

Supplementary Information

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Supplementary Tables (Tables S1 is provided as separate excel files):

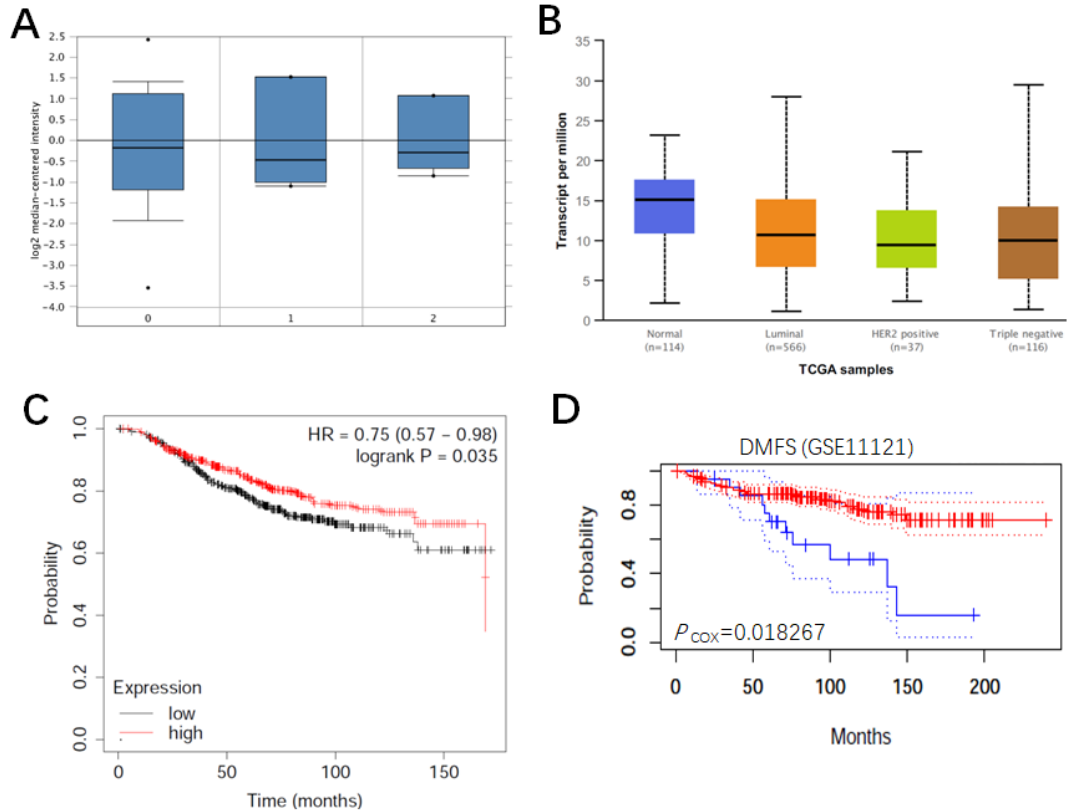
Supplementary Table S1. RNA-seq analysis of human tumor cells overexpressing Roquin2.

Supplementary Table S2. PCRarray analysis of human tumor angiogenesis genes regulated by Roquin2.

Supplementary Table S3. List of PCR Primer Sequences used in this study.

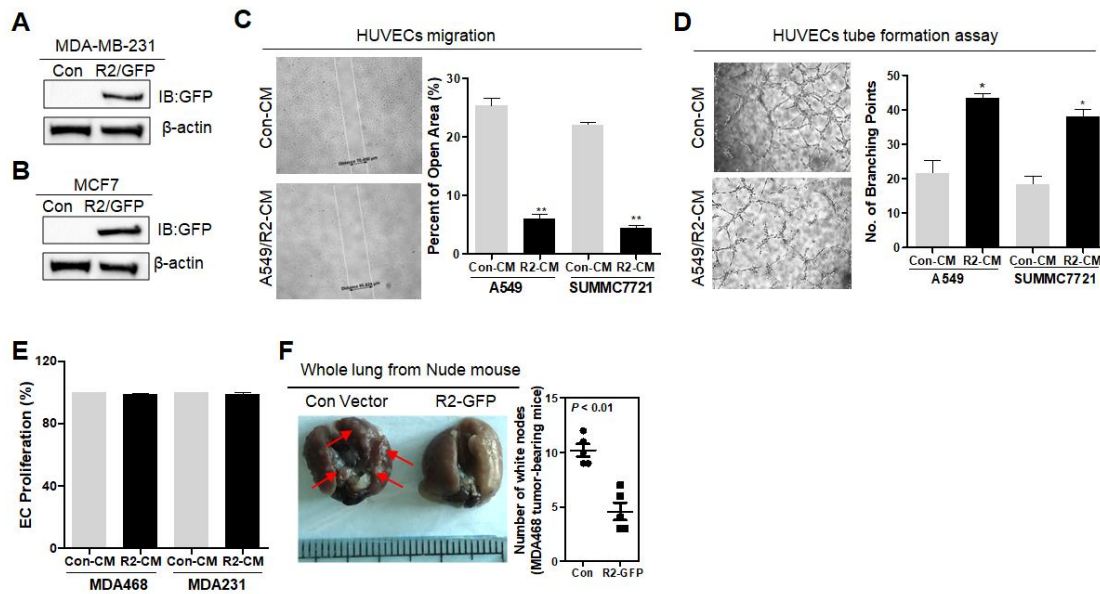
Supplementary Figures

Supplementary Fig. S1



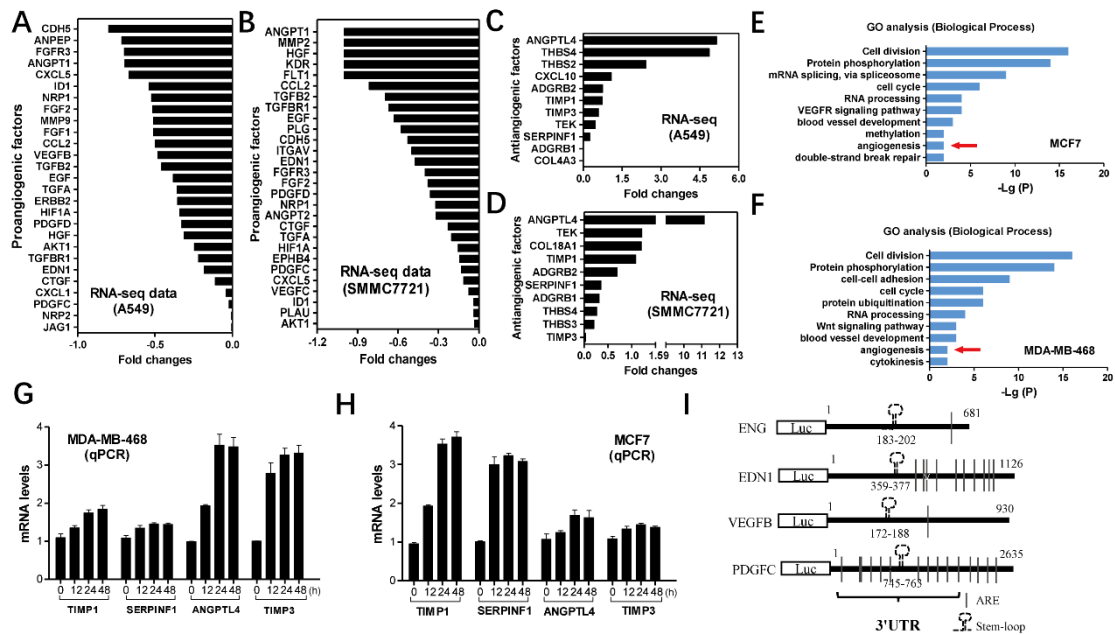
Supplementary Fig. S1. Roquin2 expression is reduced in breast cancers. (A) Comparison of Roquin2 mRNA expression between normal (0) ($n = 20$), invasive ductal breast carcinoma (1) ($n = 5$), and invasive lobular breast carcinoma (2) ($n = 5$). (<http://www.oncomine.org/>) (B) The expression levels of the Roquin2 gene were analyzed by the major subclasses of breast cancer based on the TCGA data. (<http://ualcan.path.uab.edu/index.html>) (C) Kaplan-Meier Overall Survival curve of breast cancer patients with low and high tumor Roquin2 transcripts. (<http://kmplot.com/analysis/>) (D) Kaplan-Meier Distant Metastasis Free Survival curve of breast cancer patients with low and high tumor Roquin2 transcripts. (<http://dna00.bio.kyutech.ac.jp/Prognoscan/index.html>)

Supplementary Fig. S2



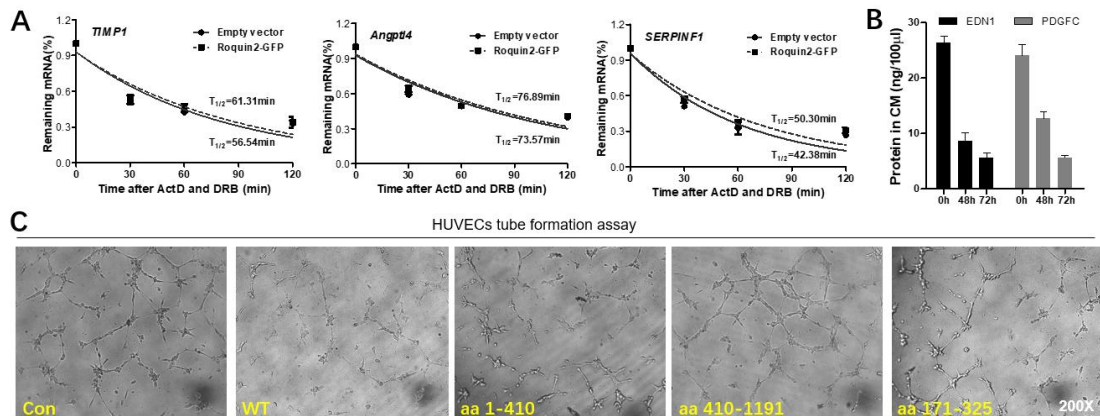
Supplementary Fig. S2. Roquin2 inhibits tumor cells-induced angiogenesis. (A, B) Cell lysates from MDA-MB-231 (A) and MCF7 (B) cells expressing Roquin2-GFP fusion protein or GFP were harvested for immunoblotting analysis with anti-GFP and anti- β -actin antibodies. (C) Left: Representative photographs of migrated HUVECs after treatment 24 hours with CMs from Roquin2-overexpressing A549 and its control A549/GFP cells. Right: Quantification of the percentage of open area of HUVECs treated with indicated tumor CMs in the wound-healing assay. (D) Left: Representative photographs of tube-formed HUVECs after treatment 12 hours with CMs from Roquin2-overexpressing A549 and its control A549/GFP cells. Right: Quantification of the number of branching points of HUVECs treated with indicated tumor CMs in the tube formation assay. (E) CMs of Roquin2-expressing tumor cells had no effect on HUVECs proliferation expressed as percentage of untreated cells. (F) Left: Whole lung from nude mice bearing MDA-MB-468/GFP (control vector) or MDA-MB-468/Roquin2-GFP (R2-GFP) tumors was collected and compared. Right: Quantification of metastatic white nodules. Results shown represent the mean \pm SEM of at least three independent experiments; * $P < 0.05$; ** $P < 0.01$, unpaired Student's t-test.

Supplementary Fig. S3



Supplementary Fig. S3. Roquin2 downregulates proangiogenic factors mRNA expression by targeting 3'UTR. (A-D) RNA-sequencing data showing the proangiogenic factors mRNA were downregulated by Roquin2 in A549 (A) and SMMC7721 (B) cells, and the antiangiogenic factors mRNAs were upregulated by Roquin2 in A549 (C) and SMMC7721 (D) cells. (E, F) 'Angiogenesis' term was significant enriched as a GO terms for all regulated genes by Roquin2 in MDA-MB-468 (E) and MCF-7 (F) cells. (G, H) qPCR showing the antiangiogenic factors mRNAs were upregulated by Roquin2 without a time dependent manner in MDA-MB-468 (G) and MCF7 (H) cells. (I) Schematic representation of the luciferase reporter constructs containing 3'UTRs sequences of *ENG*, *EDN1*, *VEGFB*, and *PDGFC*.

Supplementary Fig. S4



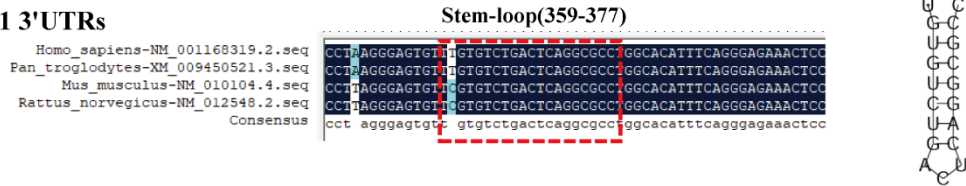
Supplementary Fig. S4. Roquin2 destabilizes mRNAs of proangiogenic factors via the ROQ domain. (A) Half-lives of indicated antiangiogenic factors mRNA were measured by qPCR in MDA-MB-231/Roquin2 cells. (B) ELISA quantification of EDN1 and PDGFC in serum-free culture medium of MDA-MB-231/Roquin2 cells at indicated times. Data are expressed in ng/100 μ l of CM. (C) Representative photographs of tube-formed HUVECs treated with indicated tumor CMs in the tube formation assay.

Supplementary Fig. S5

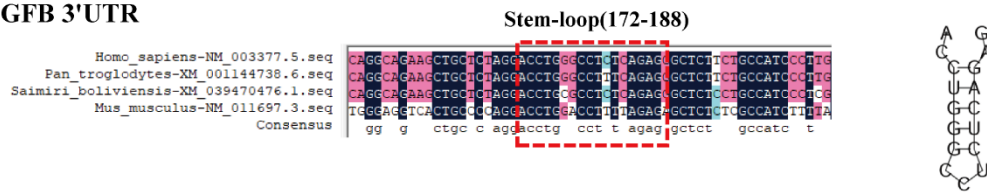
A *ENG* 3'UTRs



B *EDN1* 3'UTRs



C *VEGFB* 3'UTR



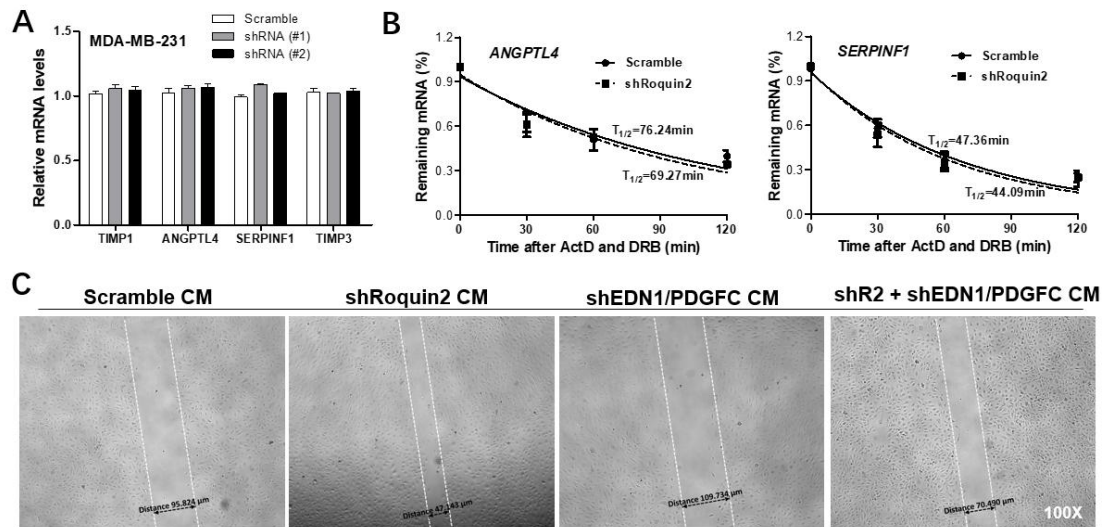
D *PDGFC* 3'UTRs



Supplementary Fig. S5. Putative stem-loop structure in the 3'UTRs of proangiogenic genes.

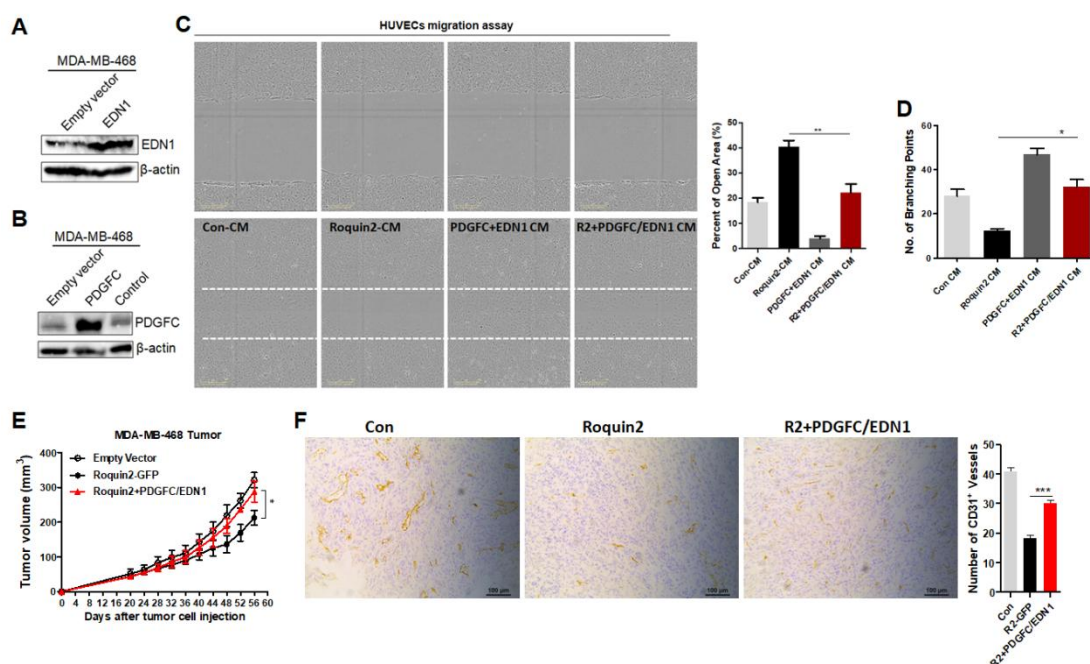
(A-D) The 3'UTR sequences from different species for each proangiogenic gene, including *ENG* (A), *EDN1* (B), *VEGFB* (C), and *PDGFC* (D), was aligned using DNAMAN software. The stem-loop sequences were predicted by RNAfold web server to fold a secondary stem-loop structure (right) and indicated by red box.

Supplementary Fig. S6



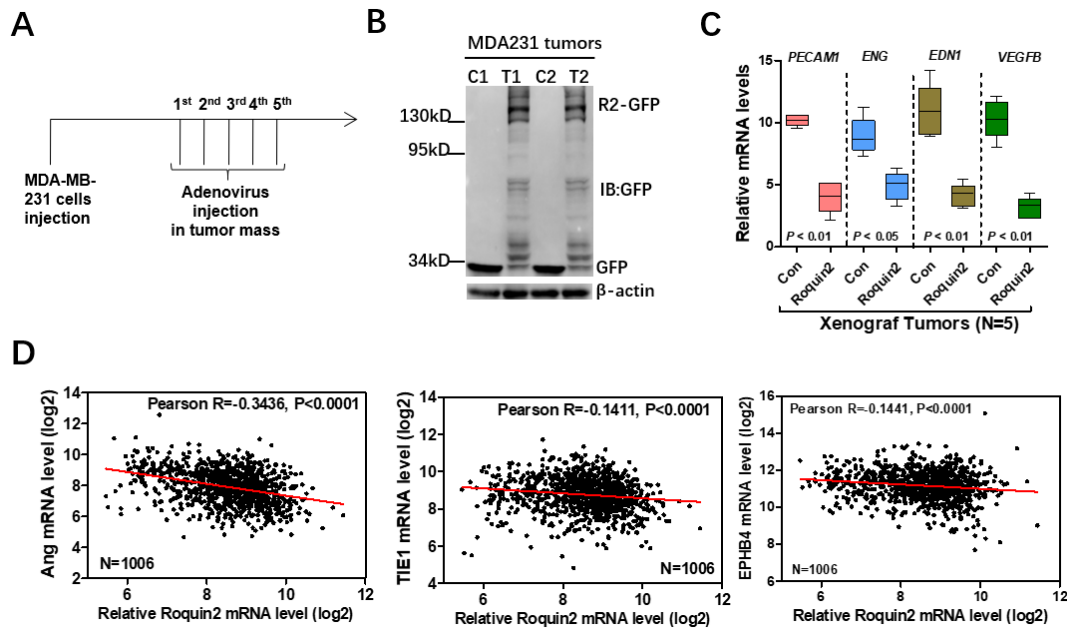
Supplementary Fig. S6. Roquin2 depletion increases proangiogenic gene transcripts stability and promotes tumor angiogenesis. (A) The antiangiogenic factors mRNAs were measured in the MDA-MB-231 cells after knocking down Roquin2 by qPCR. (B) The half-lives of *ANGPTL4* and *SERPINF1* were measured by qPCR in MDA-MB-231 cells after Roquin2 knockdown. (C) Representative photographs of migrated HUVECs treated with indicated tumor CMs in the wound-healing assay.

Supplementary Fig. S7



Supplementary Fig. S7. EDN1 and PDGFC overexpression reversed the inhibitory effects of Roquin2 on tumor angiogenesis. (A, B) EDN1 (A) and PDGFC (B) protein levels were measured in MDA-MB-468 cells by immunoblotting with anti-EDN1, anti-PDGFC and anti- β -actin antibodies. β -actin was used as a loading control. (C) Left: Representative photographs of migrated HUVECs after treatment 24 hours with indicated CMs from MDA-MB-468 cells. Right: Quantification of the percentage of open area of HUVECs treated with indicated tumor CMs in the wound-healing assay. (D) Quantification of the number of branching points of HUVECs treated with indicated tumor CMs in the tube formation assay. (E) Tumor growth curves in nude mice received MDA-MB-468/Roquin2-GFP, MDA-MB-468/Roquin2-GFP/EDN1+PDGFC and their control cells ($n = 6/\text{group}$). (F) Left: Representative histological sections from MDA-MB-468/GFP, MDA-MB-468/Roquin2 and MDA-MB-468/Roquin2/EDN1+PDGFC tumors stained with a specific anti-CD31 antibody. Scale bar, 100 μm . Right: Quantification of the number of CD31⁺ vessels per section. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.

Supplementary Fig. S8



Supplementary Fig. S8. Adenoviral expressing Roquin2 suppresses tumor progression and angiogenesis of the established breast tumors. (A) Experimental flow chart for tumor treatment with Roquin2-expressing adenovirus *in vivo*. MDA-MB-231 cells (3×10^6 cells/100 μ L PBS) were injected into nude mice to establish tumor mass. Tumors were treated with adenovirus every one day when tumors grow to ~ 5 mm in diameter. (B) Roquin2-GFP fusion protein expression in xenograft tumors was confirmed by immunoblotting with an anti-GFP antibody. (C) Measurement of the expression levels of *PECAM1*, *ENG*, *EDN1*, and *VEGFB* in Xenograft tumors. (D) Pearson's Correlation analysis between *Roquin2* and *angiogenin* (*ANG*), *Tie1*, and *EPHB4* expression levels in log₂ values in human breast cancer patients ($n = 1006$).

Supplementary Table S2. PCRarray analysis of human tumor angiogenesis genes regulated by Roquin2

| Gene Symbol | Gene Name | Control | Roquin2-Ov erepression | fold change |
|-------------|--|---------|---------------------------|----------------|
| AKT1 | V-akt murine thymoma viral oncogene homolog 1 | 29.13 | 29.46 | -0.09 |
| ANG | Angiogenin, ribonuclease, RNase A family, 5 | 26.01 | 27.92 | -0.69 |
| ANGPT1 | Angiopoietin 1 | 32.45 | 32.68 | -0.02 |
| ANGPT2 | Angiopoietin 2 | 32.46 | 32.33 | 0.26 |
| ANGPTL4 | Angiopoietin-like 4 | 30.12 | 29.07 | 1.38 |
| ANPEP | Alanyl (membrane) aminopeptidase | 30.55 | 33.07 | -0.80 |
| BAI1 | Brain-specific angiogenesis inhibitor 1 | 35.16 | 36.55 | -0.56 |
| CCL11 | Chemokine (C-C motif) ligand 11 | - | - | NA |
| CCL2 | Chemokine (C-C motif) ligand 2 | 30.11 | 33.42 | -0.88 |
| CDH5 | Cadherin 5, type 2 (vascular endothelium) | 37.53 | 37.01 | 0.65 |
| COL18A1 | Collagen, type XVIII, alpha 1 | 31.45 | 31.09 | 0.47 |
| COL4A3 | Collagen, type IV, alpha 3 (Goodpasture antigen) | 32.12 | 31.09 | 1.35 |
| CTGF | Connective tissue growth factor | 30.45 | 31.95 | -0.59 |
| CXCL1 | Chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) | 24.06 | 25.80 | -0.64 |
| CXCL10 | Chemokine (C-X-C motif) ligand 10 | 32.14 | 32.06 | 0.21 |
| CXCL5 | Chemokine (C-X-C motif) ligand 5 | 22.21 | 26.44 | -0.94 |
| CXCL6 | Chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2) | - | - | NA |
| CXCL9 | Chemokine (C-X-C motif) ligand 9 | 38.35 | 38.32 | 0.17 |
| EDN1 | Endothelin 1 | 21.61 | 24.54 | -0.85 |
| EFNA1 | Ephrin-A1 | 28.38 | 28.34 | 0.18 |
| EFNB2 | Ephrin-B2 | 32.36 | 30.96 | 2.03 |
| EGF | Epidermal growth factor | 34.08 | 36.04 | -0.70 |
| ENG | Endoglin | 32.07 | 35.46 | -0.89 |
| EPHB4 | EPH receptor B4 | 27.15 | 29.88 | -0.83 |
| ERBB2 | V-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian) | 31.02 | 33.12 | -0.73 |
| F3 | Coagulation factor III (thromboplastin, tissue factor) | 30.83 | 29.82 | 1.31 |
| FGF1 | Fibroblast growth factor 1 (acidic) | 35.12 | 36.37 | -0.52 |
| FGF2 | Fibroblast growth factor 2 (basic) | 25.15 | 26.51 | -0.55 |
| FGFR3 | Fibroblast growth factor receptor 3 | 31.07 | 33.91 | -0.84 |
| FIGF | C-fos induced growth factor (vascular endothelial growth factor D) | 33.35 | 33.25 | 0.23 |
| FLT1 | Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor) | - | - | NA |
| FN1 | Fibronectin 1 | 27.88 | 26.94 | 1.20 |
| HGF | Hepatocyte growth factor (hepapoietin A; scatter factor) | 34.10 | 34.43 | -0.08 |
| HIF1A | Hypoxia inducible factor 1, alpha subunit (basic) | 26.12 | 27.79 | -0.64 |

| | | | | |
|----------|--|-------|-------|-------|
| | helix-loop-helix transcription factor) | | | |
| HPSE | Heparanase | 29.01 | 30.31 | -0.53 |
| ID1 | Inhibitor of DNA binding 1, dominant negative helix-loop-helix protein | 22.12 | 23.84 | -0.65 |
| IFNA1 | Interferon, alpha 1 | 34.87 | 33.01 | 3.16 |
| IFNG | Interferon, gamma | - | - | NA |
| IGF1 | Insulin-like growth factor 1 (somatomedin C) | 33.11 | 33.13 | 0.13 |
| IL1B | Interleukin 1, beta | 32.25 | 33.10 | -0.36 |
| IL6 | Interleukin 6 (interferon, beta 2) | 28.85 | 30.03 | -0.50 |
| IL8 | Interleukin 8 | 27.02 | 27.37 | -0.10 |
| ITGAV | Integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) | 29.48 | 30.30 | -0.35 |
| ITGB3 | Integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) | 36.25 | 34.55 | 2.73 |
| JAG1 | Jagged 1 | 28.03 | 28.30 | -0.05 |
| KDR | Kinase insert domain receptor (a type III receptor tyrosine kinase) | - | - | NA |
| LECT1 | Leukocyte cell derived chemotaxin 1 | - | - | NA |
| LEP | Leptin | 33.76 | 34.02 | -0.04 |
| MDK | Midkine (neurite growth-promoting factor 2) | 33.55 | 34.32 | -0.33 |
| MMP14 | Matrix metalloproteinase 14 (membrane-inserted) | - | - | NA |
| MMP2 | Matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) | 30.11 | 31.99 | -0.69 |
| MMP9 | Matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase) | 30.05 | 29.12 | 1.19 |
| NOS3 | Nitric oxide synthase 3 (endothelial cell) | - | - | NA |
| NOTCH4 | Notch 4 | 35.33 | 33.55 | 2.94 |
| NRP1 | Neuropilin 1 | 26.15 | 26.06 | 0.22 |
| NRP2 | Neuropilin 2 | 28.25 | 28.09 | 0.28 |
| PDGFA | Platelet-derived growth factor alpha polypeptide | 25.14 | 26.65 | -0.60 |
| PECAM1 | Platelet/endothelial cell adhesion molecule | 30.63 | 33.18 | -0.80 |
| PF4 | Platelet factor 4 | 34.03 | 34.71 | -0.28 |
| PGF | Placental growth factor | 28.35 | 29.42 | -0.45 |
| PLAU | Plasminogen activator, urokinase | 28.60 | 29.46 | -0.37 |
| PLG | Plasminogen | 34.26 | 38.48 | -0.94 |
| PROK2 | Prokineticin 2 | - | - | NA |
| PTGS1 | Prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) | 36.45 | 35.03 | 2.07 |
| S1PR1 | Sphingosine-1-phosphate receptor 1 | 35.98 | 35.24 | 0.92 |
| SERPINE1 | Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 | 27.57 | 27.77 | 0 |
| SERPINF1 | Serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1 | 32.06 | 32.53 | -0.17 |
| SPHK1 | Sphingosine kinase 1 | 33.22 | 31.10 | 3.99 |

| | | | | |
|--------|---|-------|-------|-------|
| TEK | TEK tyrosine kinase, endothelial | 37.33 | 37.31 | 0.16 |
| TGFA | Transforming growth factor, alpha | 31.47 | 31.76 | -0.06 |
| TGFB1 | Transforming growth factor, beta 1 | 25.12 | 26.30 | -0.49 |
| TGFB2 | Transforming growth factor, beta 2 | 28.02 | 29.22 | -0.50 |
| TGFBR1 | Transforming growth factor, beta receptor 1 | 30.59 | 30.84 | -0.03 |
| THBS1 | Thrombospondin 1 | 29.02 | 30.60 | -0.62 |
| THBS2 | Thrombospondin 2 | 36.83 | 36.06 | 0.95 |
| TIE1 | Tyrosine kinase with immunoglobulin-like and EGF-like domains 1 | 37.43 | 40 | -0.81 |
| TIMP1 | TIMP metalloproteinase inhibitor 1 | 27.81 | 27.22 | 0.73 |
| TIMP2 | TIMP metalloproteinase inhibitor 2 | 30.34 | 30.56 | 0.01 |
| TIMP3 | TIMP metalloproteinase inhibitor 3 | 33.41 | 34.13 | -0.30 |
| TNF | Tumor necrosis factor | 33.14 | 33.76 | -0.25 |
| TYMP | Thymidine phosphorylase | 28.62 | 28.32 | 0.41 |
| VEGFA | Vascular endothelial growth factor A | 26.54 | 26.04 | 0.62 |
| VEGFB | Vascular endothelial growth factor B | 24.41 | 25.33 | -0.40 |
| VEGFC | Vascular endothelial growth factor C | 27.32 | 28.81 | -0.59 |
| ACTB | Actin, beta | 21.28 | 22.99 | |
| B2M | Beta-2-microglobulin | 24.44 | 23.87 | |
| GAPDH | Glyceraldehyde-3-phosphate dehydrogenase | 19.85 | 20.05 | |
| HPRT1 | Hypoxanthine phosphoribosyltransferase 1 | 28.76 | 28.70 | |
| RPLP0 | Ribosomal protein, large, P0 | 18.66 | 19.54 | |
| HGDC | Human Genomic DNA Contamination | | | |
| RTC | Reverse Transcription Control | | | |
| RTC | Reverse Transcription Control | | | |
| RTC | Reverse Transcription Control | | | |
| PPC | Positive PCR Control | 21.39 | 21.74 | |
| PPC | Positive PCR Control | 21.58 | 21.73 | |
| PPC | Positive PCR Control | 21.54 | 21.91 | |

Supplementary Table S3. List of PCR Primer Sequences

| Gene name | Primer (sense) | Primer (anti-sense) |
|--------------------------------------|---|---|
| <i>HuRoquin2</i> (qPCR) | AAGACCATGTGATTCTGGAGGAGCAA A | ACCATCTTCCCATTGCAACAGGTTTT |
| <i>huGAPDH</i> (qPCR) | ACCTGCCAAATATGATGACATCAAGAA GGT | GTTGCTGTAGCCAAATTCGTTGTCATACC |
| <i>HuPDGFC</i> (qPCR) | AGGCGGAATCCAACCTGAGTAGTAAAT | CATCTTCTGGGTCTTCAAGCCCAAATC |
| <i>HuVEGFB</i> (qPCR) | ATG GAT AGA TGT GTA TAC TCG CGC TAC C | TTT TTA GGT CTG CAT TCA CAC TGG CTG |
| <i>HuENG</i> (qPCR) | TCAAGATCTTTCCAGAGAAAAACATTC GTGG | AACAAGCTCTTTCTTTAGTACCAGGGTCAT |
| <i>HuEDN1</i> (qPCR) | ATGGATAAAGAGTGTGTCTACTTCTGC CA | CTGAGTCTTTTCTGCTTGGCAAAAATT |
| <i>HuTIMP1</i> (qPCR) | ATACCAGCGTTATGAGATCAAGATGAC CA | AAAAGTGCAGGTAGTGATGTGCAAGAG |
| <i>HuSERPINF1</i> (qPCR) | TGGTACCTATAAGGAGCTCCTTGACAC G | ATCTCATCGGGAATTTCTTTGTGGAC |
| <i>HuANGPTLA</i> (qPCR) | TGCAGACACAACCTCAAGGCTCAGAAC A | ATCGTGGCGCCTCTGAATTACTGT |
| <i>HuTIMP3</i> (qPCR) | GATGAAGATGTACCGAGGCTTCACCAA | GGTGATACCGATAGTTCAGCCCCTT |
| <i>HuICOS</i> (qPCR) | TTTAACAGGAGAAATCAATGGTTCTGC CAA | GGATAACTGAGAATGGCAGAATTCAGACTC |
| <i>HuPDGFC</i> (full-length 3UTR) | TTCTAGACCGCATCACCACCAGCAGCT CTTGCCCA | GGCCGGCCTGACATTTAAGGCTTGCTTTTATT TTAGTA AACAT |
| <i>HuVEGFB</i> (full-length 3UTR) | TTCTAGACAGCTCAACCCAGACACCTG CAGGTGCC | GGCCGGTGC CTG GCA GGA AGA ACA AGT GTT CTT TTC TAT TA |
| <i>HuENG</i> (full-length 3UTR) | TTCTAGACCGCGCTCGCCAGCAGGA GAGACTGAGCA | GGCCGGCCATGGTCTGATTTATTGGTGGTGA ATACACA |
| <i>HuEDN1</i> (full-length 3UTR) | TTCTAGACAGACCTTCGGGGCCTGTCT GAAGCCATAG | GGCCGGCCTACAGTAAGGAAAAAATATTTAT TTTCTA AAGT |
| <i>HuTIMP1</i> (full-length 3UTR) | TTCTAGAATCCTGCCCGAGTGGAAGC TGAAGCCT | GGCCGGCCTGCTGGGTGGTAACTCTTTAT TTCATTGTC |
| <i>HuANGPTLA</i> (full-length 3UTR) | TTCTAGACGTCCTGGCTGGGCCTGGTC CCAGGCCAC | GGCCGGCCTGTTCTGAGGTTGCTTTTATTCCA AGA ACTCT |
| <i>HuSERPINF1</i> (full-length 3UTR) | TTCTAGATATCCCAGTTTAATATTCCA ATACCCTAGA | GGCCGGCCTAACAGAAGTTAGGGATA AAGCTCTTTTAT |
| <i>HuTIMP3</i> (full-length 3UTR) | TTCTAGAGCGCCAGACCTGCCCCACC TCACTTCCCT | GGCCGGCCGTGATAGAAATAAAACCCTTTAC TGTTTA |
| <i>Huβ-actin</i> (full-length 3UTR) | TTCTAGAGCGGACTATGACTTAGTTGC GTTACACCCCTTCTTGACAA | GGCCGGCCTTTAAGGTGTGCACTTTTATTCAA CTGGTCTCAAG |
| <i>HuEDN1</i> (full-length) | TTCTAGAATGGATTATTGGTCTCATGAT TTTCTCTCTGC | GGCCGGTCACCAATGTGCTCGGTTGTGGGTC ACATAA |
| <i>HuPDGFC</i> (full-length) | TTCTAGAATGAGCCTCTTCGGGCTTC TCCTGCTGACAT | GGCCGGCTATCCTCCTGTGCTCCCTCTGCAC ACA |

| | | | |
|---------------------------------|----------|--------------------------------|----------------------------------|
| <i>Huβ-actin</i> | (w/PDGFC | CTGTTGGCTTTTCTAATCTACTGACTTG | GTACAGGTAAGCCCTGGCTGCCT |
| stem-loop) | | AGACCAGTTGAAT | |
| <i>Huβ-actin</i> | (w/PDGFD | AAAGATGAGGCTTTCTTAACTGACTTG | GTACAGGTAAGCCCTGGCTGCCT |
| stem-loop) | | AGACCAGTTGAAT | |
| <i>HuPDGFC</i> (truncated 3UTR) | | TTCTAGACCGCATCACCACCAGCAGCT | GGCCGGCCTTATAATGTCAAAGGAGAATATA |
| | | CTTGCCCAGA | AAAAT |
| <i>HuEDN1</i> (truncated 3UTR) | | TTCTAGACAGACCTTCGGGGCCTGTCT | GGCCGGAACACTCCCTTAGGACCTTCGTCAG |
| | | GAAGCCATAG | AAACT |
| <i>HuEDN1</i> (3UTR-mut1) | | ATTATAAACCTAAGCCTCCAAGAGTGT | GTCAAAGGAGAATATAAAAAATGTACACAAT |
| | | TAAA | GA AAC |
| <i>HuEDN1</i> (3UTR-mut2) | | ATTATAAACCTCCGCCTCGGAGAGTGT | GTCAAAGGAGAATATAAAAAATGTACACAAT |
| | | TAAA | GA AAC |
| <i>HuPDGFC</i> (3UTR-mut1) | | 5'ATTATAACTGCCGGCTTTTCTTTTCTT | GTCAAAGGAGAATATAAAAAATGTACACAAT |
| | | GTAAAA -3' | GA AAC |
| <i>HuPDGFC</i> (3UTR-mut2) | | 5'ATTATAACTGTTCACCTTTTGAATCTT | GTCAAAGGAGAATATAAAAAATGTACACAAT |
| | | GTAAAA -3' | GA AAC |
| <i>HuPDGFC</i> (RNA-ChIP) | | 5'-GTACATTTTATATTCTCCTTTTGAC-3 | 5'-GCTAAAAATAGTTGATCTAAGTTGTC-3' |
| <i>HuEDN1</i> (RNA-ChIP) | | 5'AGATTCCACACAGGGGTGGAGTTTCT | 5'-GTGGACTTTGGAGTTTCTCCCTGAAA-3' |
| | | -3' | |
