**Supplementary Table 1** Characterization of hUCMSCs

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| **Assay** | **Methodology** |
| **Immunophenotyping of hUCMSCs** | The isolated and expanded hUCMSCs were characterized by flow cytometry. 1x105 cells in 100 µL suspension were stained for 30 min with anti-marker monoclonal antibodies. Tested markers included CD73, CD90, CD105, CD44 and cocktails of CD34, CD45, CD11b, CD19 and HLA-DR (Human MSC Analysis Kit, BD Biosciences, USA). For an isotype control, non-specific mouse Ig was substituted for the primary antibody. After incubation, the cells were washed in PBS and analysed using a flow cytometer (FACSCalibur, Becton Dickinson, USA). |
| **Tri-differentiation of hUCMSCs** | |
| *Adipocytes differentiation* | Cultured hUCMSCs were treated in adipogenic differentiation medium consisting of complete medium supplemented with 1 µM dexamethasone and 0.2 mM indomethacin, 0.01 mg/mL insulin and 0.5 mM 3-isobutil-1-metil-xantina. The medium was changed every 3 days, and the cells were subjected to Oil Red O staining after about 14 days of culture. |
| *Chondrocytes differentiation* | Three dimension (3D) hUCMSCs cultures were maintained in a chemically defined basal medium consisting of complete medium supplemented with 50 µg/mL ascorbate-2-phosphate, 1.0 mM sodium piruvate, 40 µg/mL proline, 10 ng/mL transforming growth factor-β3, 6.25 µg/mL human insulin, 6.25 µg/mL transferrin, 6.25 µg/mL bovine insulin, 6.25 µg/ mL selenous acid, 1.25 µg/mL linoleic acid, and 5.35 µg/mL bovine serum albumin. The 3D chondrogenic culture utilised 1.0x106 hUCMSCs per pellet. hUCMSCs were suspended in 1 mL of chondrogenic medium with medium changes every 3–4 days. Chondrogenic pellets were harvested after 5 weeks in culture. To assess chondrogenesis, Alcian Blue-PAS was used to stain cartilage matrix. |
| *Osteoblasts differentiation* | hUCMSCs were treated in osteogenic differentiation medium consisting of complete medium supplemented with 50 µg/mL ascorbate-2-phosphate, 10 mM β-glycerophosphate, and 100 nM dexamethasone. The medium was changed every 3 days continuously for 2–3 weeks. Alizarin Red S was used to stain matrix mineralisation associated with osteoblasts. |

**Supplementary Table 2** List of proteins that were significantly up-regulated in TNF-α induced and uninduced hUCMSCs secretome, based on the *t*-test difference between both samples.

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| Sample | Accession number | Gene Symbol | Protein | Student’s *t test* difference |
| Induced hUCMSCs secretome | P02462 | COL4A1 | Collagen alpha-1 (IV) | -1.2687 |
| P21333 | FLNA | Filamin-A | -0.9641 |
| P04406 | GAPDH | Glyceraldehyde-3-phosphate dehydrogenase | -1.0224 |
| P28799 | GRN | Granulin | -0.9438 |
| P35527 | KRT9 | Keratin, type I cytoskeletal 9 | -2.2949 |
| P11047 | LAMC1 | Laminin subunit gamma-1 | -0.9349 |
| A0A3B3ITK0 | THBS2 | Thrombospondin | -0.7007 |
| P31946 | YWHAB | 14-3-3 protein beta/alpha | -0.6681 |
| Uninduced hUCMSCs secretome | P13500 | CCL2 | C-C motif chemokine 2 | 1.4063 |
| A0A0S2Z4F1 | EFEMP1 | EGF containing fibulin-like extracellular matrix protein 1 | 1.2189 |
| D6RF35 | GC | Vitamin D-binding protein | 1.2245 |
| P24592 | IGFBP6 | Insulin-like growth factor-binding protein 6 | 1.9286 |
| Q14766 | LTBP1 | Latene-transforming growth factor beta-binding protein 1 | 0.6020 |
| P23284 | PPIB | Peptidyl-prolyl cis-trans isomerise B | 0.9380 |
| P06703 | S100A6 | Protein S100-A6 | 1.1269 |
| P07093 | SERPINE2 | Gilia-derived nexin | 1.0610 |

Negative values indicate up-regulation in the TNF-α induced hUCMSCs secretome and positive values correspond to the up-regulated proteins in the uninduced hUCMSCs secretome, generated from the volcano plot in Figure 3b.