Figure S1. Analysis of the knockdown of ZNF469 expression in dermal fibroblasts. (A) Uncropped western blots of ZNF469 and GAPDH in dermal fibroblasts (left) and keloid fibroblasts (right) after transfection with sh1-ZNF469 or sh2-ZNF469, with and without Dox induction. These are uncropped versions of the blots shown in Fig. 1B and 6B, respectively. (B) Immunofluorescence staining of ZNF469 in control and ZNF469-knockdown dermal fibroblasts. DAPI nuclear staining is blue and ZNF469 immunostaining is green. ZNF469, zinc finger 469; sh, short hairpin; Dox, doxycycline; MW, molecular weight; DAPI, 4',6-diamidino-2-phenylindole.

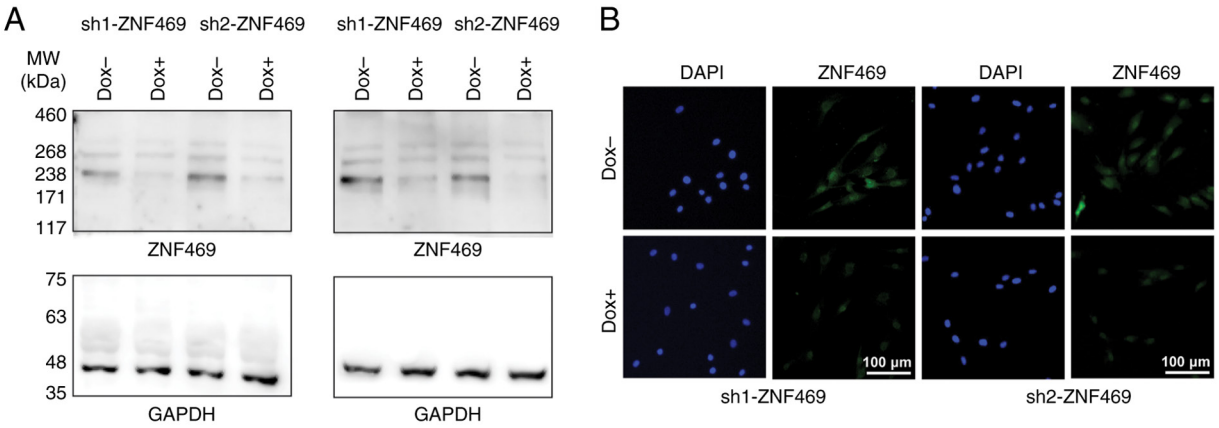

Figure S2. Immunofluorescence staining of type I collagen in dermal fibroblasts following the induction of ZNF469 knockdown by Dox treatment for 8 days. Fluorescent images showing DAPI nuclear staining in blue and type I collagen staining in green were captured under identical exposure settings. These images support the quantitative data in Fig. 1H. Scale bar, 100 μm. ZNF469, zinc finger 469; Dox, doxycycline; sh, short hairpin; DAPI, 4',6-diamidino-2-phenylindole.

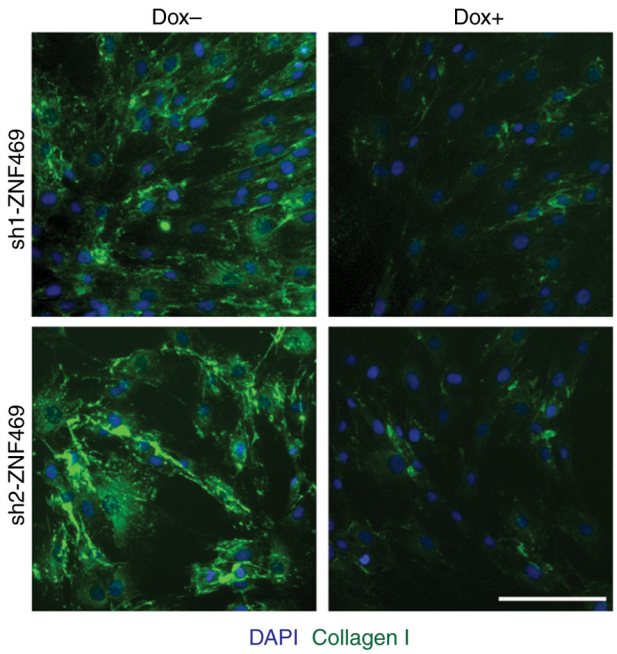

Figure S3. Gene set enrichment analysis leading edge analysis plot. The plot shows leading-edge genes corresponding to the gene expression patterns shown in the heatmap in Fig. 2E, for cells with and without doxycycline-induced zinc finger 469 knockdown.

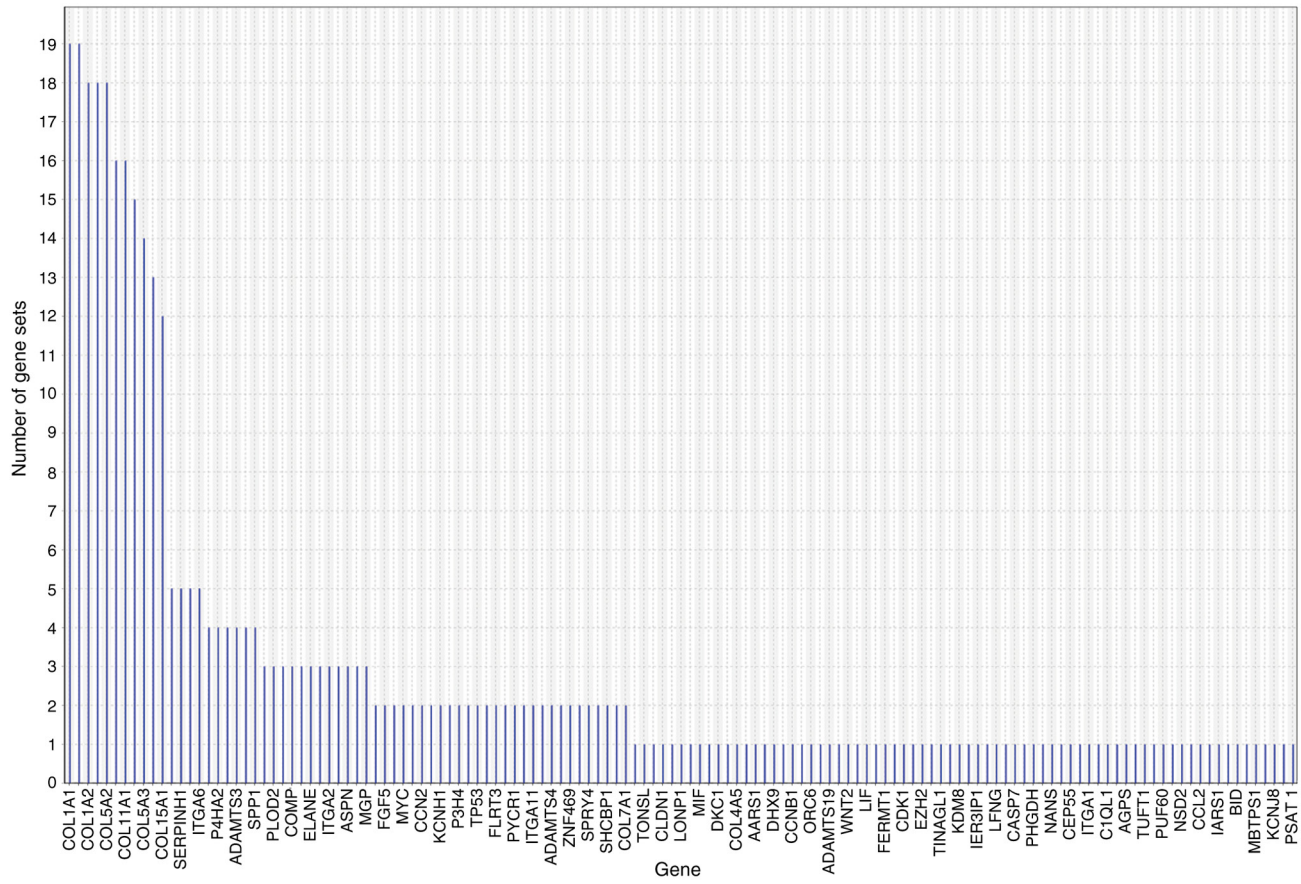

Figure S4. Heat map of angiogenic marker expression based on the RNA-sequencing data of dermal fibroblasts with or without Dox-induced zinc finger 469 knockdown. The red color indicates upregulated gene expression, while blue indicates downregulated gene expression. Dox, doxycycline.

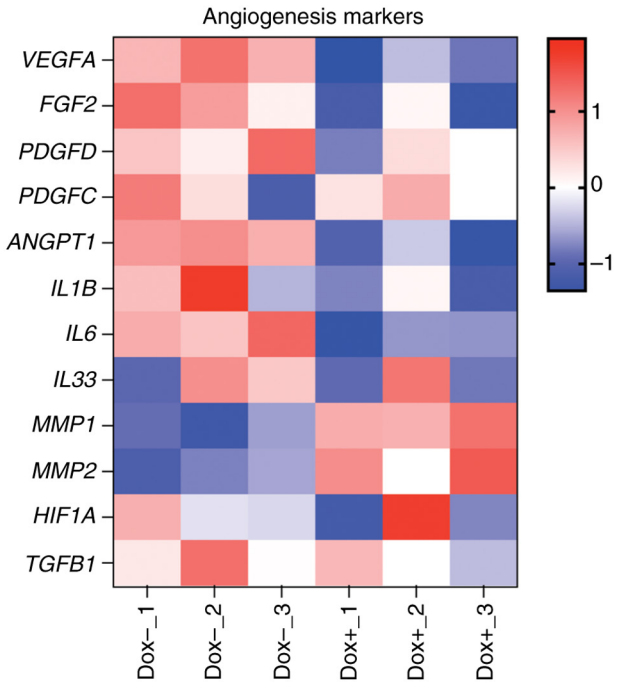

Figure S5. UMAP plots of ZNF469 and COL1A1 expression in scar tissue cell populations. The plots are for individual samples, which are presented in combined form in Fig. 4A. UMAP, Uniform Manifold Approximation and Projection; ZNF469, zinc finger 469; COL1A1, collagen type I α 1; KF, keloid scar fibroblasts; NF, normal scar fibroblasts.

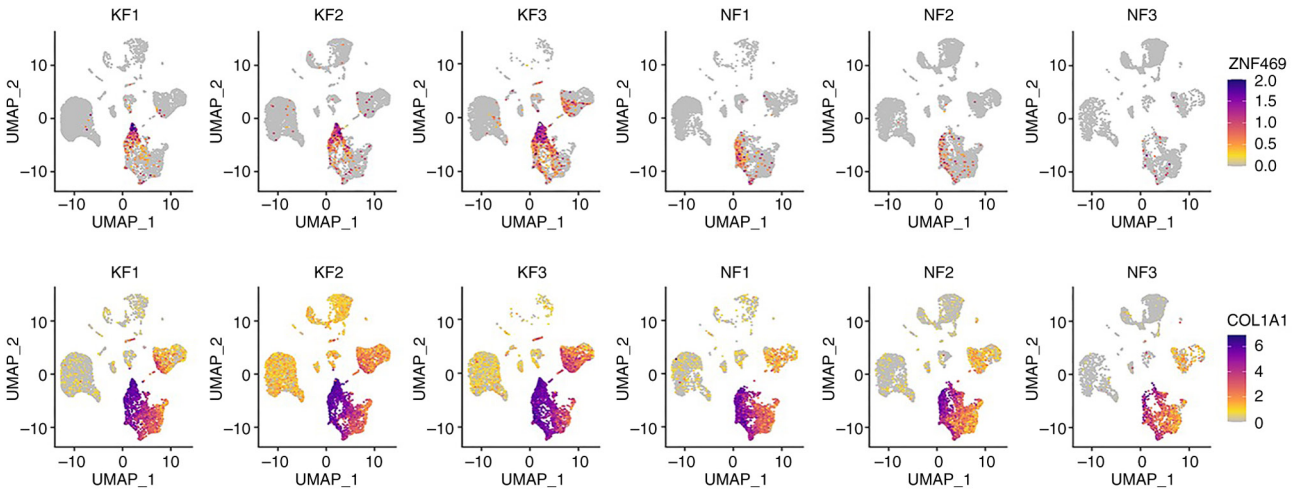

Figure S6. Dot plots for ZNF469 and COL1A1 expression profiles as identified by UMAP-based clustering. Plots are for different (A) scar tissue cell populations and (B) fibroblast subpopulations, and are derived from the UMAP data presented in Fig. 4A and B. ZNF469, zinc finger 469; COL1A1, collagen type I α 1; fib, fibroblast.

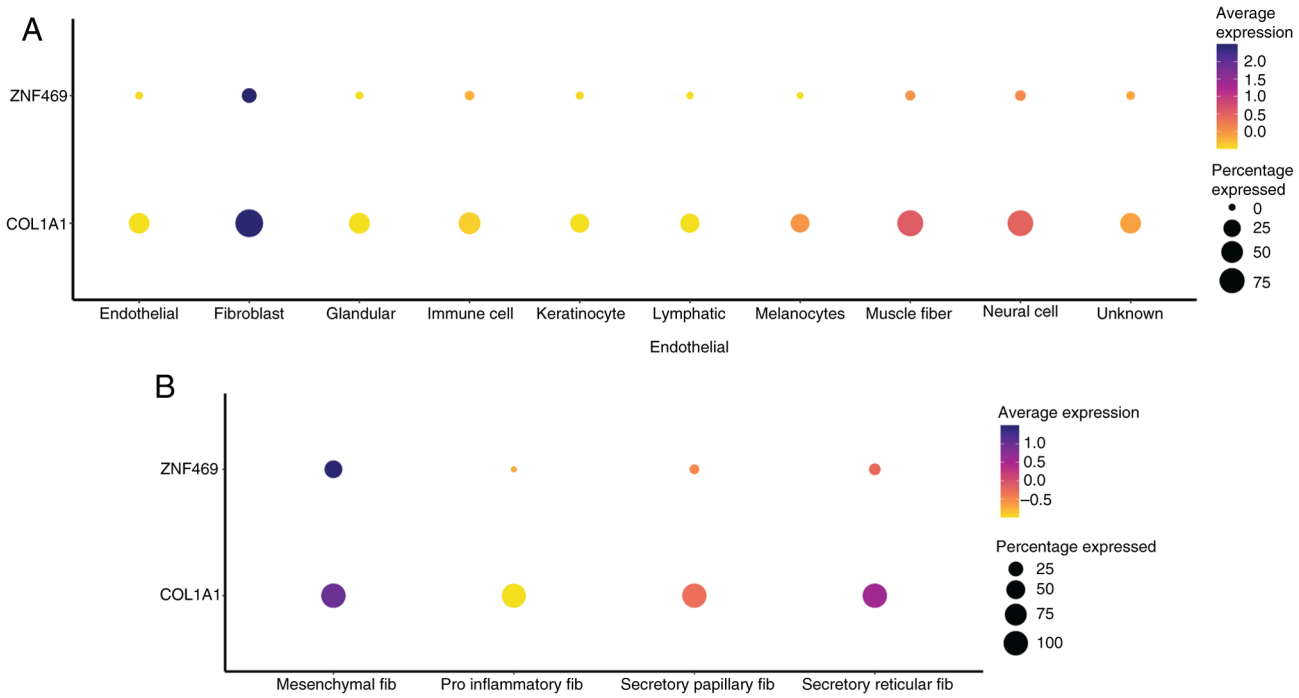
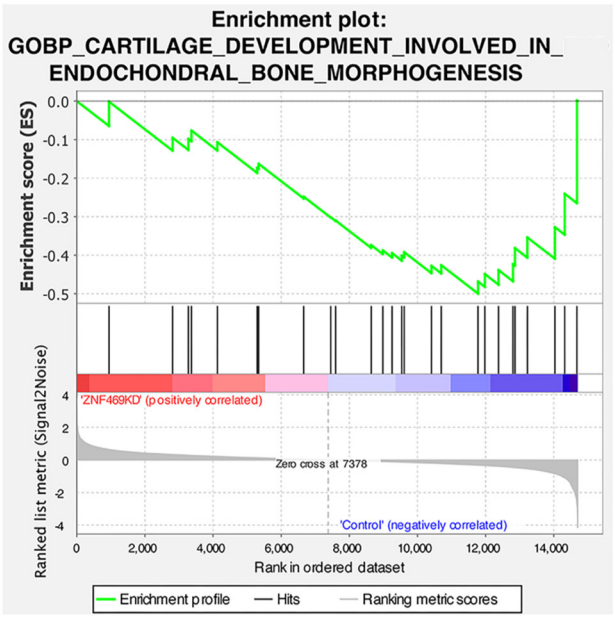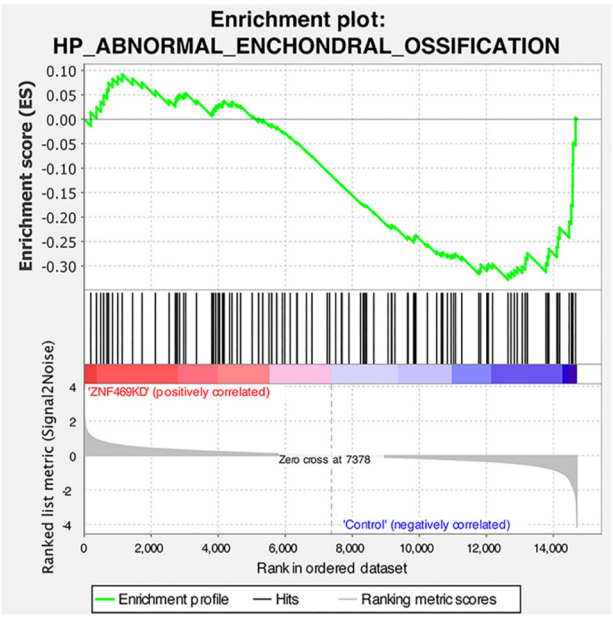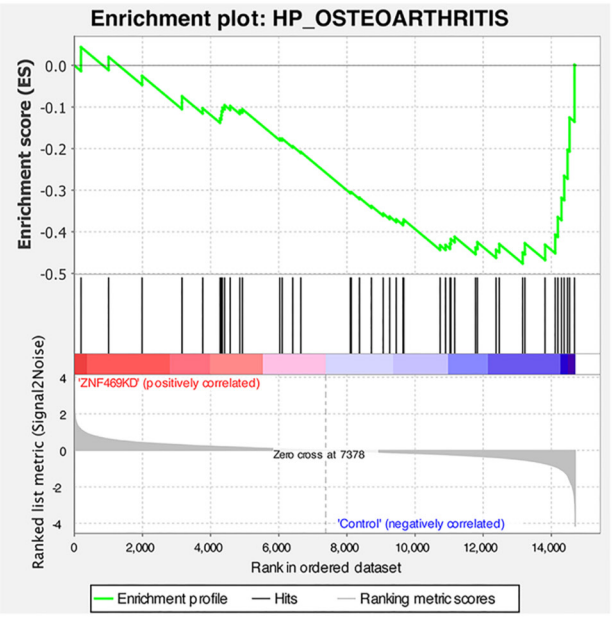
Figure S7. Gene set enrichment analysis plots of bone- and cartilage-related pathways, associated with the results in Fig. 5A and B. GOBP, Gene Ontology biological process; HP, human phenotype.