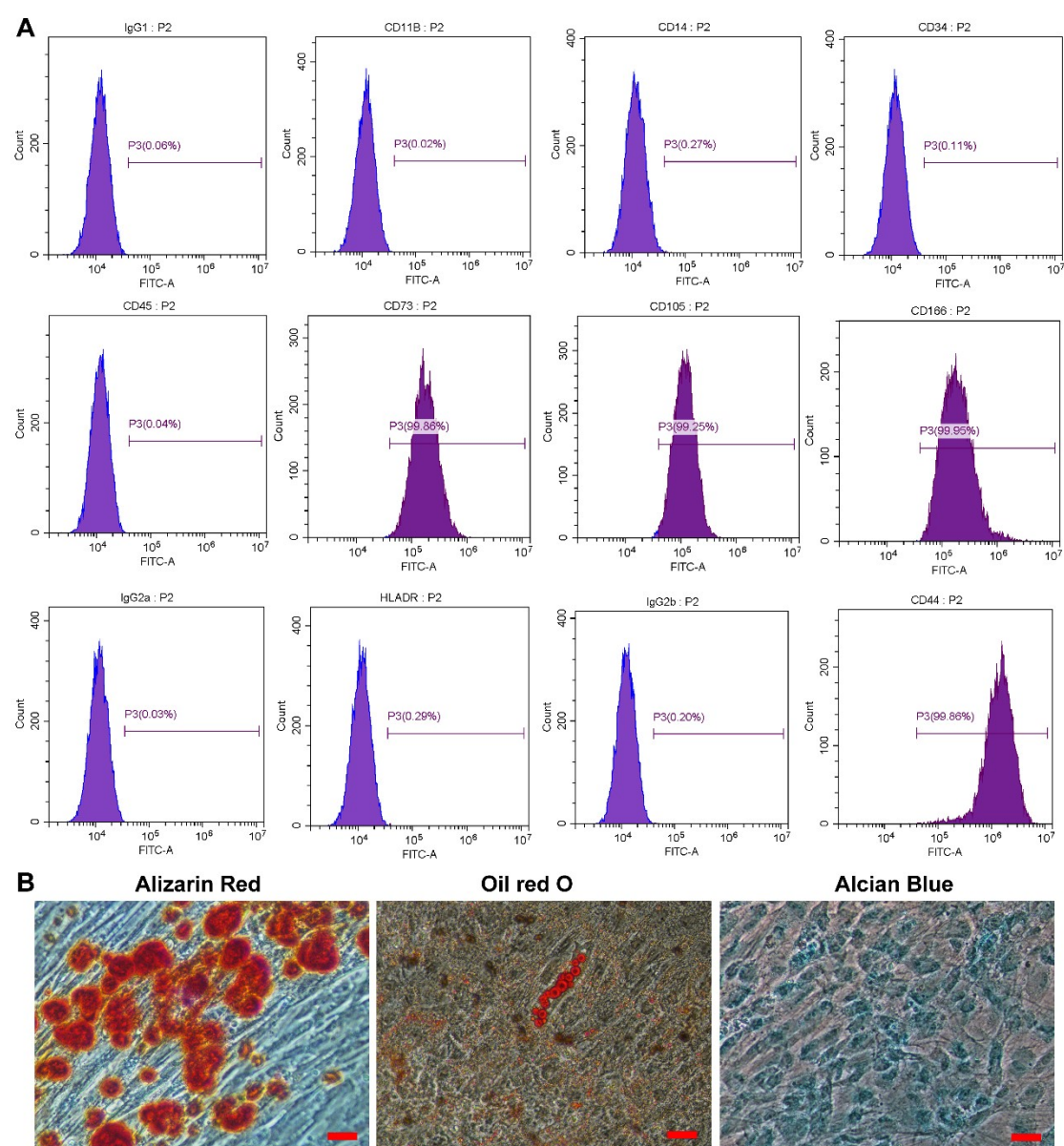
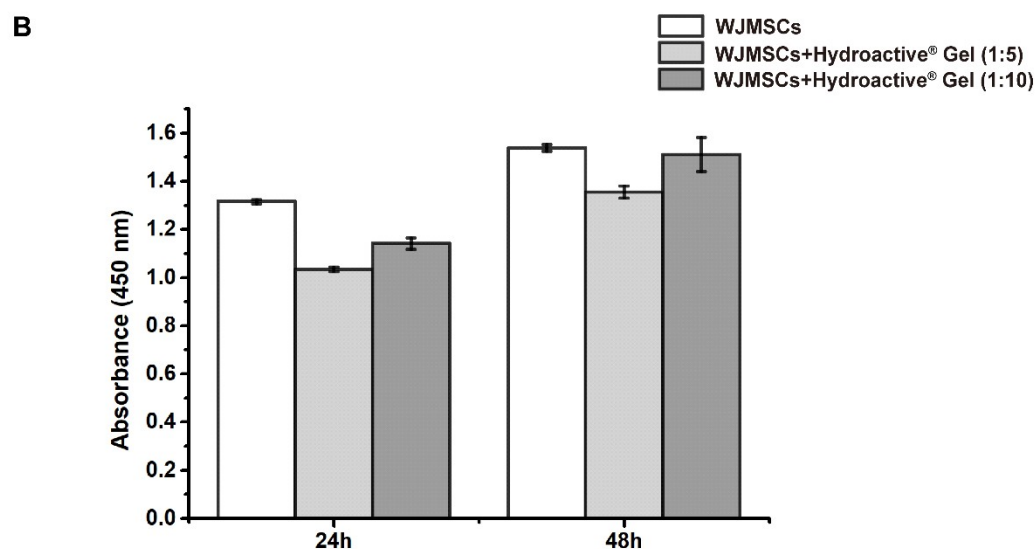
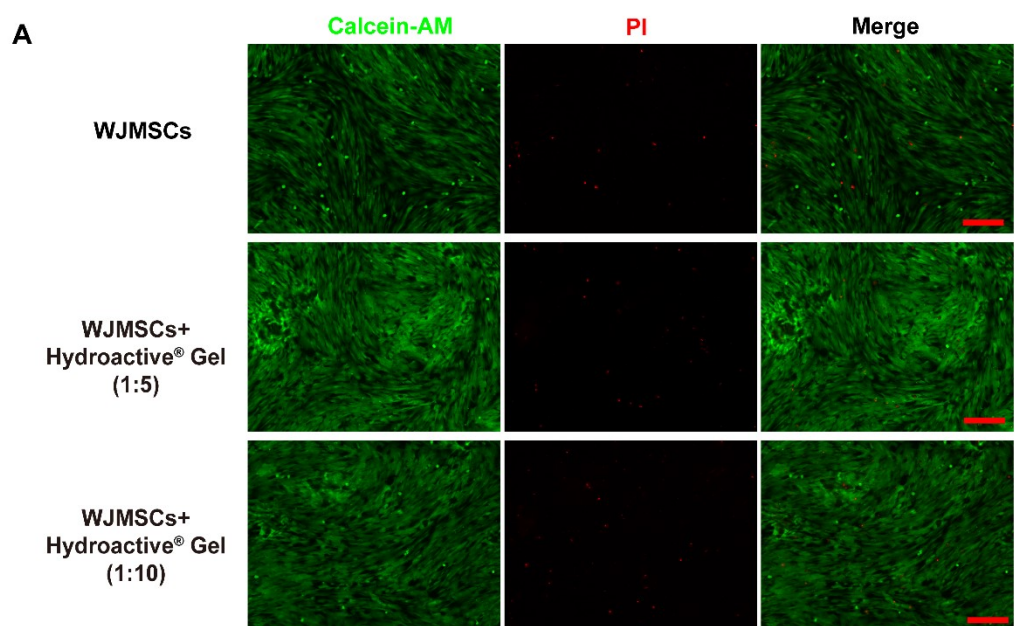


Supplementary materials

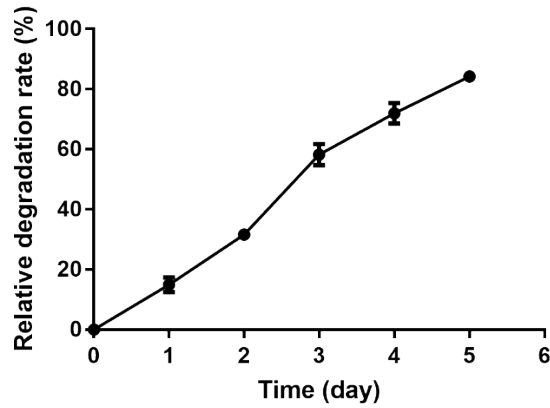
Supplementary Figure S1. Surface marker identification and tri-lineage differentiation ability of WJMSCs. **A.** Flow cytometry analysis of WJMSCs negative maker (CD11b, CD14, CD34, CD45, HLA-DR) and positive markers (CD44, CD73, CD105, CD166). Isotypic antibodies (IgG1, IgG2a and IgG2b) were used as negative controls. **B.** Representative images of WJMSCs differentiating into adipocytes after Oil Red O staining. Representative Alizarin Red staining images of WJMSCs differentiating into osteocytes after Alizarin Red staining. Representative images of WJMSCs differentiating into chondrocytes after Alcian Blue staining, Scale bar, 50 μ m.



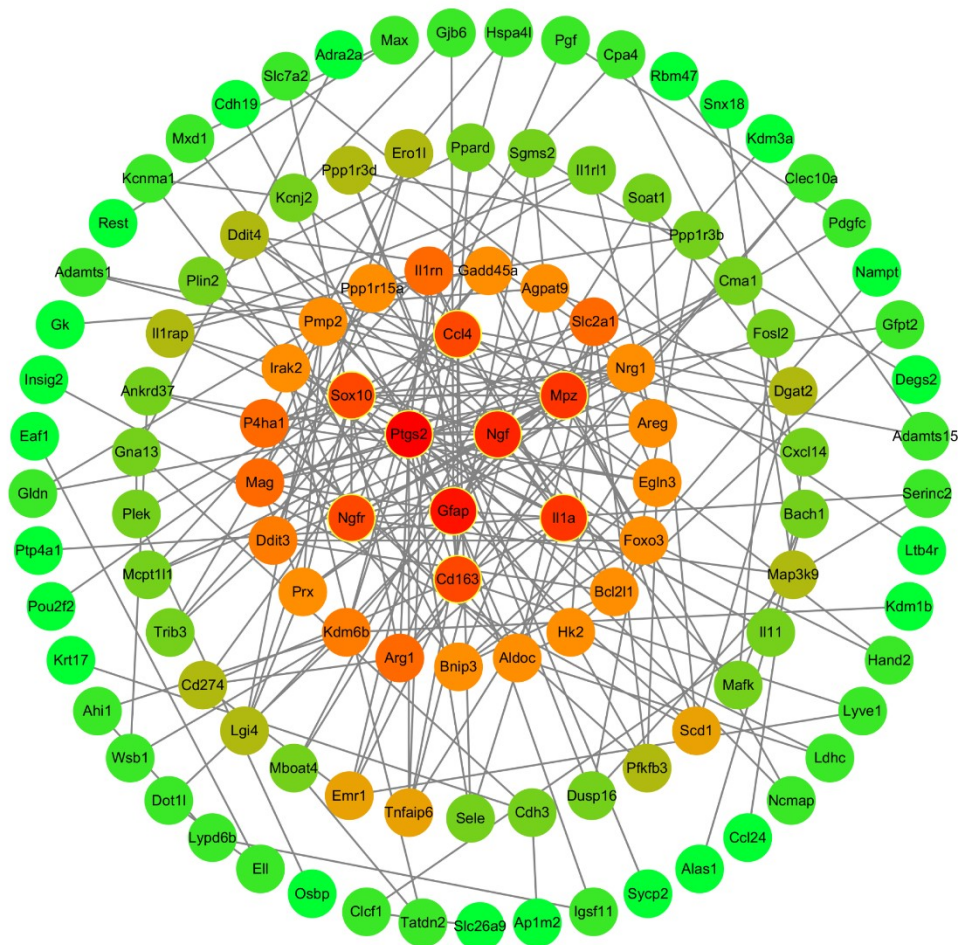
Supplementary Figure S2. The survival and viability of WJMSCs encapsulated with various dilution ratio Hydroactive® Gel. **A.** The survival of WJMSCs encapsulated with various dilution ratio Hydroactive® Gel was detected using Live/Dead™ Cell Imaging Kit. Calcein staining (green) represents live cells, while PI staining (red) represents dead cells. Scar bar: 100 μ M. **B.** The cell viability of WJMSCs encapsulated with various dilution ratio Hydroactive® Gel was detected by CCK-8 at 24h and 48h, respectively. Error bars represent mean \pm SEM; n=3 independent experiments. Significance was determined using one-way ANOVA.



Supplementary Figure S3. Degradation of Hydroactive® Gel was detected *in vitro*. Statistical analysis of the degradation rate of Hydroactive® Gel at different times.



Supplementary Figure S4. PPI network of DEGs in D3CON vs. D3MSC. The network displays gene interactions. Nodes represent genes, and edges represent gene interactions. The genes with more interactions are shown in red, genes with less interactions are shown in green, and hub genes are highlighted with a yellow circle.



Supplementary Figure S5. PPI network of DEGs in D14CON vs. D14MSC. The network displays gene interactions. Nodes represent genes, and edges represent gene interactions. The genes with more interactions are shown in red, genes with less interactions are shown in green, and hub genes are highlighted with a yellow circle.

