanase), Rho-GDI (alpha), phosphohistidine phosphatase, mRNA capping enzyme, similar to apobec2 protein, galectin 1, albumin, vitamin D binding protein prepeptide, protein kinase C interacting protein-1, RIKEN cDNA 1700012G19, myosin heavy chain 2 (MYH2), troponin T type 1 (TNNT1), ryanodine receptor 1 (skeletal) (RYR1), calsequestrin 1 (fast-twitch, skeletal muscle) (CASQ1), junctophilin 1 (JPH1), adenosine monosphosphate deaminase (AMPD1), phosphorylase glycogen muscle (PYGM), and enolase 3 (beta, muscle) (ENO3);

(B) MLCF3, myosin light polypeptide 2 (slow), MLC1F, myosin binding protein C, myosin binding protein H, alpha actin (fragment), actin (skeletal muscle), actin alpha (cardiac), troponin T class IIa beta-1, troponin T beta/alpha, capZ beta, triosephosphate isomerase 1, glycosylase I, glyoxalase I, enolase 3 (beta muscle), glycerol 3-P dehydrogenase, isocitrate dehydrogenase 3 (NAD+), cytochrome c oxidase (polypeptide Va), creatine kinase (muscle form), Cu/Zn superoxide dismutase, phosphohistidine phosphatase, protein kinase C interacting protein-1, and RIKEN cDNA 1700012G19, wherein a decrease in expression in the one or more transcripts is indicative of aging;

(C) troponin T class Ia alpha-1, troponin T class IIa beta-1, desmin, gelsolin (cytosolic), beta-tubulin, p23, ferritin heavy chain (H-ferritin), aldehyde dehydrogenase (mitochondrial), glutathione transferase (omega 1), Hsp20, Hsp20, disulfide isomerase ER60 (ERp57), 14-3-3 protein, guanine deaminase (guanase), Rho-GDI (alpha), mRNA capping enzyme, similar to apobec2 protein, galectin 1, albumin, vitamin D binding protein prepeptide, wherein an increase in expression in the one or more transcripts is indicative of aging;

(D) myristoylated alanine-rich C-kinase substrate, alpha-internexin, isoform B of methyl-CpG-binding protein 2, histone H1.4, isoform 1 of serum albumin, guanine nucleotide-binding protein (G(1)/G(S)/G(T) subunit beta-1, adenylate kinase 1, fructose-biphosphate aldolase A, tenascin-R, isoform 2 of clusterin, synaptic transmission, cation

transport, isoform 1 of myeline proteolipid protein, neuromodulin, dihydropyrimidinase-related protein 2, dihydropteridine reductase, matrin-3, alpha-enolase, isoform 1 of gelsolin, APP isoform of APP714 of amyloid beta A4 protein (fragment), annexin A6, isoform tau-E of microtubule-associated protein tau, MAP1A 331 kDa protein, neuroblast differentiation-associated protein AH NAK, cell cycle exit and neuronal differentiation protein 1, glyceraldehyde-3-phosphate dehydrogenase, HIST1H1D, isoform KGA of glutaminase kidney isoform, superoxide dismutase (Mn) (SOD2), isoform 1 of myelin basic protein (MBP), and vimentin (VIM);

(E) amyloid beta (A4) precursor protein (APP), myristoylated alanine-rich protein kinase C substrate (MARCKS), internexin neuronal intermediate filament protein alpha (INA), methyl CpG binding protein (MECP), histone cluster 1 H1e (HIST1H1E), albumin (ALB), guanine nucleotide binding protein (G protein) beta polypeptide (GNB1), adenylate kinase 1 (AK1), aldose A fructose-biphosphate (ALDOA), tenascin R (TNR), clusterin (CLU), synapsin 1 (SYN1), ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac musle (ATP5A1), proteolipid protein 1 (PLP1), growth associated protein 43 (GAP43), dihydropyrimidinase-like 2 (DPYSL2), quinoid dihydropteridine reductase (QDPR), matrin 3 (MATR3), enolase 1 (alpha) (ENO1), gelsolin (GSN), annexin A6 (ANXA6), microtubule associated protein tau (MAPT), microtuble-associated protein 1A (MAP1A), AHNAK nucleoprotein, cell cycle exit and neuronal differentiation 1 (CEND1), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), histone cluster 1, H1d (HIST1H1D), glutaminase (GLS), superoxide dismutase (SOD2), MBP, VIM, ELAV-like protein 3 (ELAVL3), neurogranin (NRGN), receptor expression enhancing protein 2 (REEP2), glutamate decarboxylase 1 (GAD1), protocadherin alpha-1 (PCDHA1), glial fibrillary acidic protein (GFAP), S100 calcium binding protein (S100B), family with sequence similarity 19 (chemokine (C-C- motif)-like), member A1 (FAM19A1), aquaporin 4 (AQP4), c-type lectin domain family 2, member L (CLEC2L), neurofilament triplet L protein (NF-L),

peroxiredoxin (EC 1.11.1.), aconitate hydratase (EC 4.2.1.3), enolase 2 (EC 4.2.1.11), and T-complex protein 1;

(F) amyloid beta (A4) precursor protein (APP), marcks, internexin neuronal intermediate filament protein alpha (INA), methyl CpG binding protein (MECP), histone cluster 1 H1e (HIST1H1E), albumin (ALB), guanine nucleotide binding protein (G protein) beta polypeptide (GNB1), adenylate kinase 1 (AK1), aldose A fructose-biphosphate (ALDOA), tenascin R (TNR) and clusterin (CLU);

(G) proteolipid protein 1 (PLP1), growth associated protein 43 (GAP43), dihydropyrimidinase-like 2 (DPYSL2), quinoid dihydropteridine reductase (QDPR), matrin 3 (MATR3), enolase 1 (alpha) (ENO1), and gelsolin (GSN);

(H) microtubule associated protein tau (MAPT), microtuble-associated protein 1A (MAP1A), AHNAK nucleoprotein, cell cycle exit and neuronal differentiation 1 (CEND1) and glyceraldehyde-3-phosphate dehydrogenase (GAPDH);

(I) neurofilament triplet L protein (NF-L), peroxiredoxin (EC 1.11.1.), aconitate hydratase (EC 4.2.1.3), enolase 2 (EC 4.2.1.11), and T-complex protein 1;

(J) myosin, heavy chain 6, cardiac muscle, alpha (MYH6), actin, alpha, cardiac muscle 1 (ACTC1), troponin I type 3 (cardiac) (TNNI3), natriuretic peptide A (NPPA), A kinase (PRKA) anchor protein 6 (AKAP6), nestin (NES), ATPase, Na+,K+ transporting, alpha 3 polypeptide (ATP1A3), cadherin 2, type 1, N-cadherin (neuronal) (CDH2), plakophilin 2 (PKP2), ATP synthase subunit d (Atp5h), ATP synthase subunit o (Atp5o), ATP synthase subunit delta (Atp5d), ATP synthase subunit alpha (Atp5a1), ATP synthase subunit beta (Atp5b), cytochrome c (Cycs), mito, pyruvate dehydgrenase E1 component subunit beta (Pdhb), phosphoglycerate kinase 1 (Pgk1), heat shock protein 70 (Hspa9), 60 kDa heat shock protein (Hspd1), desmin (Desm), troponin T2 (Tnnt2), tropomyosin alpha 1 (Tpm1), voltage dependent anion channel-1 (Vdac1), and elongation factor 2 (Eef2);

(K) ATP synthase subunit d (Atp5h), ATP synthase subunit o (Atp5o), ATP synthase subunit delta (Atp5d), ATP synthase subunit alpha

(Atp5a1), ATP synthase subunit beta (Atp5b), cytochrome c (Cycs), mito, pyruvate dehydgrenase E1 component subunit beta (Pdhb), phosphoglycerate kinase 1 (Pgk1), heat shock protein 70 (Hspa9), 60 kDa heat shock protein (Hspd1), desmin (Desm), troponin T2 (Tnnt2), tropomyosin alpha 1 (Tpm1), voltage dependent anion channel-1 (Vdac1), and elongation factor 2 (Eef2);

wherein optionally the biomarker is elongation factor 2 (Eef2) and an increase in the expression of Eef2 is indicative of aging;

(L) ATP synthase subunit alpha (Atp5a1), ATP synthase subunit beta (Atp5b), cytochrome c (Cycs), mito, pyruvate dehydgrenase E1 component subunit beta (Pdhb), phosphoglycerate kinase 1 (Pgk1), heat shock protein 70 (Hspa9), desmin (Desm), troponin T2 (Tnnt2), tropomyosin alpha 1 (Tpm1), voltage dependent anion channel-1 (Vdac1), wherein a decrease in the expression of the one or more transcripts is indicative of aging;

(M) podocin (NPHS2), nephrin (NPHS1), kin of IRRE like (NEPH1 or KIRREL), podocalyxin-like (PODXL), fibroblast growth factor 1 (FGF1), crumbs family member 2 (CRB2), solute carrier family 22 (organic anion transporter), member 8 (SLC22A8), solute carrier family 22 (organic anion transporter), member 13 (SLC22A13), aminocarboxymuconate semialdehyde decarboxylase (ACMSD), agmatine ureohydrolase (agmatinase) (AGMAT), betaine-homocysteine S-methyltransferase (BHMT), chromosome 11 open reading frame 54 (C11orf54), cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), dihycropyrimidinase (DPYS), gamma-glutamyltransferase 1 (GGT1), 4-hydroxyphenylpyruvate dioxygenase (HPD), heat-responsive protein 12 (HRSP12), low density lipoprotein receptor-related protein 2 (LRP2), pyruvate kinase, liver and RBC (PKLR), X-prolyl aminopeptidase (aminopeptidase P)2, membrane-bound (XPNPEP2), uromodulin (UMOD), calbindin (CALB1), solute carrier family 12 (sodium/potassium/chloride transporter), member 1 (SLC12A1), solute carrier family 12 (sodium/chloride transporter), member 3 (SLC12A3), calcium-sensing receptor (CASR), aquaporin (AQP2),ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2

(ATP6V0D2), parvalbumin (PVALB), transmembrane protein 213 (TMEM213), transferrin, isocitrate dehydrogenase 1 (IDH), 3-hydroxyisobutyrate dehydrogenase, afenopin, heat shock protein (HSP) 9A, ATP synthase, ornithine aminotransferase, glutamate dehydrogenase, phosphoglycerate mutase, catalase, and glutathione (GSH);

(N) transferrin, isocitrate dehydrogenase 1 (IDH), and 3-hydroxyisobutyrate dehydrogenase, wherein an increase in the expression of the one or more transcripts is indicative of aging;

(O) afenopin, phosphoglycerate mutase, and glutathione (GSH), wherein a decrease in the expression of the one or more transcripts is indicative of aging;

(P) apolipoprotein B (APOB), apolipoprotein A-I (APOA1), fibrinogen gamma chain (FGG), complement component 2 (C2), kininogen 1 (KNG1), fibrinogen alpha chain (FGA), hydroxyacid oxidase (glycolate oxidase) 1 (HAO1), retinol dehydrogenase 16 (all-trans) (RDH16), aldolase B, fructose-bisphosphate (ALDOB), bile acid CoA: amino acid N-acyltransferase (glycine N-choloyltransferase) (BAAT), aldo-keto reductase family 1, member C4 (AKR1C4), solute carrier family 27 (fatty acid transporter), member 5 (SLC27A5), epoxide hydrolase, 3-ketoacyl-CoA thiolase A, sarcosine oxidase, and 2,4-dienoyl reductase;

(Q) epoxide hydroxylase, 3-ketoacyl-CoA thiolase A, sarcosine oxidase, and 2,4-dienoyl reductase, wherein an increase in expression of the one or more transcripts is indicative of aging;

(R) defensin, alpha 1 (DEFA1), defensin, alpha 1B (DEFA1B), defensin, alpha 3 (DEFA3), defensin, alpha 4 (DEFA4), cathepsin G (CTSG), myeloperoxidase (MPO), hemoglobin, beta (HBB), hemoglobin, alpha 1 (HBA1), hemoglobin, alpha 2 (HBA2), S100 calcium binding protein 12 (S100A12), chromosome 19 open reading frame 59 (C19orf59), pyruvate dehydrogenase (lipoamide) beta, fatty acid-binding protein 5, galectin-3, c-synuclein, heterobiomarkerous nuclear ribonucleoprotein A1, myosin light chain, regulatory B (Mrlcb), transgelin, similar to purine-nucleoside phosphorylase (punA), heterobiomarkerous nuclear

ribonucleoprotein A2/B1 isoform A2 (Hnrpa2b1), Huntingtin interacting protein K (HYPK), beta-actin FE-3 (Actg1), caldesmon 1 (Cald1, calponin-1 (Cnn1), E-FABP (C-FABP) (Fabp5), capping protein (actin filament), gelsolin-like (CAPG), similar to coactosin-like 1 (Cotl1), calponin-1 (calponin H1, smooth muscle; basic calponin) (Cnn1), vinculin (VCL), VIM, beta-tropomyosin (TPM2), transgelin 2 (Tagln2), tropomyosin 1, alpha isoform c (TPM1), calponin 3, acidic (CNN3), calponin 2 isoform a (Calponin 2), F-actin capping protein beta subunit (Capzb), alpha-globulin (Hba1), alpha-actin (aa 40-375) (Acta2), smooth muscle protein SM22 homolog-bovine (fragments) (Tagln2), thioredoxin 2 (Txn1), peroxideroxin 2 (Prdx2), peroxiderodoxin 5 precursor (Prdx5), and Cu-Zn superoxide dismutase A5 (GSTA5);

(S) fatty acid-binding protein 5, galectin-3, c-synuclein, heterobiomarkerous nuclear ribonucleoprotein A1, myosin light chain, regulatory B, peroxiredoxin 5 precursor, and transgelin;

(T) beta-actin FE-3 (Actg1), caldesmon 1 (Cald1, calponin-1 (Cnn1), E-FABP (C-FABP) (Fabp5), galectin-3 (LGALS3), gamma synuclein (Sncg), heterobiomarkerous nuclear ribonucleoprotein A1 isoform a (HNRPA1), heterobiomarkerous nuclear ribonucleoprotein A2/B1 isoform A2 (Hnrpa2b1), Huntingtin interacting protein K (HYPK), myosin light chain, regulatory B (Mrlcb), peroxiredoxin 5 precursor (Prdx5), similar to purine-nucleoside phosphorylase (punA), pyruvate dehydrogenase (lipoamide) beta (PDHB), and transgelin (Tagln);

(U) transgelin (Tagln), capping protein (actin filament), gelsolin-like (CAPG), caldesmon 1 (Cald1), beta-actin FE-3 (Actg1), similar to coactosin-like 1 (Cotl1), calphonin-1 (calphonin H1, smooth muscle; basic calponin) (Cnn1), vinculin (VCL), VIM, beta-tropomyosin (TPM2), myosin light chain, regulatory B (Mrlcb), transgelin 2 (Tagln2), tropomyosin 1, alpha isoform c (TPM1), calponin 3, acidid (CNN3), calponin 2 isoform a (Calponin 2), F-actin capping protein beta subunit (Capzb), alpha-globulin (Hba1), alpha-actin (aa 40-375) (Acta2), smooth muscle protein SM22 homolog-bovine (fragments) (Tagln2), thioredoxin 2 (Txn1), peroxideroxin 2 (Prdx2),

peroxiderodoxin 5 precursor (Prdx5), and Cu-Zn superoxide dismutase A5 (GSTA5);

(V) collagen, type XVII, alplha 1 (COL17A1), tumor protein p73 (TP73), keratin 10 (KRT10), caspase 14, apoptosis-related cysteine peptidase (CASP14), filaggrin (FLG), keratinocyte proline-rich protein (KPRP), corneodesmosin (CDSN), kallikrein-related peptidase 5 (KLK5), melan-A (MLANA), dopachrome tautomerase (DCT), tyrosinase (TYR), CD1a molecule (CD1A), CD207 molecule, langerin, (CD207), annexin A6 (ANXA6), glutaminyl-tRNA synthetase (QARS), cation-independent mannose-6-phosphate (IGF2R), twinfilin-2 (TWF2), 40S ribosomal protein S5 (RPS5), putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 (DHX15), 26S proteasome non-ATPase regulatory subunit 1 (PSMD1), 40S ribosomal protein S29 (RPS29), synaptopodin-2 (SYNPO2), T-complex protein 1 subunit zeta (CCT6A), annexin 5 (ANXA5), tRNA-splicing ligase RtcB homolog (C22orf28), serine/arginine-rich splicing factor 9 (SRSF9), myosin light polypeptide 6 (MYL6), protein phosphatase 1 regulatory subunit 7 (PPP1R7), UPF0568 protein C14orf166 (C14orf166), 26 proteasome non-ATPase regulatory subunit 14 (PSMD14), serine hydroxymethyltransferase, mitochondrial (SHMT2), heat shock 70 kDa protein 1A/1B (HSPA1A), ATP-dependent RNA helicase DDX1 (DDX1), calmodulin (CALM1), AP-2 complex subunit alpha-2 (AP2A2), Rho guanine nucleotide exchange factor 2 (ARHGEF2), annexin A4 (ANXA4), erythrocyte band 7 integral membrane protein (STOM), ATP-dependent RNA helicase DDX3X (DDX3X), calpain small subunit 1 (CAPNS1), NAD(P)H dehydrogenase [quinone] 1 (NQO1), Protein S100-A16 (S100A16), clathrin light chain B (CLTB), brain acid soluble protein 1 (BASP1), DnaJ homolog subfamily C member 3 (DNAJC3), AP-2 complex subunit alpha-1 (AP2A1), 40S ribosomal protein (RPS6), glycyl-tRNA synthetase (GARS), EH domain-containing protein 2 (EHD2), oligoribonuclease, mitochondrial (REXO2), thrombospondin-1 (THBS1), glycylpeptide N-tetradecanoyltransferase 1 (NMT1), adenylyl cyclase-associated protein 1 (CAP1), heat shock-related 70 kDa protein 2 (HSPA2),

histone H2A type 1-A (HIST1H2AA), and T-complex protein 1 subunit alpha (TCP1);

(W) mitochondrially encoded cytochrome c oxidase II (MTCO2), NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (NDUFA5), NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 (NDUFA9), NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10 (NDUFA10) and NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase) (NDUFS6), wherein a decrease in expression of the one or more transcripts is indicative of aging;

(X) annexin A6 (ANXA6), glutaminyl-tRNA synthetase (QARS), cation-independent mannose-6-phosphate (IGF2R), twinfilin-2 (TWF2), 40S ribosomal protein S5 (RPS5), putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 (DHX15), 26S proteasome non-ATPase regulatory subunit 1 (PSMD1), 40S ribosomal protein S29 (RPS29), synaptopodin-2 (SYNPO2), T-complex protein 1 subunit zeta (CCT6A), annexin 5 (ANXA5), tRNA-splicing ligase RtcB homolog (C22orf28), serine/arginine-rich splicing factor 9 (SRSF9), myosin light polypeptide 6 (MYL6), protein phosphatase 1 regulatory subunit 7 (PPP1R7), UPF0568 protein C14orf166 (C14orf166), 26 proteasome non-ATPase regulatory subunit 14 (PSMD14), serine hydroxymethyltransferase, mitochondrial (SHMT2), heat shock 70 kDa protein 1A/1B (HSPA1A), ATP-dependent RNA helicase DDX1 (DDX1), calmodulin (CALM1), AP-2 complex subunit alpha-2 (AP2A2), Rho guanine nucleotide exchange factor 2 (ARHGEF2), annexin A4 (ANXA4), erythrocyte band 7 integral membrane protein (STOM), ATP-dependent RNA helicase DDX3X (DDX3X), calpain small subunit 1 (CAPNS1), NAD(P)H dehydrogenase [quinone] 1 (NQO1), Protein S100-A16 (S100A16), clathrin light chain B (CLTB), brain acid soluble protein 1 (BASP1), DnaJ homolog subfamily C member 3 (DNAJC3), AP-2 complex subunit alpha-1 (AP2A1), 40S ribosomal protein (RPS6), glycyl-tRNA synthetase (GARS), EH domain-containing protein 2 (EHD2), oligoribonuclease, mitochondrial (REXO2), thrombospondin-1 (THBS1), glycylpeptide N-

tetradecanoyltransferase 1 (NMT1), adenylyl cyclase-associated protein 1 (CAP1), heat shock-related 70 kDa protein 2 (HSPA2), histone H2A type 1-A (HIST1H2AA), and T-complex protein 1 subunit alpha (TCP1);

(Y) annexin A6 (ANXA6), glutaminyl-tRNA synthetase (QARS), cation-independent mannose-6-phosphate (IGF2R), putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 (DHX15), 40S ribosomal protein S29 (RPS29), synaptopodin-2 (SYNPO2), annexin 5 (ANXA5), serine/arginine-rich splicing factor 9 (SRSF9), myosin light polypeptide 6 (MYL6), heat shock 70 kDa protein 1A/1B (HSPA1A), calmodulin (CALM1), annexin A4 (ANXA4), erythrocyte band 7 integral membrane protein (STOM), NAD(P)H dehydrogenase [quinone] 1 (NQO1), clathrin light chain B (CLTB), brain acid soluble protein 1 (BASP1), 40S ribosomal protein (RPS6), EH domain-containing protein 2 (EHD2), thrombospondin-1 (THBS1), heat shock-related 70 kDa protein 2 (HSPA2), wherein an increase in expression of the one or more transcripts is indicative of aging;

(Z) twinfilin-2 (TWF2), 40S ribosomal protein S5 (RPS5), 26S proteasome non-ATPase regulatory subunit 1 (PSMD1), T-complex protein 1 subunit zeta (CCT6A), tRNA-splicing ligase RtcB homolog (C22orf28), protein phosphatase 1 regulatory subunit 7 (PPP1R7), UPF0568 protein C14orf166 (C14orf166), 26 proteasome non-ATPase regulatory subunit 14 (PSMD14), serine hydroxymethyltransferase , mitochondrial (SHMT2), ATP-dependent RNA helicase DDX1 (DDX1), AP-2 complex subunit alpha-2 (AP2A2), Rho guanine nucleotide exchange factor 2 (ARHGEF2), ATP-dependent RNA helicase DDX3X (DDX3X), calpain small subunit 1 (CAPNS1), Protein S100-A16 (S100A16), DnaJ homolog subfamily C member 3 (DNAJC3), AP-2 complex subunit alpha-1 (AP2A1), glycyl-tRNA synthetase (GARS), oligoribonuclease, mitochondrial (REXO2), glycylpeptide N-tetradecanoyltransferase 1 (NMT1), adenylyl cyclase-associated protein 1 (CAP1), histone H2A type 1-A (HIST1H2AA), and T-complex protein 1 subunit alpha (TCP1), wherein a decrease in the expression of the one or more transcripts is indicative of aging; or

(AA) Abcg1, Abra, Actn3, Alas2, Alox15, Angptl4, Apod, Apold1, Arc, Arhgap24, Arl4c, Arntl, Arrdc2, Asb5, Atf3, Bag2, Bcl11a, Bcl6, Bdh1, Bdnf, Best3, Bhlhe40, Calhm1, Calml3, Car12, Ccl5, Cd74, Cdc42se1, Chac1, Chst5, Ciart, Cidec, Cish, Cited4, Ckap4, Cldn2, Clic6, Cpt1a, Csrnp1, Cxcl13, Dbp, Dnajb5, Dynll1, Dyrk2, Edn1, Egr1, Egr3, Elfn1, Emb, Enah, Fam107b, Fam110a, Fam134b, Fam167a, Fam46a, Fasn, Fgfr3, Fhl2, Fos, Fosb, Frk, Fst, Gdf15, Gem, Gngt1, Gnl3, Hba1, Hba2, Hbb, Hbb-b1, Hbegf, Hmox1, Hpdl, Hspa1b, Id4, Il2rb, Irs1, Irs2, Junb, Jund, Kbtbd8, Kcnk5, Kctd7, Kirrel2, Ky, Lamc2, Lipg, LOC689064, Lonrf3, Lrrc38, Lrrc52, Lrrn2, Lsr, Maff, Mchr1, Mfrp, Mllt11, Mns1, Mogat1, Mphosph6, Mpz, Muc20, Mybpc2, Myf6, Myh1, Myh2, Myh4, Myocd, Nedd9, Nfil3, Nkg7, Nr1d1, Nr4a2, Nr4a3, Ntf4, Nuak1, Parp16, Pdc, Pde7a, Pfkfb2, Pfkfb3, Pgam1, Phlda1, Pik3ip1, Plk3, Postn, Ppargc1a, Ppp1r14c, Pragmin, Prf1, Ptpn14, Pvalb, Rab23, Rab30, Rbm20, Rcan1, Rell1, Rfx1, RGD1307461, RGD1309676, RGD1359290, RGD1564428, Rhpn2, Rn45s, Rnd1, Rp1, Rrad, RT1-Ba, RT1-Bb, RT1-Da, RT1-Db1, Rtn4rl1, Scd1, Sdc4, Sec14l5, Siglec5, Sik1, Slc18a2, Slc2a5, Slc30a4, Slc4a1, Slc4a5, Slpi, Smad7, Snhg4, Spag8, Stc1, Sv2c, Terf2ip, Thrsp, Tmc8, Tmem171, Tmx4, Tnfrsf12a, Tnni2, Ttc30b, Txnip, Txnip, Ucp3, Unc5b, Zfp112, Zfp13, Zfp385b, Zfp474, Zfyve28, Zic1 and Zmynd10.