**Supplementary Information**

Green polymer-based nanocomposites containing ceria and their use in the process of stem cell proliferation

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**Table S1.** Selected gene groups for PCR-RT analysis.

| **Function** | **Description** | **GeneBank** | **Symbol** | **Forward 5'-3'** | **Rewerse 5'-3'** |
| --- | --- | --- | --- | --- | --- |
| Glutathione Peroxidases (GPx) | Glutathione peroxidase 1 | NM\_000581 | GPX1 | CCTCCCCTTACAGTGCTTGTTC | GCACACATGGCGCAATTG |
| Glutathione peroxidase 2 (gastrointestinal) | NM\_002083 | GPX2 | CCGATCCCAAGCTCATCATT | TCTCAAAGTTCCAGGCCACAT |
| Glutathione peroxidase 3 (plasma) | NM\_002084 | GPX3 | CATCCCCTTCAAGCAGTATGCT | GCCCGTCAGGCCTCAGTAG |
| Glutathione peroxidase 4 (phospholipid hydroperoxidase) | NM\_002085 | GPX4 | CCGATACGCTGAGTGTGGTTT | GCTCCTGCTTCCCGAACTG |
| Glutathione peroxidase 5 (epididymal androgen-related protein) | NM\_001509 | GPX5 | TCACCACACTCTCTTCCTGCAT | AGAGTGGGAATTCTGGCAGTATG |
| Glutathione S-transferase pi 1 | NM\_000852 | GSTP1 | CAGGAGGGCTCACTCAAAGC | GTGAGGTCTCCGTCCTGGAA |
| Glutathione transferase zeta 1 | NM\_001513 | GSTZ1 | CCCAGAACGCCATCACTTG | TGCCCGCTGTGCTCTGT |
| Peroxiredoxins (TPx) | Peroxiredoxin 1 | NM\_002574 | PRDX1 | CTGGGACCCATGAACATTCC | AAGACCCCATAATCCTGAGCAA |
| Peroxiredoxin 2 | NM\_005809 | PRDX2 | TCCTTCGCCAGATCACTGTTAA | CAGCCGCAGAGCCTCATC |
| Peroxiredoxin 3 | NM\_006793 | PRDX3 | GCATTTGAGCGTCAACGATCT | TCACCAAGCGGAGGGTTTC |
| Peroxiredoxin 4 | NM\_006406 | PRDX4 | GAGGCATCCCGGGTATCG | GGCTTGGAAATCTTCGCTTTG |
| Peroxiredoxin 5 | NM\_181652 | PRDX5 | AGATGATTCGCTGGTGTCCAT | ACTATGCCATCCTGTACCACCAT |
| Peroxiredoxin 6 | NM\_004905 | PRDX6 | GGCCGCATCCGTTTCC | CCCGAGGGTGGGAGAAGA |
| Other Peroxidases | Catalase | NM\_001752 | CAT | CAGGGCATCAAAAACCTTTCTG | CGGATGCCATAGTCAGGATCTT |
| Cytochrome b-245, beta polypeptide | NM\_000397 | CYBB | CCTTTGAGTGGTTTGCAGATCTG | AGCCGGCATTGTTCCTTTC |
| Cytoglobin | NM\_134268 | CYGB | GCAGCACCTCGAGCAGAAG | CCTTGGCACCCAGAAATGG |
| Dual oxidase 1 | NM\_175940 | DUOX1 | TGAGCGGCACTTCCAGAAG | GACGGCCAAAGTGGGTGAT |
| Dual oxidase 2 | NM\_014080 | DUOX2 | CCTTCGAGCCCTTCTTCAACT | CAGCTGAACACCCCGATCTT |
| Lactoperoxidase | NM\_006151 | LPO | CAAGCTTTTCCAGCCAACTCA | CCGGCAACGCTGTGTGT |
| Myeloperoxidase | NM\_000250 | MPO | CCTGAAATTGGCGAGGAAACT | GCCGCCCATCCAGATGT |
| Prostaglandin-endoperoxide synthase 1 | NM\_000962 | PTGS1 | TGTTCGGTGTCCAGTTCCAATA | TGCCAGTGGTAGAGATGGTTGA |
| Prostaglandin-endoperoxide synthase 2 | NM\_000963 | PTGS2 | AATTGCTGGCAGGGTTGCT | GGTCAATGGAAGCCTGTGATACTT |
| Other Antioxidants | Albumin | NM\_000477 | ALB | TGAGAAAACGCCAGTAAGTGACA | GAAAAGCATGGTCGCCTGTT |
| Apolipoprotein E | NM\_000041 | APOE | CTGCGTTGCTGGTCACATTC | CTCTGTCTCCACCGCTTGCT |
| Glutathione reductase | NM\_000637 | GSR | TGCAGGGACTTGGGTGTGA | GCCTTCGTTGCTCCCATCT |
| Metallothionein 3 | NM\_005954 | MT3 | AGTGCGAGGGATGCAAATG | GCCTTTGCACACACAGTCCTT |
| Sulfiredoxin 1 | NM\_080725 | SRXN1 | TGCTGTATCCCCAAGAATCATG | GCTAGTTTGGCCCTTCCTCTTC |
| Superoxide dismutase 1, soluble | NM\_000454 | SOD1 | TGGTGTGGCCGATGTGTCT | GTGCGGCCAATGATGCA |
| Superoxide dismutase 2, mitochondrial | NM\_000636 | SOD2 | TCCGCAGAAAGGAACATTAAGG | TGACCTCCATTCTTTGCTCTCA |
| Superoxide dismutase 3, extracellular | NM\_003102 | SOD3 | GCGGAGCCCAACTCTGACT | TGCCAGATCTCCGTGACCTT |
| Genes Involved in Reactive Oxygen Species (ROS) Metabolism | Arachidonate 12-lipoxygenase | NM\_000697 | ALOX12 | CCACCCACCACCAAGGAA | TGCCGGACATCAGGTAGTGA |
| Nitric oxide synthase 2, inducible | NM\_000625 | NOS2 | CCGCATGACCTTGGTGTTT | TCCAGCATCTCCTCCTGGTAGA |
| NADPH oxidase 4 | NM\_016931 | NOX4 | AAGAGCCCAGATTCCAAGCTAATT | CGGCACAGTACAGGCACAAA |
| NADPH oxidase, EF-hand calcium binding domain 5 | NM\_024505 | NOX5 | AGGCACCAGAAAAGAAAGCATACT | ATGTTGTCTTGGACACCTTCGAT |
| Uncoupling protein 2 (mitochondrial, proton carrier) | NM\_003355 | UCP2 | CAGTTCTACACCAAGGGCTCTGA | CCTGTGGTGCTGCCTGCTA |
| Aldehyde oxidase 1 | NM\_001159 | AOX1 | GGTGTTCCGTGTTTTTCGCTAT | GGTCCATGCAGGCCTCTCT |
| BCL2/adenovirus E1B 19kDa interacting protein 3 | NM\_004052 | BNIP3 | TCCATCTCTGCTGCTCTCTCATT | AGGTTGTCAGACGCCTTCCA |
| Epoxide hydrolase 2, cytoplasmic | NM\_001979 | EPHX2 | AACTGGGCCTCTCTCAAGCA | AGCCATGTACCACACCAGCAT |
| MpV17 mitochondrial inner membrane protein | NM\_002437 | MPV17 | TCTATGGCCTGCTGTGCAGTT | GGACAACGGCCAACCTGTA |
| ATX1 antioxidant protein 1 homolog (yeast) | NM\_004045 | ATOX1 | TGCTTGCAACCCTGAAGAAA | GGACCAGGCCCCTGCTA |
| Chemokine (C-C motif) ligand 5 | NM\_002985 | CCL5 | TGCATCTGCCTCCCCATATT | AGTGGGCGGGCAATGTAG |
| 24-dehydrocholesterol reductase | NM\_014762 | DHCR24 | CATGCTGGTGCCCATGAAG | GACGTGGATGTCGTTTTGGAA |
| Forkhead box M1 | NM\_021953 | FOXM1 | AGGAAACGCTGCCCATCTC | CGTGAGCCTCCAGGATTCAG |
| Ferritin, heavy polypeptide 1 | NM\_002032 | FTH1 | CTGGCTTGGCGGAATATCTCT | GCCCGAGGCTTAGCTTTCAT |
| Glutamate-cysteine ligase, modifier subunit | NM\_002061 | GCLM | CCGCCTGCGGAAGAAGT | CATTCAAGGTTTTTTGGATACAATCA |
| Glutathione synthetase | NM\_000178 | GSS | GCAGGAAAAGACACTCGTGATG | CATGCTCGATGGCTTTGGT |
| Heme oxygenase (decycling) 1 | NM\_002133 | HMOX1 | TCCGATGGGTCCTTACACTCA | GCCTGCATTCACATGGCATA |
| Heat shock 70kDa protein 1A | NM\_005345 | HSPA1A | GCTGATTGGCCGCAAGTT | TGGAAAGGCCAGTGCTTCAT |
| Mannose-binding lectin (protein C) 2, soluble | NM\_000242 | MBL2 | AGTGAAGGCCTTGTGTGTCAAGT | TCCATTCTCTGCAGCATTCCT |
| NAD(P)H dehydrogenase, quinone 1 | NM\_000903 | NQO1 | CAGCAGACGCCCGAATTC | TGGTGTCTCATCCCAAATATTCTC |
| Ring finger protein 7 | NM\_014245 | RNF7 | AAAGGAAAGAGCTCCAAATTGAATC | CATAAGCATGCAAAAAGTTCTCTGA |
| Sirtuin 2 | NM\_012237 | SIRT2 | GCTGGAACAGGAGGACTTGGT | TGGCGCTGACGCAGTGT |
| Sequestosome 1 | NM\_003900 | SQSTM1 | GGAAGGTGAAACACGGACACTT | ACGTGGGCTCCAGTTTCCT |
| Pathway Activity Signature Genes | Aldo-keto reductase family 1 | NM\_001354 | AKR1C2 | GATTGCCCTGCGCTACCA | TGTCTGATGCGCTGCTCATT |
| BCL2-associated athanogene 2 | NM\_004282 | BAG2 | CTCACCGTTGAAGTGTCAGTAGAAA | ATCAATAATCCTTGTGGCATGCT |
| Four and a half LIM domains 2 | NM\_001450 | FHL2 | CCTGCAGGAAGCAGCTGTCT | AGTTCAGGCAGTAGGCAAAGTCA |
| Galactosidase, alpha | NM\_000169 | GLA | GGATGGCTCCCCAAAGAGAT | GGCGAATCCCATGAGGAAA |
| Heat shock protein 90kDa alpha (cytosolic), class A member 1 | NM\_001017963 | HSP90AA1 | TTGGCAGTGAAGCATTTTTCAG | GAGCACGTCGTGGGACAAA |
| Phospholysine phosphohistidine inorganic pyrophosphate phosphatase | NM\_022126 | LHPP | TGCGCACCGGGAAGTT | CACGTACCCATCAGCCTTCA |
| Trafficking protein particle complex 6A | NM\_024108 | TRAPPC6A | GGTGTTCCAGAAGCAGATGGA | AGCTGTTGTCTTGCAGGACGTA |
| Mitochondrial dysfunction | Mitochondrial ribosomal protein L43 | NM\_176794 | MRPL43 | CAGTTGCACCGCAGATCCT | GGAAGATCGGATGACTGAACTGA |
| NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3kDa | NM\_019056 | NDUFB11 | GCAGCACCTTTGTGGCCTAT | TCCCATCCCACGCTCTTG |
| Polymerase (RNA) mitochondrial (DNA directed) | NM\_005035 | POLRMT | CACAGGTGCTGGAAGGTTTCA | CCGTACACCACCGTCATCAC |
| Sirtuin 1 | NM\_012238 | SIRT1 | TGAGCCTGATGTTCCAGAGAGA | AGCTTCATTAATTGCCTCTTGATCAT |
| Sirtuin 3 | NM\_012239 | SIRT3 | CCAGTGGCATTCCAGACTTCA | GATCGTACTGCTGGAGGTTGCT |
| Transcription factor B1, mitochondrial | NM\_016020 | TFB1M | GCCATCGAGGGCTCAGAA | CAGCCTGCCCGTGCTTT |
| Transcription factor B2, mitochondrial | NM\_022366 | TFB2M | AAGGCGTCTAAGGCCAGCTT | TTTGCGCCAGGGTCTCA |
| Copper chaperone for superoxide dismutase | NM\_005125 | CCS | GCCGCGCCATCTTCAG | ATCAGGCTGCGGCCAAT |
| Selenoprotein P, plasma, 1 | NM\_203472 | SELENOS | CTGAAACGGAAATCGGACAGA | CGCCTCCTTCACCAGACAAC |
| Anti Apoptotic | B-cell CLL/lymphoma 2 | NM\_000633.2 | BCL2 | CTGGGATGCCTTTGTGGAACT | AGACAGCCAGGAGAAATCAAACAG |
| aculoviral IAP repeat containing 3 | NM\_001165.4 | BIRC3 | GGACAGGAGTTCATCCGTCAAG | TCTCCTGGGCTGTCTGATGTG |
| myeloid cell leukemia 1 | NM\_021960.4 | MCL1 | CACGAGACGGCCTTCCAA | CACTCGAGACAACGATTTCACATC |
| TNF receptor-associated factor 2 | NM\_021138.3 | TRAF2 | GGCCGTCTGTCCCAGTGAT | TTCGTGGCAGCTCTCGTATTC |
| Autophagy | autophagy related 3 | NM\_022488.4 | ATG3 | CCATTGAAAATCACCCTCATCTG | CACCTCAGCATGCCTGCAT |
| autophagy related 12 | NM\_004707.3 | ATG12 | CCCGGGAACAGAGGAACCT | GGAGTGTCTCCCACAGCCTTT |
| nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 | NM\_003998.3 | NFKB1 | GGCTACACCGAAGCAATTGAAG | CAGCGAGTGGGCCTGAGA |
| ribosomal protein S6 kinase, 70kDa, polypeptide 1 | NM\_003161.3 | RPS6KB1 | TGGCATAGAGCAGATGGATGTG | AGAGTTCGGCTGTCGTATTGGA |
| Necrosis | coiled-coil domain containing 103 | NM\_213607.2 | CCDC103 | GCTGCAAGGGCTTGTTTCAG | GCCCCTCCTTCACGGATCT |
| forkhead box I1 | NM\_012188.4 | FOXI1 | CGCCTCACTCTCAGCCAGAT | CCGGCCTTGCTCTTGTTGTA |
| junctophilin 3 | NM\_020655.3 | JPH3 | CCAGGATCACTGCCAAAGAGTT | CGCTTCGGCCTCTGGTACT |
| RAB25, member RAS oncogene family | NM\_020387.2 | RAB25 | TGTCTTCAAGGTGGTGCTGATC | CGCGTGAATCGGGAGAGTAG |
| Pro apoptotic | BCL2-associated X protein | NM\_004324.3 | BAX | GTGGCAGCTGACATGTTTTCTG | GCAAAGTAGAAAAGGGCGACAA |
| CD40 molecule, TNF receptor superfamily member 5 | NM\_001250.4 | CD40 | ACACTGCCACCAGCACAAATACT | CTGTTTCTGAGGTGCCCTTCTG |
| CASP8 and FADD-like apoptosis regulator | NM\_003879.5 | CFLAR | GTGTGTATGGTGTGGATCAGACTCA | GGCATGAATCTCCCATGAACA |
| Fas cell surface death receptor | NM\_000043.4 | FAS | GAATCATCAAGGAATGCACACTCA | AAAGCCACCCCAAGTTAGATCTG |
| Tumor necrosis factor receptor superfamily, member 10a | NM\_003844.3 | TNFRSF1 | CTGGCGCTTGGGTCTCCTA | TGCGTTGCTCAGAATCTCGTT |
| House keeping | glyceraldehyde-3-phosphate dehydrogenase | NM\_002046.5 | GAPDH | GTGGAAGGACTCATGACCACAGT | GCCATCACGCCACAGTTTC |
| ribosomal protein, large, P0 | NM\_001002.3 | RPLP0 | ATGCAGCAGATCCGCATGT | TTGCGCATCATGGTGTTCTT |
| beta-actin | XM\_006715764.1 | Actin | TCGTGCGTGACATTAAGGAGAA | AGCAGCCGTGGCCATCT |