

Figure S1 Isolation and identification of BMSCs, BAMSCs and WAMSCs. (A-C) Images of three types of mesenchymal stem cells in bright field of an ordinary light microscope. (D) The proportion of CD44, CD105, CD90.2 and CD34 positive cells in total cells of BMSCs. (E) The proportion of CD44, CD105, CD73 and CD34 positive cells in total cells of BAMSCs. (F) The proportion of CD44, CD73, CD90.2 and CD34 positive cells in total cells of WAMSCs. (G-I) Statistical analysis of the proportion of positive cells expressed several surface markers in total cells of BMSCs, BAMSCs or WAMSCs. Scale bar: 50 μ m. n=3. BMSCs, bone marrow-derived mesenchymal stem cells; BAMSCs, brown adipose-derived mesenchymal stem cells; WAMSCs, white adipose-derived mesenchymal stem cells.

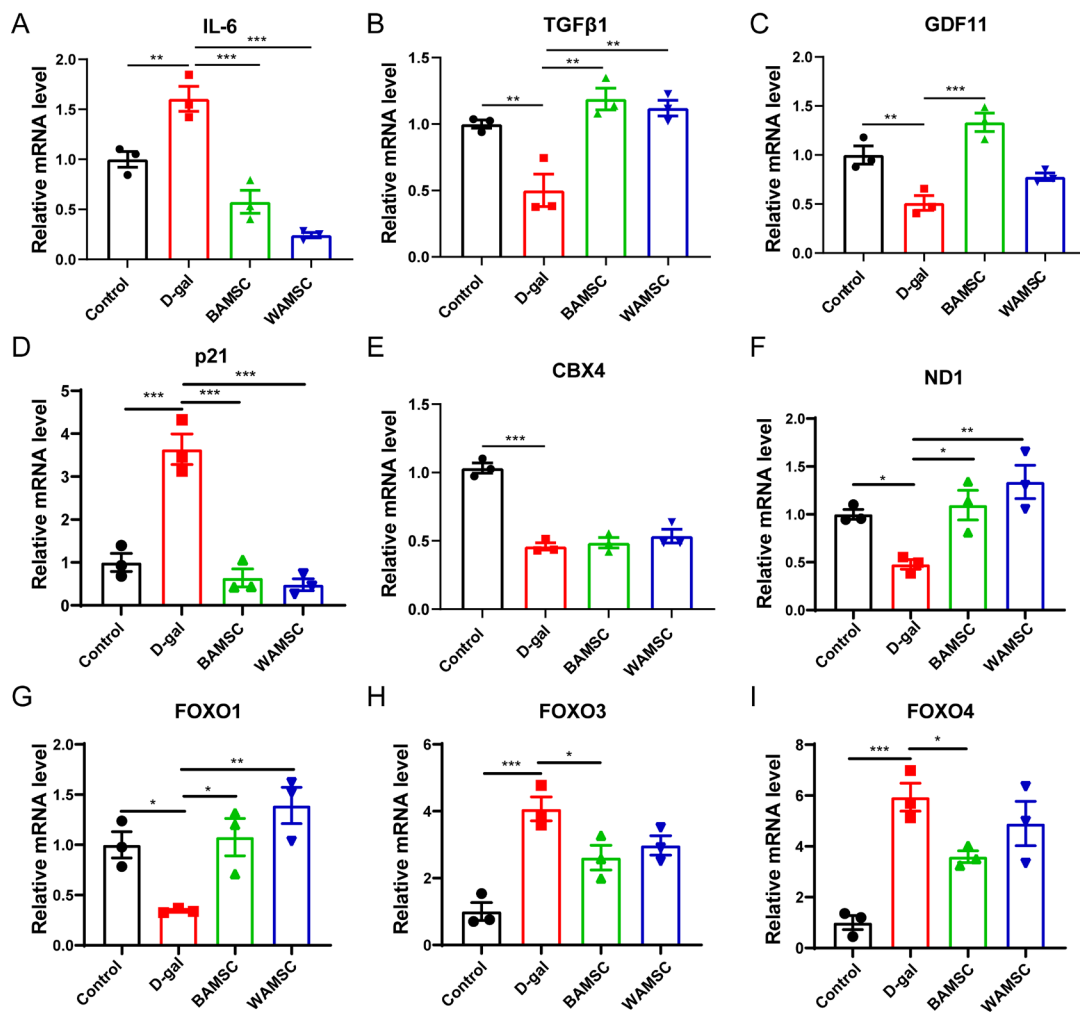


Figure S2 BAMSCs and WAMSCs ameliorate changes in D-gal induced senescent cells. (A-C) RT-PCR assessment of SASP components IL-6 (A), TGFβ1 (B) and GDF11 (C) expression in different cell groups. (D,E) The mRNA expression analysis of aging related factors of p21 (D) and CBX4 (E) in different cell groups. (F) Mitochondrial copy number characterization gene, ND1 expression analysis between different groups. (G-I) RT-PCR assessment of aging related members of FOXO family. Data were expressed as mean ± SE and analyzed using one-way ANOVA. n=3, *P<0.05, **P<0.01, ***P<0.001. BAMSCs, brown adipose-derived mesenchymal stem cells; WAMSCs, white adipose-derived mesenchymal stem cells; D-gal, D-galactose; RT-PCR, real-time polymerase chain reaction; SASP, senescence-associated secretory phenotype; IL, interleukin; TGF, transforming growth factor; GDF11, growth differentiation factor 11; CBX4, Chromobox 4; ND1, NADH-ubiquinone oxidoreductase chain 1; FOXO, Forkhead; SE, standard error.