

Description of Additional Supplementary Files

Supplementary Data 1. Quality control metrics, cell counts, differentially expressed genes for each subcluster, and Ro/e data from single-cell sequencing.

Differential gene expression between groups was assessed using a two-sided Wilcoxon rank-sum test. Multiple comparisons correction was applied using the Benjamini–Hochberg procedure, and adjusted p-values (FDR) < 0.05 were considered statistically significant. The Ro/e statistical test compares the observed number of cells with the expected number under random distribution to determine the enrichment or depletion of cell clusters in a given tissue. If the observed cell count is higher than expected, the cluster is considered enriched; if lower than expected, it is considered depleted. This is a two-tailed test based on a chi-square goodness-of-fit framework with multiple comparisons.

Supplementary Data 2. Clinical baseline characteristics. Detailed statistical methods are provided in Supplementary Data 2.

Supplementary Data 3. Public dataset information and related differentially expressed genes (DEGs). Differential gene expression between groups was assessed using a two-sided Wilcoxon rank-sum test. Multiple comparisons correction was applied using the Benjamini–Hochberg procedure, and adjusted p-values (FDR) < 0.05 were considered statistically significant.

Supplementary Data 4. Clinical trial profile of adipose-derived stem cells (ADSCs).