Video S1. Time-lapse video of HPMECs treated with 10 μM of RA undergoing angiogenesis. Imaging was performed in a pre-equilibrated, humidified incubator chamber maintained at 37°C with 5% CO_2 and approximately 21% oxygen. Images were captured every 20 minutes over a period of 4 hours using an inverted Zeiss Axio Observer widefield epifluorescence microscope with an EC Plan-Neofluar 10×/0.30 objective lens.

Video S2. Time-lapse video of HPMECs treated with ethanol vehicle control. Imaging conditions were identical to those in Video S1, with images taken every 20 minutes for 4 hours in a pre-equilibrated, humidified incubator chamber maintained at 37°C with 5% CO_2 and approximately 21% oxygen, using the same microscope and objective lens.

Tables S1-S6 are provided as a separate Microsoft Excel file.

Table S1. List of DEGs at 40 minutes post-treatment comparing EtOH control and RA-treated HPMECs.

Table S2. List of DEGs at 4 hours post-treatment comparing EtOH control and RA-treated HPMECs.

Table S3. The top 15 upregulated genes at 4 hours post-RA treatment. RARE (retinoic acid response element)-containing genes are highlighted in blue.

Table S4. The top 15 upregulated genes at 40 minutes post-RA treatment. No RARE-containing genes were identified.

Table S5. Evaluation of extracellular TGFα levels in the culture supernatants of HPMECs treated with EtOH control and RA. ELISA assay was performed using a Human TGF-alpha DuoSet ELISA kit.

Table S6. Detailed sample information for microarray profiling.

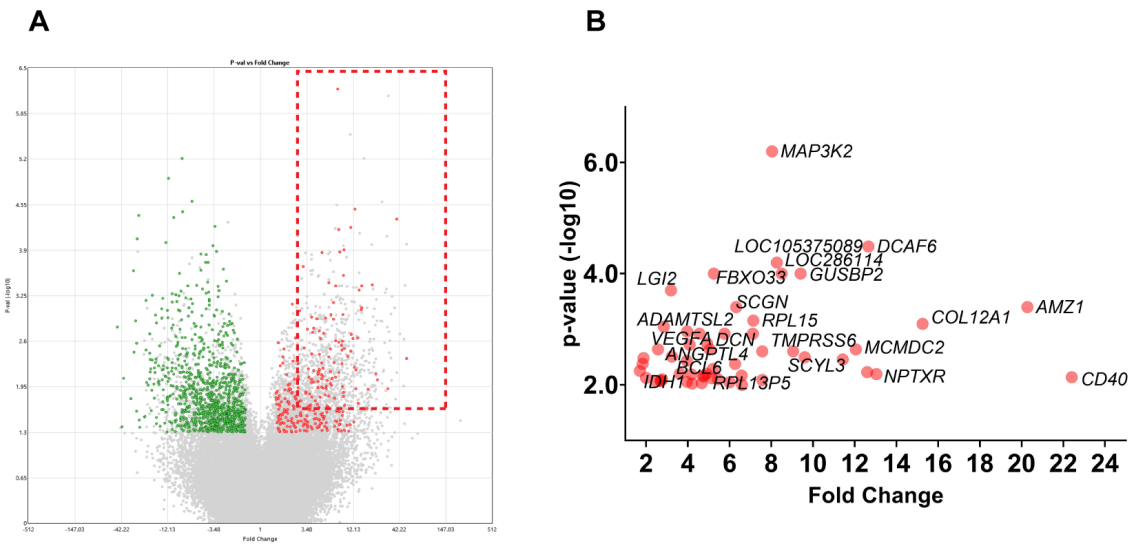

Figure S1. Differentially expressed genes (DEGs) in EtOH control versus RA-treated HPMECs at 40 minutes post-treatment. (A) Volcano plot showing DEGs between EtOH control and RA-treated HPMECs at 40 minutes post-treatment. Upregulated genes are shown in red; downregulated genes are shown in green. **(B)** Extrapolated volcano plot highlighting the top upregulated genes after 40 minutes of RA treatment.

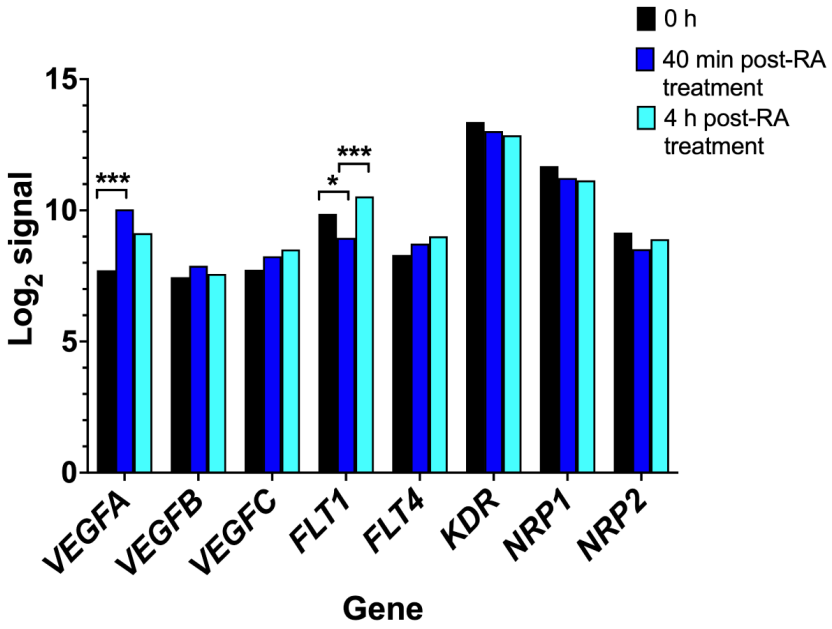

Figure S2. Upregulation of *VEGFA* and *FLT1* in HPMECs following RA treatment. Histogram showing expression levels of key genes in VEGF signalling, including *VEGFA, VEGFB, VEGFC*, *FLT1* (*VEGFR1), FLT4 (VEGFR3), KDR (VEGFR2), NRP1, and NRP2*.

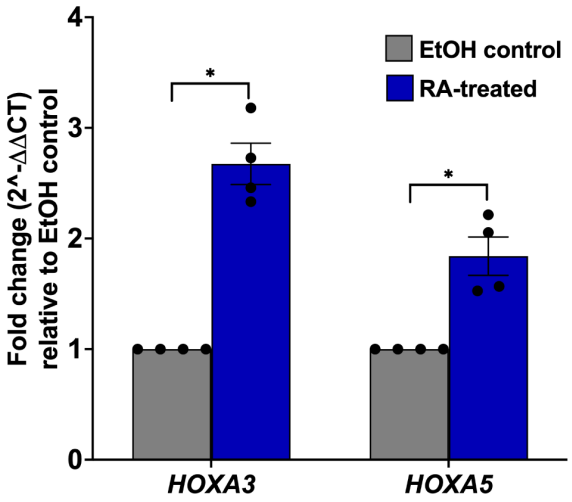

Figure S3. Upregulation of *HOXA3 and HOXA5* in RA-treated HPMECs. Histogram showing increased transcript levels of *HOXA3* and *HOXA5* at 4 hours post-RA treatment, assessed by qRT-PCR. HPMEC monolayers were cultured on fibronectin-coated plates. *HOXA3* and *HOXA5* were among the top upregulated genes identified in the microarray analysis. $n = 4$ independent experiments; each experiment was run in triplicate. Each dot represents the mean value per experiment. Data are presented as mean ± SEM; Mann–Whitney *U*-test, $*p < 0.05$.

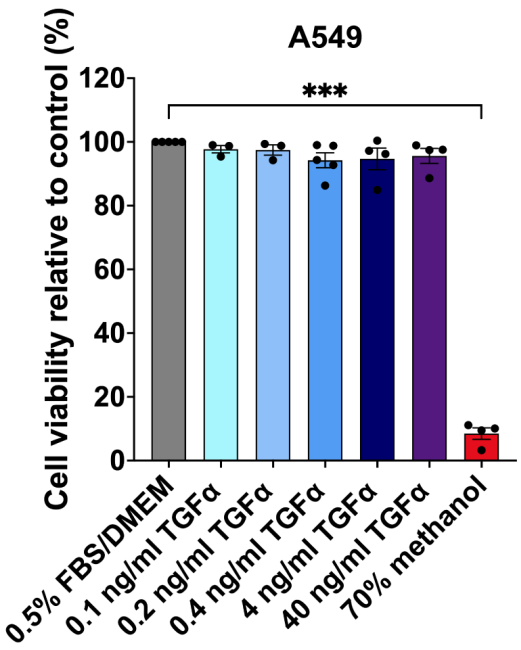

Figure S4. MTT metabolic assay results in A549 cells. Histogram showing cell viability in A549 cells treated with varying concentrations of TGFα. DMEM with 0.5% FBS served as a negative control, and 70% methanol-treated cells served as a positive control for cell death. Data are presented as mean ± SEM; Kruskal-Wallis with Dunn's multiple comparisons test, ***$p < 0.001$.

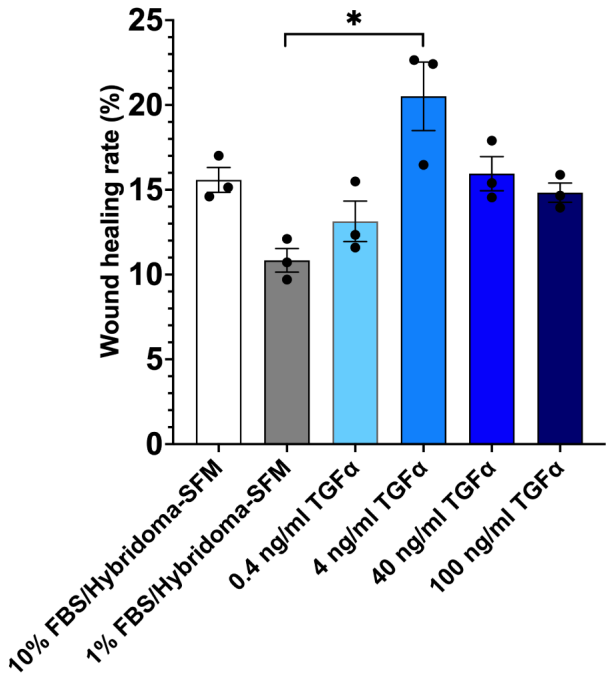

Figure S5. TGFα promotes wound healing in hAT2 cells in a dose-dependent manner. Histogram showing the percentage of wound healed at 24 hours post-scratch in hAT2 cells treated with hybridoma medium containing 10% FBS (positive control), hybridoma medium with 1% FBS (negative control), or varying concentrations of recombinant TGFα (0.4 ng/ml, 4 ng/ml, 40 ng/ml, and 200 ng/ml). *n* = hAT2 cells from 1 donor; three technical replicates per experiment; each dot represents a technical replicate. Data are presented as mean ± SEM; Kruskal-Wallis with Dunn's multiple comparisons test, **p* < 0.05.

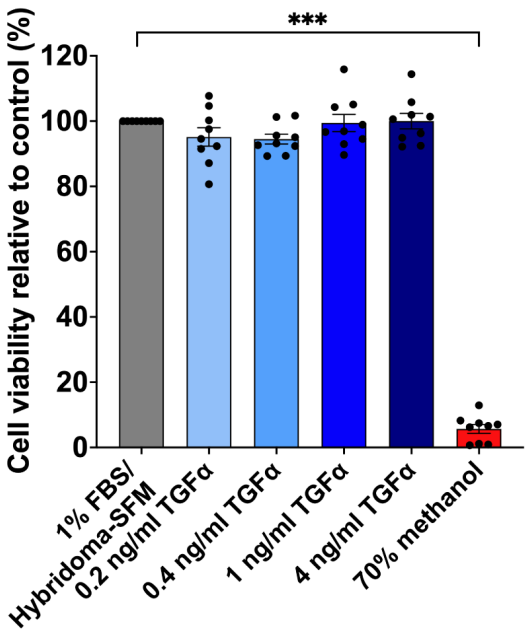

Figure S6. MTT cell viability assay in hAT2 cells. Histogram showing cell viability in hAT2 cells treated with different concentrations of TGFα (0.2 ng/ml, 0.4 ng/ml, 1 ng/ml, and 4 ng/ml). Hybridoma medium with 1% FBS served as a negative control, and 70% methanol-treated cells served as a positive control for cell death. *n* = hAT2 cells from 3 donors; three technical replicates per experiment; each dot represents a technical replicate. Data are presented as mean ± SEM; Kruskal-Wallis with Dunn's multiple comparisons test, ***$p < 0.001$.

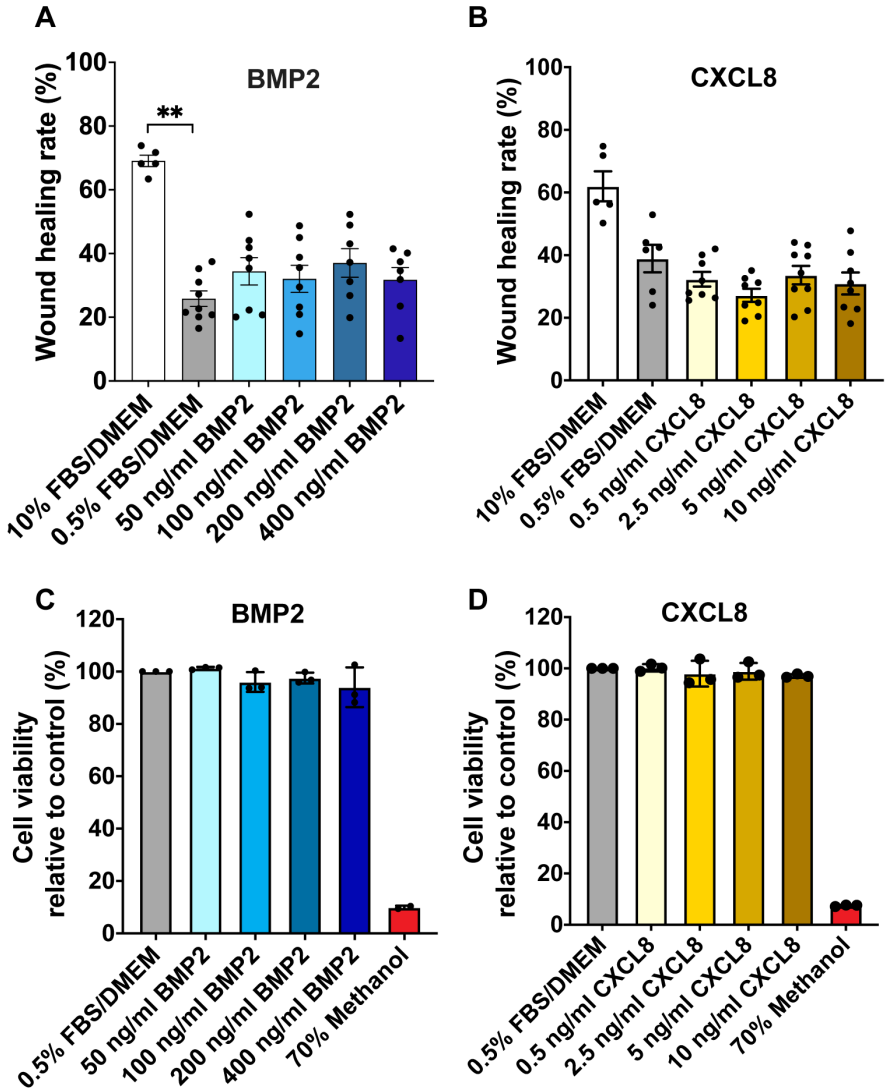

Figure S7. BMP2 and CXCL8 do not affect wound healing in A549 cells. (A-B) Percentage of wound healed at 24 hours in A549 cells treated with DMEM/10% FBS (positive control), DMEM/1% FBS (negative control), or varying concentrations of BMP2 (50 ng/ml, 100 ng/ml, 200 ng/ml, and 400 ng/ml BMP2) **(A),** and CXCL8 (0.5 ng/ml, 2.5 ng/ml, 5 ng/ml, 10 ng/ml CXCL8) **(B). (C-D)** Histograms showing cell viability in A549 cells treated with different concentrations of BMP2 and CXCL8. DMEM with 0.5% FBS served as a negative control, and 70% methanol-treated cells served as a positive control for cell death. *n* = three independent experiments; two or three technical replicates per experiment; each dot represents the mean value per experiment. Data are presented as mean ± SEM; Kruskal-Wallis with Dunn's multiple comparisons test, *$p < 0.01$.

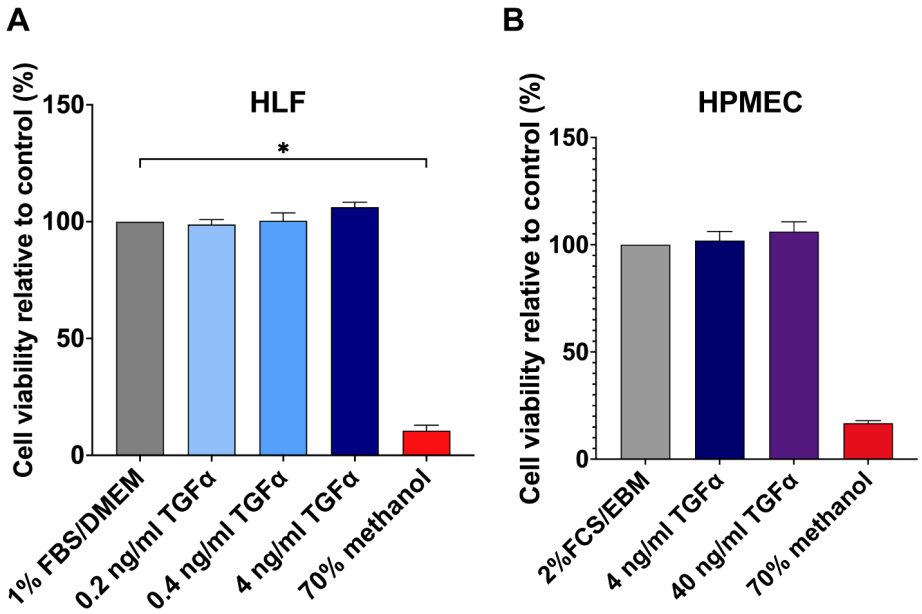

Figure S8. Assessment of cell viability in HLFs and HPMECs using MTT metabolic assays. (A-B) Cell viability in HLFs treated with TGFα at 0.2 ng/ml, 0.4 ng/ml, and 4 ng/ml **(A)** and HPMECs (4 ng/ml and 40 ng/ml) **(B)**. DMEM with 1% FBS and EBM with 2% FCS served as negative controls for HLFs and HPMECs, respectively, while 70% methanol-treated cells served as a positive control for cell death. For HLFs: *n* = HLFs from 3 donors; three technical replicates per experiment. For HPMECs: *n* = 1 experiment run in triplicate. Data are presented as mean ± SEM; Kruskal-Wallis with Dunn's multiple comparisons test was performed for HLFs, ***$p < 0.001$.

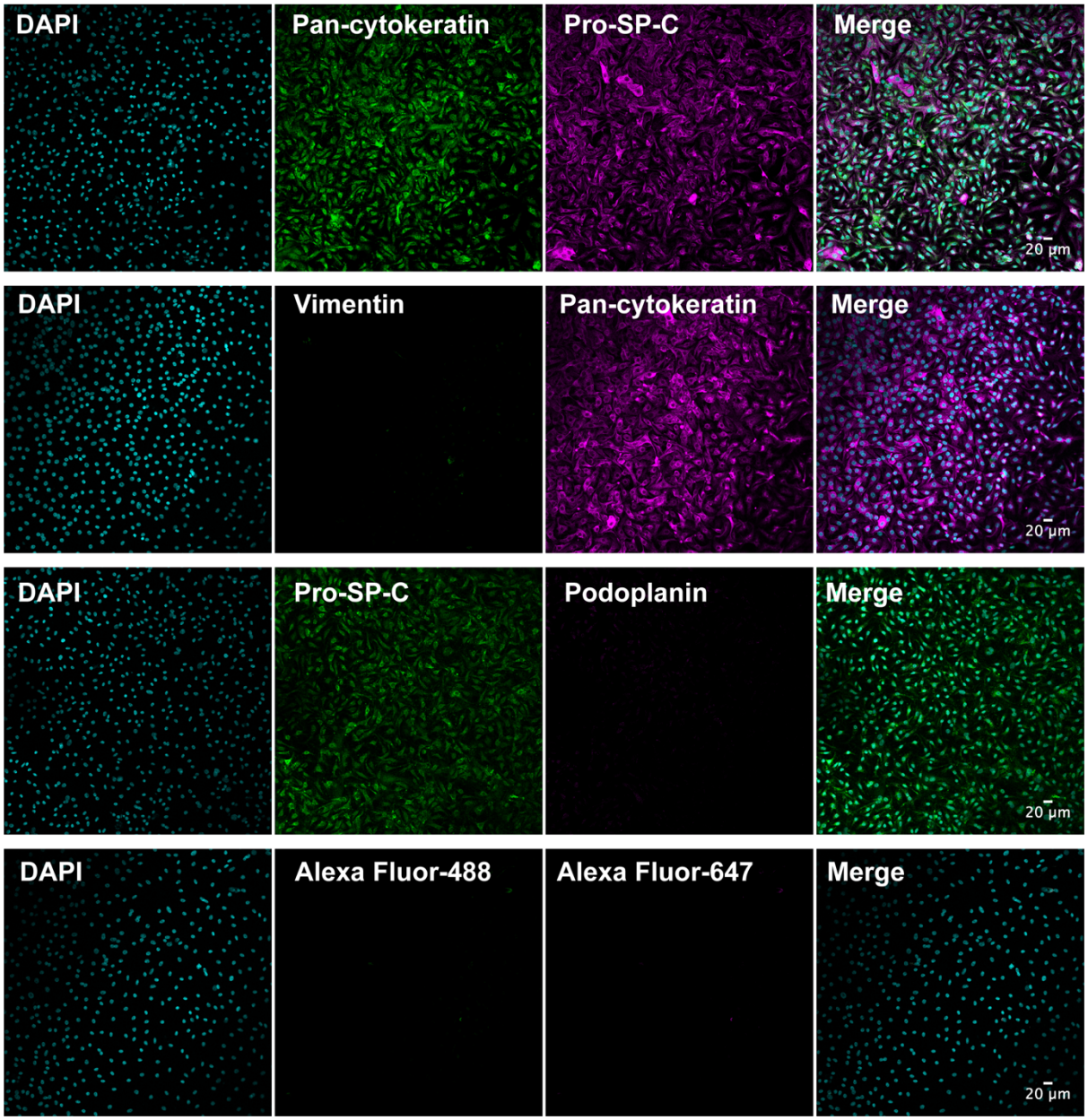

Figure S9. Immunostaining of hAT2 cells to confirm cell specificity. Representative images of hAT2 cells immunostained for pan-cytokeratin (a pan-epithelial marker), Pro-SPC (an AT2 cell marker), vimentin (a fibroblast marker), and podoplanin (PDPN; an AT1 cell marker) at 68 hours post-seeding. Negative controls lacking primary antibody are shown in the bottom panels. Nuclei were counterstained with DAPI (cyan). Images were captured using a Leica SP8 inverted confocal microscope with a HC PL APO 10×/0.40 air objective lens.