

Supplementary materials

Table S1. Enrichment of molecular function GO terms using DAVID. GO terms were ranked according to count (%). False discovery rate (FDR) corrected p-values were determined using the Benjamini-Hochberg procedure. Top 10 are depicted.

| GO Term | Description | Count (%) | FDR |
|------------|---|-----------|---------|
| GO:0007165 | Signal transduction | 7.4 | 7.3e-1 |
| GO:0098609 | Cell-cell adhesion | 6.8 | 6.1e-60 |
| GO:0007155 | Cell adhesion | 6.1 | 1.5e-19 |
| GO:0006508 | Proteolysis | 4.9 | 2.4e-6 |
| GO:0055114 | Oxidation-reduction process | 4.9 | 3.6e-3 |
| GO:0030198 | Extracellular matrix organization | 4.3 | 8.6e-31 |
| GO:0016032 | Viral process | 4.1 | 8.3e-14 |
| GO:0000398 | mRNA splicing, via spliceosome | 3.9 | 2.6e-20 |
| GO:0043066 | Negative regulation of apoptotic process | 3.9 | 3.8e-3 |
| GO:0008284 | Positive regulation of cell proliferation | 3.9 | 7.8e-3 |

Table S2. Enrichment of molecular function GO terms using STRINGdb. False discovery rate (FDR) corrected p-values were determined using the Benjamini-Hochberg procedure. GO terms were ranked according to strength. Top 10 are depicted.

| GO Term | Description | Count | Strength | FDR |
|------------|---|----------|----------|--------|
| GO:0051920 | Peroxisredoxin activity | 7 of 7 | 1.02 | 3.1e-3 |
| GO:0044388 | Small protein activating enzyme binding | 5 of 5 | 1.02 | 2.7e-2 |
| GO:0008379 | Thioredoxin peroxidase activity | 5 of 5 | 1.02 | 2.7e-2 |
| GO:0048407 | Platelet-derived growth factor binding | 9 of 11 | 0,93 | 9.1e-4 |
| GO:0030020 | Extracellular matrix structural constituent conferring tensile strength | 21 of 28 | 0,9 | 2.1e-8 |
| GO:0004298 | Threonine-type endopeptidase activity | 16 of 21 | 0,9 | 1.8e-6 |
| GO:0032050 | Clathrin heavy chain binding | 6 of 8 | 0,9 | 2.3e-2 |
| GO:0031995 | Insulin-like growth factor ii binding | 6 of 8 | 0,9 | 2.3e-2 |
| GO:0015037 | Peptide disulfide oxidoreductase activity | 9 of 13 | 0,86 | 2.3e-2 |
| GO:0043394 | Proteoglycan binding | 25 of 37 | 0,85 | 2.0e-9 |

Table S3. Information concerning antioxidant proteins identified in AOD.

| Accession | Gene ID | Protein Name | Function |
|---------------|---------|--|---|
| Q06830 | PRDX1 | Peroxisredoxin-1 | Catalyzes the reduction of H ₂ O ₂ and organic hydroperoxides to water and alcohols. Protects cells against oxidative stress. |
| P32119 | PRDX2 | Peroxisredoxin-2 | Catalyzes the reduction of H ₂ O ₂ and organic hydroperoxides to water and alcohols. Protects cells against oxidative stress. |
| P30048 | PRDX3 | Thioredoxin-dependent peroxide reductase | Catalyzes the reduction of H ₂ O ₂ and organic hydroperoxides to water and alcohols. Protects cells against oxidative stress. |
| Q13162 | PRDX4 | Peroxisredoxin-4 | Catalyzes the reduction of H ₂ O ₂ and organic hydroperoxides to water and alcohols. Protects cells against oxidative stress. |
| P30044 | PRDX5 | Peroxisredoxin-5 | Catalyzes the reduction of H ₂ O ₂ and organic hydroperoxides to water and alcohols. Protects cells against oxidative stress. |
| P30041 | PRDX6 | Peroxisredoxin-6 | Catalyzes the reduction of H ₂ O ₂ and organic hydroperoxides to water and alcohols. Protects cells against oxidative stress. |
| P00441 | SOD1 | Superoxide dismutase | Attaches to Cu and Zn to break down superoxide radicals. Protects the cell from reactive oxygen species toxicity. |
| P99999 | CYCS | Cytochrome c | Transfers electrons to the cytochrome oxidase complex. Involved in apoptosis. |

Table S4. Gene primers (all from Applied Biosystems)

| Gene Type | Gene | Assay ID |
|----------------|---|---------------|
| Reference | GAPDH | Hs02758991_g1 |
| Apoptotic | CASP3 | Hs00234387_m1 |
| Pro-apoptotic | BAX | Hs00180269_m1 |
| Anti-apoptotic | BCL-2 | Hs00153350_m1 |
| Osteogenic | Col1a2 (Collagen type I) | Hs01028956_m1 |
| Osteogenic | BMP-2 (bone morphogenetic protein 2) | Hs00154192_m1 |
| Osteogenic | SPP1 (Osteopontin) | Hs00960942_m1 |
| Osteogenic | RUNX2 (runt-related transcription factor 2) | Hs01047973_m1 |

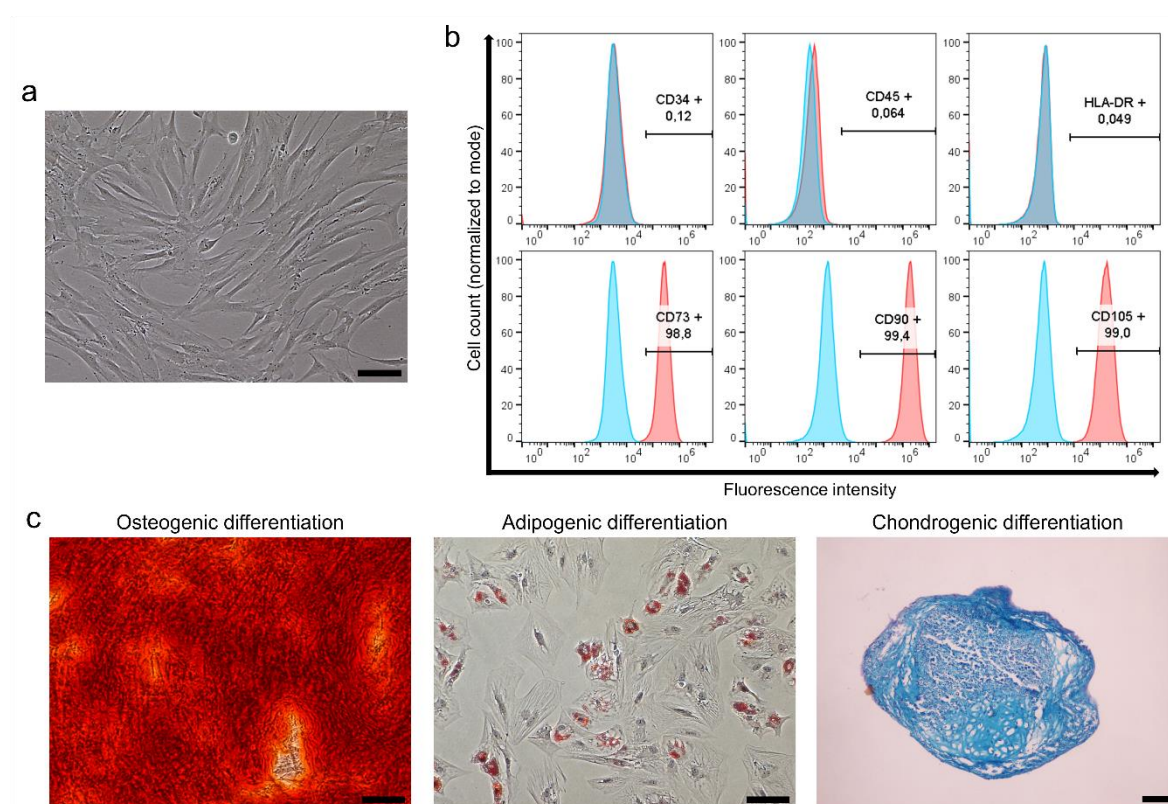


Figure S1. Characterization and multi-differentiation of hBMSC. (a) Microscopic image showing fibroblastic morphology of hBMSC. Scale bar 100 µm. (b) Histograms showing percentage of cell surface marker expression using flow cytometry analysis of hBMSC, antibody control (blue) and the stained cells (red). (c) Images showing tri-lineage differentiation into osteogenic, adipogenic and chondrogenic lineages confirmed by Alizarin red, Oil red O and Alcian blue staining, respectively. Scale bars 100 µm.