Supporting information

Metal-Phenolic Network Coatings Delivering Stem Cells from Apical Papilla Derived Nanovesicles for Bone Defect Regeneration

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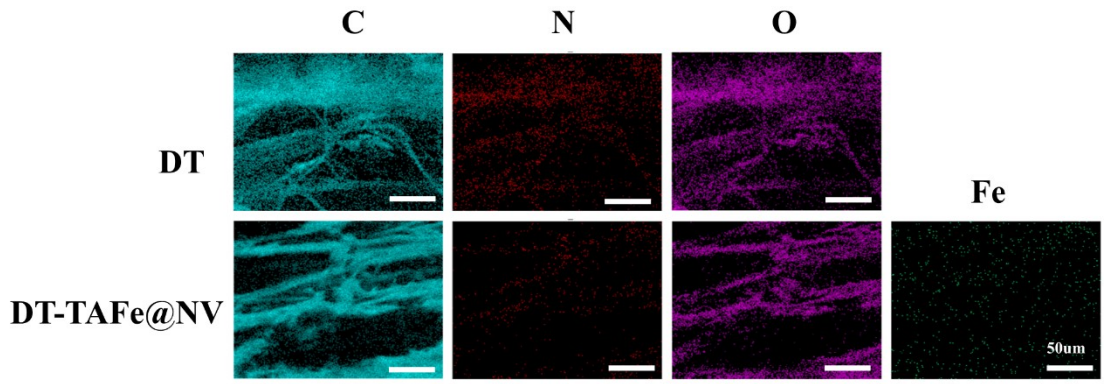

Figure S1. EDS energy spectra of DT and DT-TAFe.

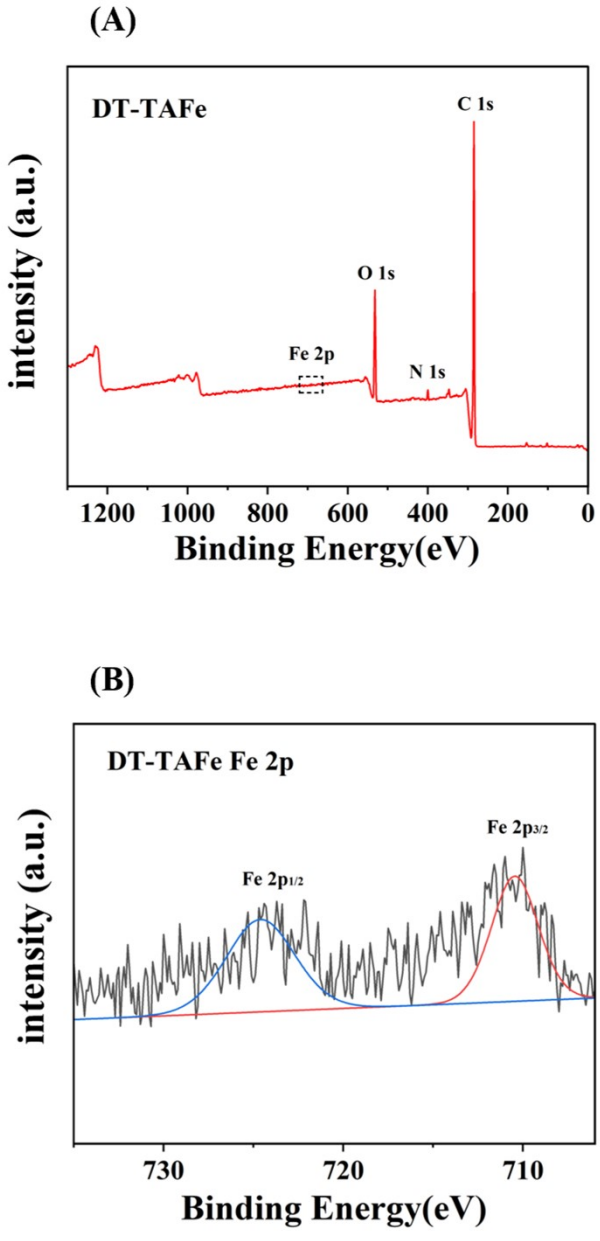

Figure S2. (A) XPS analysis of DT-TAFe, (B) Fe 2p fine spectrum of DT-TAFe.

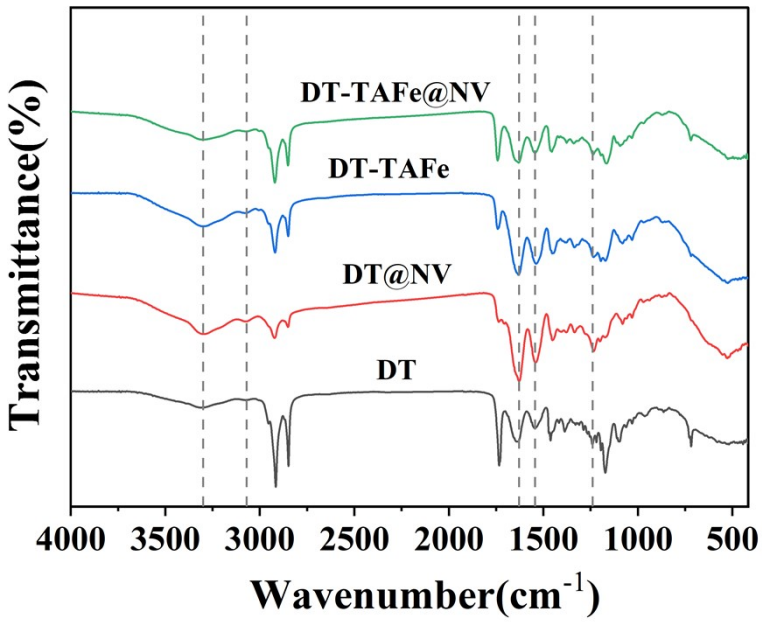

Figure S3. FTIR profiles of DT, DT @NV, DT-TAFe and DT-TAFe@NV.

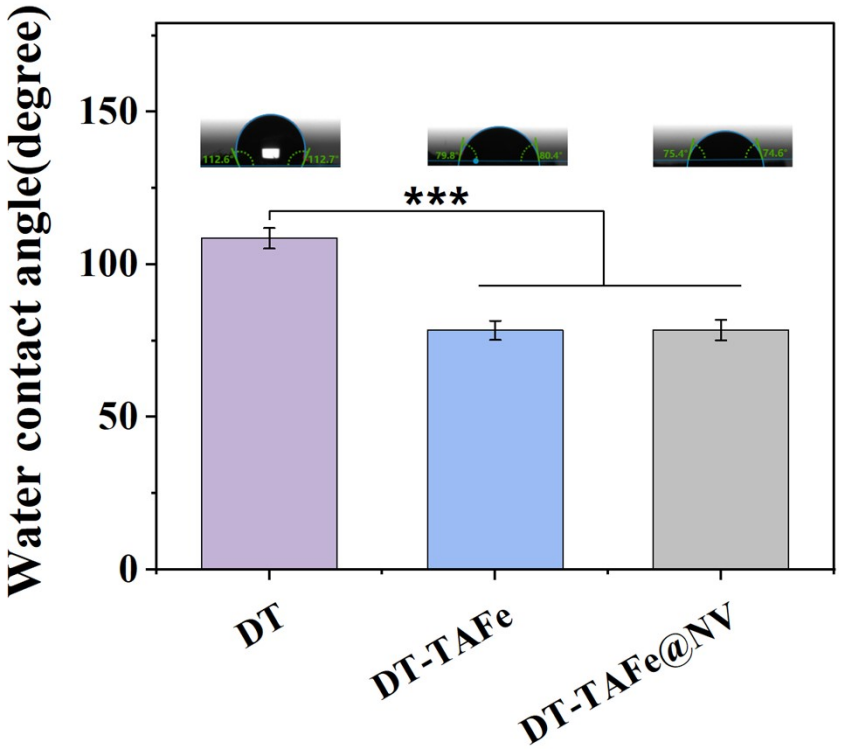

Figure S4. Water contact angles for DT, DT-TAFe and DT-TAFe@NV (n = 3, $p < 0.05$, $p < 0.01$, $p < 0.001$). ***.

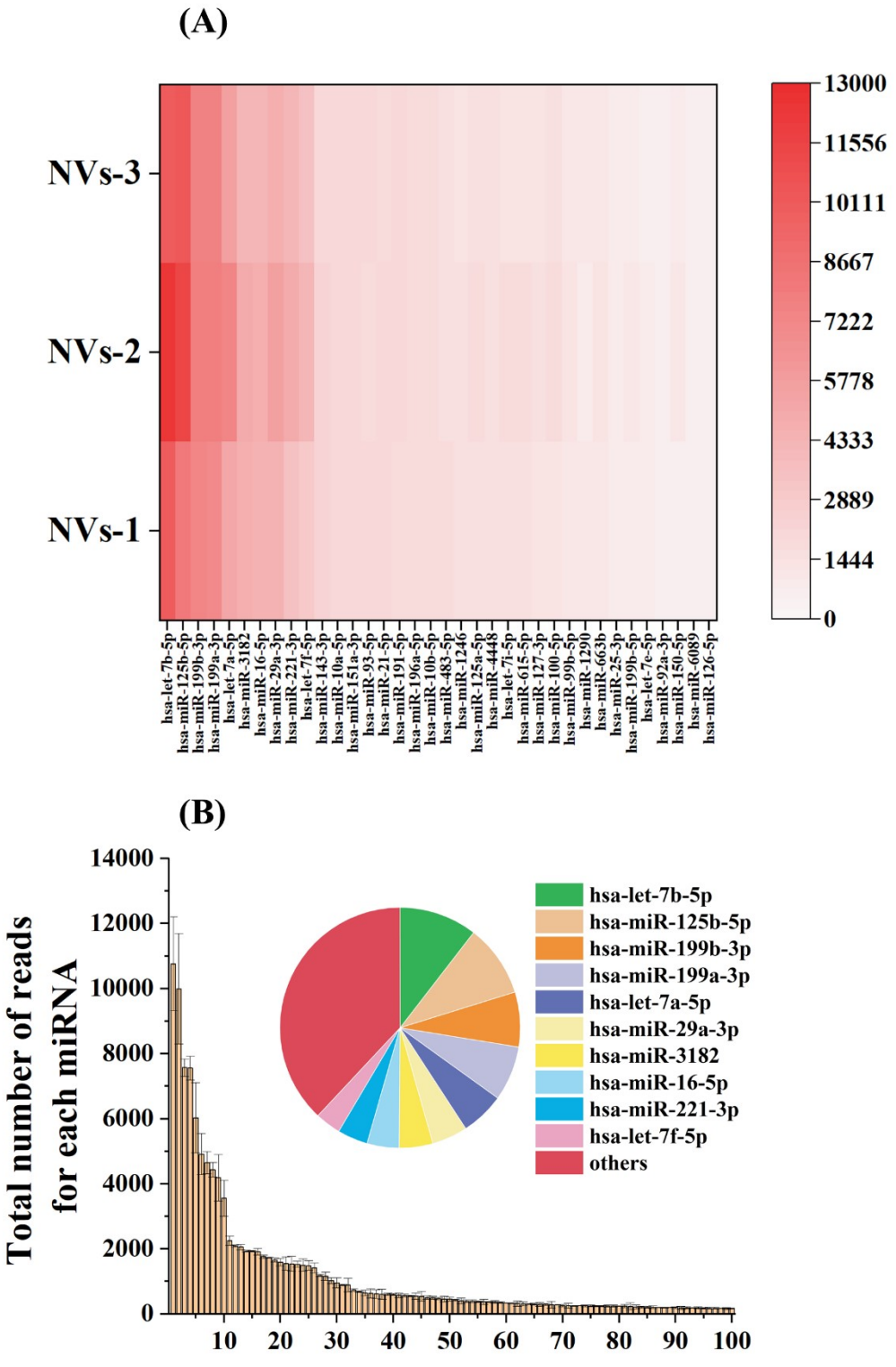

Figure S5. (A)Heatmap of the expression of three groups of SCAPs-NVs, (B) Histogram of miRNAs highly expressed in SCAPs-NVs and pie chart presenting the top 10 expressed micro RNAs.

For miRNA sequencing the library building method of QIAseq was used. Total RNA was first extracted from SCAPs-NV as starting material for library construction. Then, in an unbiased reaction, the junctions are sequentially attached to the '3 and 5' ends of the miRNAs to complete the junction ligation. Next, universal cDNA synthesis is performed and unique molecular indexes (UMIs) are assigned to each miRNA molecule at an early stage to eliminate PCR and sequencing bias. Afterwards, the library is amplified using the QIAseq miRNA Index Kit. Finally, magnetic bead purification is performed again to remove residual impurities. After completing the above steps, the quality of the library is assessed using e.g. Bioanalyzer. Finally, the libraries are sequenced to obtain the amount of miRNA expression.

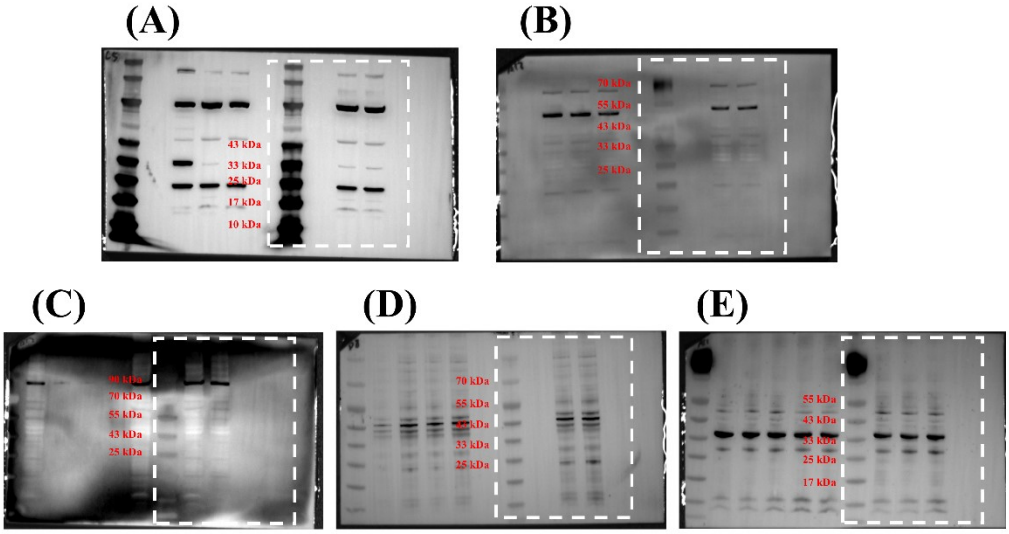

Figure S6. Raw image of western blot result in Fig. 2E. (A, B, C, D, E) A, B, C, D, E are the raw images of the Western blotting results of CD9, CD63, Calnexin, TSG101 and β-actin for each group of samples, respectively.

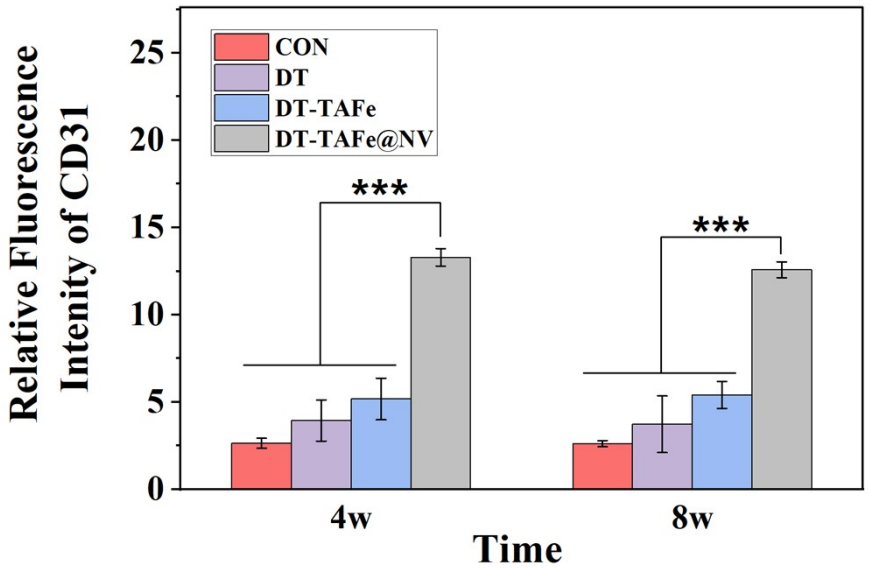

Figure S7. Semi-quantitative analysis of the immunofluorescence intensity of CD31