

Additional File 1:

ERG is a regulator of dynamic and reversible endothelial plasticity

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Table S1: Guide RNA sequences for stable *ERG* gene disruption

	<u>Forward primer</u>	<u>Reverse primer</u>
Hs_ERG_exon6_5'1	CACCGGGGAAGTTGCGATCTGCCG ACCCCTTCAACGCTAGACGGCTCA AA	AAACTCGGCAGATCA ACTTCCCC
Hs_ERG_exon6_3'2	CACCGAAGAATATTTCTTCTCCTCC CTTCTTATAAAGAAGAGGAGGCAA A	AAACGGAGGAGAAG AAATATTCTTC

Table S2: EC and EndMT Gene Lists

Endothelial cell (n=353)	Endothelial-to-mesenchymal transition (n=463)
<i>A2M</i>	<i>ABCA10</i>
<i>ACKR1</i>	<i>ABCA6</i>
<i>ACVRL1</i>	<i>ABCA8</i>
<i>ADAM15</i>	<i>ABCA9</i>
<i>ADAMTS1</i>	<i>ABCC9</i>
<i>ADAMTS4</i>	<i>ABI3BP</i>
<i>ADAMTS9</i>	<i>ACKR3</i>
<i>ADCY4</i>	<i>ACKR4</i>
<i>ADGRF5</i>	<i>ACTA2</i>
<i>ADGRL4</i>	<i>ACVRL1</i>
<i>ADM5</i>	<i>ADAM33</i>
<i>AFAP1L1</i>	<i>ADAMTS1</i>
<i>ANXA2R</i>	<i>ADAMTS12</i>
<i>APLN</i>	<i>ADAMTS15</i>
<i>APLNR</i>	<i>ADAMTS2</i>
<i>APOL3</i>	<i>ADAMTS4</i>
<i>APOLD1</i>	<i>ADAMTS5</i>
<i>AQP1</i>	<i>ADAMTS8</i>
<i>ARAP3</i>	<i>ADAMTSL2</i>
<i>ARHGAP29</i>	<i>ADGRA2</i>
<i>ARHGAP31</i>	<i>ADGRD1</i>
<i>ARHGEF15</i>	<i>ADH1B</i>
<i>ART4</i>	<i>ADRA2C</i>
<i>ATOH8</i>	<i>AEBP1</i>
<i>AVPR2</i>	<i>AGTR1</i>
<i>BCL6B</i>	<i>ALX4</i>
<i>BDKRB2</i>	<i>ANGPT1</i>
<i>BMP6</i>	<i>ANGPTL1</i>
<i>BMPR2</i>	<i>ANGPTL2</i>
<i>BMX</i>	<i>ANGPTL5</i>
<i>C1QTNF5</i>	<i>ANKRD35</i>
<i>C1QTNF9</i>	<i>AOC3</i>
<i>C20orf204</i>	<i>APCDD1L</i>
<i>C2CD4B</i>	<i>APOD</i>
<i>C2CD4C</i>	<i>ARSI</i>

<i>CALCRL</i>	<i>ASPN</i>
<i>CALHM5</i>	<i>ATG5</i>
<i>CARD10</i>	<i>AXL</i>
<i>CARD6</i>	<i>B3GNT9</i>
<i>CASKIN2</i>	<i>BARX1</i>
<i>CASP12</i>	<i>BDKRB2</i>
<i>CAV1</i>	<i>BGN</i>
<i>CAVIN1</i>	<i>BMP2</i>
<i>CAVIN2</i>	<i>BMP4</i>
<i>CCDC68</i>	<i>BMP5</i>
<i>CCDC85B</i>	<i>BMP7</i>
<i>CCL14</i>	<i>BMPR2</i>
<i>CCL23</i>	<i>BOC</i>
<i>CCM2L</i>	<i>C11orf96</i>
<i>CCN2</i>	<i>C16orf89</i>
<i>CD34</i>	<i>C1QTNF1</i>
<i>CD93</i>	<i>C1QTNF2</i>
<i>CDH24</i>	<i>C1QTNF5</i>
<i>CDH5</i>	<i>C1QTNF7</i>
<i>CLDN5</i>	<i>C1R</i>
<i>CLEC14A</i>	<i>C1S</i>
<i>CLEC1A</i>	<i>C7</i>
<i>CLEC1B</i>	<i>CALHM2</i>
<i>CLEC3B</i>	<i>CALHM5</i>
<i>CLEC4M</i>	<i>CCDC80</i>
<i>CLIC2</i>	<i>CCL11</i>
<i>CNTNAP3B</i>	<i>CCL14</i>
<i>COL15A1</i>	<i>CCL19</i>
<i>COL4A1</i>	<i>CCL23</i>
<i>CPLX1</i>	<i>CCL26</i>
<i>CPXM2</i>	<i>CCL8</i>
<i>CRHBP</i>	<i>CCN1</i>
<i>CRIP2</i>	<i>CCN2</i>
<i>CSF3</i>	<i>CCN3</i>
<i>CTHRC1</i>	<i>CCN4</i>
<i>CX3CL1</i>	<i>CCN5</i>
<i>CXCL12</i>	<i>CD248</i>
<i>CYP1A1</i>	<i>CD34</i>
<i>CYTL1</i>	<i>CD44</i>

<i>CYYR1</i>	<i>CD70</i>
<i>DCHS1</i>	<i>CD90</i>
<i>DEPP1</i>	<i>CDC42EP2</i>
<i>DIPK1B</i>	<i>CDH11</i>
<i>DIPK2B</i>	<i>CDH13</i>
<i>DKK2</i>	<i>CDH2</i>
<i>DLL4</i>	<i>CFD</i>
<i>DNASE1L3</i>	<i>CFH</i>
<i>DOC2B</i>	<i>CHRD</i>
<i>DOCK6</i>	<i>CHRD1</i>
<i>DYNLT5</i>	<i>CILP</i>
<i>DYSF</i>	<i>CLDN6</i>
<i>EBF3</i>	<i>CLEC11A</i>
<i>ECSCR</i>	<i>CLEC1B</i>
<i>EDN1</i>	<i>CLEC3B</i>
<i>EDNRB</i>	<i>CLEC4M</i>
<i>EFCC1</i>	<i>CLMP</i>
<i>EFNB2</i>	<i>CLOCK</i>
<i>EGFL7</i>	<i>CNN1</i>
<i>EHD3</i>	<i>COL12A1</i>
<i>ELFN1</i>	<i>COL14A1</i>
<i>ELK3</i>	<i>COL15A1</i>
<i>EMCN</i>	<i>COL1A1</i>
<i>EMP1</i>	<i>COL1A2</i>
<i>ENG</i>	<i>COL3A1</i>
<i>ENSG00000284969</i>	<i>COL4A1</i>
<i>ENTPD1</i>	<i>COL4A2</i>
<i>EPAS1</i>	<i>COL5A1</i>
<i>EPHB4</i>	<i>COL5A2</i>
<i>ERG</i>	<i>COL6A1</i>
<i>ESAM</i>	<i>COL6A2</i>
<i>ESM1</i>	<i>COL6A3</i>
<i>ETS1</i>	<i>COL6A5</i>
<i>EXOC3L1</i>	<i>COL6A6</i>
<i>EXOC3L2</i>	<i>COL8A1</i>
<i>F2R</i>	<i>COL8A2</i>
<i>F2RL3</i>	<i>COMP</i>
<i>F8</i>	<i>COPZ2</i>
<i>FAM107A</i>	<i>CPXM1</i>

<i>FAM110D</i>	<i>CPZ</i>
<i>FAM124B</i>	<i>CRHBP</i>
<i>FAM167B</i>	<i>CRISPLD2</i>
<i>FAM241A</i>	<i>CRLF1</i>
<i>FAM43A</i>	<i>CSF1</i>
<i>FAT4</i>	<i>CTHRC1</i>
<i>FCGR2B</i>	<i>CTSK</i>
<i>FCN2</i>	<i>CTSL</i>
<i>FCN3</i>	<i>CXCL12</i>
<i>FGD5</i>	<i>CXCL14</i>
<i>FGF23</i>	<i>CYBRD1</i>
<i>FLI1</i>	<i>CYGB</i>
<i>FLT1</i>	<i>CYP1B1</i>
<i>FLT4</i>	<i>CYP2W1</i>
<i>FMO2</i>	<i>DBN1</i>
<i>FOXC1</i>	<i>DCHS1</i>
<i>FOXC2</i>	<i>DCN</i>
<i>FOXF1</i>	<i>DDR2</i>
<i>FOXP1</i>	<i>DES</i>
<i>FZD4</i>	<i>DKK2</i>
<i>GALNT15</i>	<i>DNASE1L3</i>
<i>GASK1B</i>	<i>DPT</i>
<i>GBP4</i>	<i>DUT</i>
<i>GDF3</i>	<i>EBF1</i>
<i>GGT5</i>	<i>EBF2</i>
<i>GIMAP1</i>	<i>EBF3</i>
<i>GIMAP4</i>	<i>ECM1</i>
<i>GIMAP5</i>	<i>ECM2</i>
<i>GIMAP6</i>	<i>EFEMP1</i>
<i>GIMAP7</i>	<i>EFEMP2</i>
<i>GIMAP8</i>	<i>ELANE</i>
<i>GIPC3</i>	<i>ELN</i>
<i>GJA4</i>	<i>EMILIN1</i>
<i>GJA5</i>	<i>EN1</i>
<i>GNG11</i>	<i>F10</i>
<i>GPR146</i>	<i>F2R</i>
<i>GPR4</i>	<i>F2RL2</i>
<i>GPR68</i>	<i>FAM167B</i>
<i>GRAP</i>	<i>FAM180A</i>

<i>GRAPL</i>	<i>FAM180B</i>
<i>HEG1</i>	<i>FAM43B</i>
<i>HHEX</i>	<i>FAP</i>
<i>HIF3A</i>	<i>FAT4</i>
<i>HLA-E</i>	<i>FBLN1</i>
<i>HLX</i>	<i>FBLN2</i>
<i>HMCN1</i>	<i>FBLN5</i>
<i>HOXD10</i>	<i>FBLN7</i>
<i>HOXD9</i>	<i>FBN1</i>
<i>HSPA12B</i>	<i>FCGR2B</i>
<i>HSPG2</i>	<i>FCN2</i>
<i>HYAL2</i>	<i>FCN3</i>
<i>ICAM1</i>	<i>FGF10</i>
<i>ICAM2</i>	<i>FGF16</i>
<i>ICAM4</i>	<i>FGF2</i>
<i>IFI27</i>	<i>FGF7</i>
<i>IFI44</i>	<i>FGFR1</i>
<i>IFI44L</i>	<i>FIBIN</i>
<i>IFITM1</i>	<i>FKBP10</i>
<i>IGFBP4</i>	<i>FKBP7</i>
<i>IL18BP</i>	<i>FMO2</i>
<i>IL33</i>	<i>FMOD</i>
<i>IL3RA</i>	<i>FN1</i>
<i>IL6</i>	<i>FNDC1</i>
<i>ITGA1</i>	<i>FOXF1</i>
<i>ITGA10</i>	<i>FOXF2</i>
<i>ITM2A</i>	<i>FST</i>
<i>JAG2</i>	<i>FSTL1</i>
<i>JAM2</i>	<i>FZD4</i>
<i>JCAD</i>	<i>GABRP</i>
<i>KANK3</i>	<i>GALNT15</i>
<i>KCTD12</i>	<i>GALNT16</i>
<i>KDR</i>	<i>GAS1</i>
<i>KIF17</i>	<i>GAS7</i>
<i>KIF26A</i>	<i>GATA4</i>
<i>KLF2</i>	<i>GATA6</i>
<i>LAYN</i>	<i>GDF10</i>
<i>LCN6</i>	<i>GDF6</i>
<i>LDLRAD2</i>	<i>GEM</i>

<i>LEPR</i>	<i>GFPT2</i>
<i>LIFR</i>	<i>GFRA1</i>
<i>LIMS2</i>	<i>GGT5</i>
<i>LMCD1</i>	<i>GLT8D2</i>
<i>LMO2</i>	<i>GPC3</i>
<i>LRRC32</i>	<i>GPNUMB</i>
<i>LRRC70</i>	<i>GPX8</i>
<i>LYVE1</i>	<i>GSC</i>
<i>MADCAM1</i>	<i>GSN</i>
<i>MAP3K6</i>	<i>GSTM5</i>
<i>MAPK11</i>	<i>GXYLT2</i>
<i>MAPK12</i>	<i>HAND1</i>
<i>MCAM</i>	<i>HAPLN1</i>
<i>MCF2L</i>	<i>HAS2</i>
<i>MEOX1</i>	<i>HDAC3</i>
<i>MEOX2</i>	<i>HDAC9</i>
<i>MFNG</i>	<i>HGF</i>
<i>MLKL</i>	<i>HIC1</i>
<i>MMRN2</i>	<i>HMCN1</i>
<i>MRTFB</i>	<i>HMCN2</i>
<i>MYCT1</i>	<i>HMGA2</i>
<i>NES</i>	<i>HOXC6</i>
<i>NEURL1B</i>	<i>HOXC8</i>
<i>NHSL2</i>	<i>HS3ST3A1</i>
<i>NOS3</i>	<i>HSPB6</i>
<i>NOSTRIN</i>	<i>HSPG2</i>
<i>NOTCH1</i>	<i>HTRA1</i>
<i>NOTCH4</i>	<i>HTRA3</i>
<i>NOVA2</i>	<i>ID1</i>
<i>NPDC1</i>	<i>IGDCC4</i>
<i>NPR1</i>	<i>IGF1</i>
<i>NR5A2</i>	<i>IGFBP4</i>
<i>NRN1</i>	<i>IGFBP5</i>
<i>NRP1</i>	<i>IGFBP6</i>
<i>NUAK1</i>	<i>IL15RA</i>
<i>OIT3</i>	<i>IL33</i>
<i>OLFM1</i>	<i>IL6</i>
<i>OLFML2A</i>	<i>INHBA</i>
<i>OR52N5</i>	<i>INMT</i>

<i>OSMR</i>	<i>ISLR</i>
<i>PABPC4L</i>	<i>ISM1</i>
<i>PALM2AKAP2</i>	<i>ITGA11</i>
<i>PALMD</i>	<i>ITGBL1</i>
<i>PCDH1</i>	<i>ITIH5</i>
<i>PCDH12</i>	<i>ITM2A</i>
<i>PCDH17</i>	<i>KCND1</i>
<i>PDE2A</i>	<i>KCNE4</i>
<i>PDGFB</i>	<i>KDEL3R</i>
<i>PEAR1</i>	<i>KDM4B</i>
<i>PECAM1</i>	<i>KERA</i>
<i>PGM5</i>	<i>KIAA0408</i>
<i>PIK3R3</i>	<i>KIRREL1</i>
<i>PKHD1L1</i>	<i>KLF2</i>
<i>PKN3</i>	<i>KLF4</i>
<i>PLA1A</i>	<i>KRT24</i>
<i>PLAT</i>	<i>LAMA2</i>
<i>PLEKHG1</i>	<i>LAMA4</i>
<i>PLSCR4</i>	<i>LAMB1</i>
<i>PLVAP</i>	<i>LAMC1</i>
<i>PLXND1</i>	<i>LARP7</i>
<i>PODXL</i>	<i>LEPR</i>
<i>POSTN</i>	<i>LGALS3</i>
<i>PRKCH</i>	<i>LHFPL6</i>
<i>PRSS23</i>	<i>LHX5</i>
<i>PRX</i>	<i>LOX</i>
<i>PTCHD3</i>	<i>LOXL1</i>
<i>PTPRB</i>	<i>LPAR4</i>
<i>PXDN</i>	<i>LRP1</i>
<i>QRFPR</i>	<i>LRRC17</i>
<i>RAMP2</i>	<i>LRRN4CL</i>
<i>RAMP3</i>	<i>LTBP1</i>
<i>RAPGEF3</i>	<i>LTBP2</i>
<i>RASA4</i>	<i>LTBP3</i>
<i>RASIP1</i>	<i>LTBP4</i>
<i>RASSF9</i>	<i>LUM</i>
<i>RFLNB</i>	<i>LY6A</i>
<i>RGS3</i>	<i>MAMDC2</i>
<i>RHOJ</i>	<i>MAP1LC3C</i>

<i>RIPOR1</i>	<i>MASP1</i>
<i>RND1</i>	<i>MATN4</i>
<i>ROBO4</i>	<i>MEDAG</i>
<i>RPGR</i>	<i>MEOX2</i>
<i>RSPO3</i>	<i>MFAP2</i>
<i>S1PR1</i>	<i>MFAP4</i>
<i>SCARF1</i>	<i>MFAP5</i>
<i>SELE</i>	<i>MGP</i>
<i>SELP</i>	<i>MMP11</i>
<i>SEMA3F</i>	<i>MMP14</i>
<i>SEMA6B</i>	<i>MMP19</i>
<i>SH2D3C</i>	<i>MMP2</i>
<i>SHANK3</i>	<i>MMP23B</i>
<i>SHE</i>	<i>MMP27</i>
<i>SHISA3</i>	<i>MMP3</i>
<i>SLC2A3</i>	<i>MMP9</i>
<i>SLC9A3R2</i>	<i>MN1</i>
<i>SLCO2A1</i>	<i>MRC2</i>
<i>SLCO4A1</i>	<i>MRGPRF</i>
<i>SMAD1</i>	<i>MRTFA</i>
<i>SMAD6</i>	<i>MSC</i>
<i>SNAI1</i>	<i>MT1A</i>
<i>SNCG</i>	<i>MUSK</i>
<i>SNRK</i>	<i>MXRA5</i>
<i>SOCS2</i>	<i>MXRA8</i>
<i>SOCS3</i>	<i>MYC</i>
<i>SOX17</i>	<i>MYOC</i>
<i>SOX18</i>	<i>NAMPT</i>
<i>SOX7</i>	<i>NDN</i>
<i>SPAAR</i>	<i>NFATC1</i>
<i>SPARC</i>	<i>NFATC4</i>
<i>SPARCL1</i>	<i>NFE2L2</i>
<i>SPNS2</i>	<i>NID1</i>
<i>SPRY1</i>	<i>NID2</i>
<i>SPRY4</i>	<i>NNMT</i>
<i>SRPX</i>	<i>NOTCH3</i>
<i>ST8SIA6</i>	<i>NOVA1</i>
<i>STAB1</i>	<i>NOX4</i>
<i>STAB2</i>	<i>NPPC</i>

<i>STARD8</i>	<i>NPR1</i>
<i>STC1</i>	<i>NPY1R</i>
<i>STING1</i>	<i>NPY5R</i>
<i>STOM</i>	<i>NR2F1</i>
<i>SULT1C4</i>	<i>NR4A1</i>
<i>SWAP70</i>	<i>NUPR1</i>
<i>SYT15</i>	<i>NXPH3</i>
<i>SYT15B</i>	<i>OAF</i>
<i>TAL1</i>	<i>OGN</i>
<i>TAS2R31</i>	<i>OIT3</i>
<i>TBXA2R</i>	<i>OLFML1</i>
<i>TEK</i>	<i>OLFML2A</i>
<i>TGFBR2</i>	<i>OLFML2B</i>
<i>TGFBR3</i>	<i>OLFML3</i>
<i>TGM2</i>	<i>OMD</i>
<i>THBD</i>	<i>OSR1</i>
<i>THSD1</i>	<i>P2RX2</i>
<i>TIE1</i>	<i>PCDH18</i>
<i>TIMP3</i>	<i>PCDHB11</i>
<i>TM4SF1</i>	<i>PCDHB12</i>
<i>TM4SF18</i>	<i>PCDHB15</i>
<i>TMEM100</i>	<i>PCDHB16</i>
<i>TMEM121</i>	<i>PCDHB3</i>
<i>TMEM204</i>	<i>PCDHB4</i>
<i>TMEM255B</i>	<i>PCDHGA12</i>
<i>TMEM273</i>	<i>PCDHGA2</i>
<i>TMEM44</i>	<i>PCDHGA3</i>
<i>TMEM88</i>	<i>PCDHGB7</i>
<i>TMTC1</i>	<i>PCDHGC3</i>
<i>TNFRSF10D</i>	<i>PCOLCE</i>
<i>TNFRSF4</i>	<i>PCOLCE2</i>
<i>TNS2</i>	<i>PDCD1LG2</i>
<i>TPO</i>	<i>PDGFA</i>
<i>TRAPPC3L</i>	<i>PDGFB</i>
<i>TSPAN18</i>	<i>PDGFD</i>
<i>TSPAN7</i>	<i>PDGFRA</i>
<i>USHBP1</i>	<i>PDGFRB</i>
<i>VAMP5</i>	<i>PDGFRL</i>
<i>VCAM1</i>	<i>PI16</i>

<i>VEGFC</i>	<i>PKD1L2</i>
<i>VWF</i>	<i>PLA2G2A</i>
<i>WWTR1</i>	<i>PLAC9</i>
<i>XAF1</i>	<i>PLAGL1</i>
<i>ZNF366</i>	<i>PLAT</i>
<i>ZNF792</i>	<i>PLOD1</i>
	<i>PLPP3</i>
	<i>PMP22</i>
	<i>PODN</i>
	<i>POGLUT3</i>
	<i>POSTN</i>
	<i>PRDM6</i>
	<i>PRELP</i>
	<i>PRRX1</i>
	<i>PRRX2</i>
	<i>PTGDR2</i>
	<i>PTGFR</i>
	<i>PTX3</i>
	<i>PXDN</i>
	<i>RCN3</i>
	<i>RIPOR3</i>
	<i>RSPO1</i>
	<i>RSPO3</i>
	<i>S100A4</i>
	<i>S1PR3</i>
	<i>SCARA5</i>
	<i>SCARF2</i>
	<i>SCUBE3</i>
	<i>SDC2</i>
	<i>SEMA7A</i>
	<i>SERPINA3</i>
	<i>SERPINE1</i>
	<i>SERPINF1</i>
	<i>SERPING1</i>
	<i>SERPINH1</i>
	<i>SFRP1</i>
	<i>SFRP2</i>
	<i>SFRP4</i>
	<i>SHISA3</i>

	<i>SLIT3</i>
	<i>SMAD2</i>
	<i>SMAD3</i>
	<i>SMAD4</i>
	<i>SMIM41</i>
	<i>SMOC2</i>
	<i>SMTN</i>
	<i>SNAI1</i>
	<i>SNAI2</i>
	<i>SNED1</i>
	<i>SOD2</i>
	<i>SOD3</i>
	<i>SOX11</i>
	<i>SOX2</i>
	<i>SP1</i>
	<i>SP5</i>
	<i>SPARC</i>
	<i>SPARCL1</i>
	<i>SPOCD1</i>
	<i>SPON2</i>
	<i>SPRY1</i>
	<i>SPRY2</i>
	<i>SRPX</i>
	<i>SRPX2</i>
	<i>SSC5D</i>
	<i>SSPN</i>
	<i>STAB1</i>
	<i>STAB2</i>
	<i>SULF1</i>
	<i>SVEP1</i>
	<i>TAC3</i>
	<i>TAGLN</i>
	<i>TBX15</i>
	<i>TBXA2R</i>
	<i>TCEAL7</i>
	<i>TCF21</i>
	<i>TGFB1</i>
	<i>TGFB2</i>
	<i>TGFB3</i>

	<i>TGFB1</i>
	<i>TGFBR1</i>
	<i>TGFBR2</i>
	<i>TGFBR3</i>
	<i>THBS2</i>
	<i>THBS4</i>
	<i>THY1</i>
	<i>TIMP1</i>
	<i>TIMP2</i>
	<i>TIMP3</i>
	<i>TMEM100</i>
	<i>TMEM119</i>
	<i>TMEM200B</i>
	<i>TMEM204</i>
	<i>TMEM35B</i>
	<i>TMSB4X</i>
	<i>TNC</i>
	<i>TNFAIP6</i>
	<i>TNN</i>
	<i>TNXB</i>
	<i>TRABD2B</i>
	<i>TRDV3</i>
	<i>TRIL</i>
	<i>TWIST1</i>
	<i>TWIST2</i>
	<i>VASN</i>
	<i>VCAN</i>
	<i>VEGFD</i>
	<i>VIM</i>
	<i>VIT</i>
	<i>VSTM2A</i>
	<i>WDR86</i>
	<i>WNT10B</i>
	<i>WNT11</i>
	<i>WNT2</i>
	<i>XG</i>
	<i>ZEB1</i>
	<i>ZEB2</i>

Table S4: Primers for qPCR

<u>Gene name</u>	<u>Forward primer</u>	<u>Reverse primer</u>
<i>TBP</i>	TCG GAG AGT TCT GGG ATT GT	CAC GAA GTG CAA TGG TCT TT
<i>ERG</i>	AAC AAG TAG CCG CCT TGC	AGG TGA TGC AGC TGG AGT
<i>VWF</i>	TAC AGC TTT GCG GGA TAC TG	AGG CTC ACT CTC TTG CCA TT
<i>CD31</i>	AAC CAC TGC AGA GTA CCA GG	TGG CCT CTT TCT TGT CCA GT
<i>APLN</i>	CCA AGG AGC AGC ATG AAT CT	CTT CCA GCC CAT TCC CAT C
<i>DLL4</i>	GTG CAA GAA GCG CAA TGA C	GAC AGC CCG AAA GAC AGA TAG
<i>FNI</i>	GAT TGG CCA ACA ATC AAC AG	ACT GTG ACA GCA GGA GCA TC
<i>ACTA2</i>	CCA CCG GGA GAA AAT GAC TC	ATA CAT GGC TGG GAC ATT GA

Supplementary Figures:

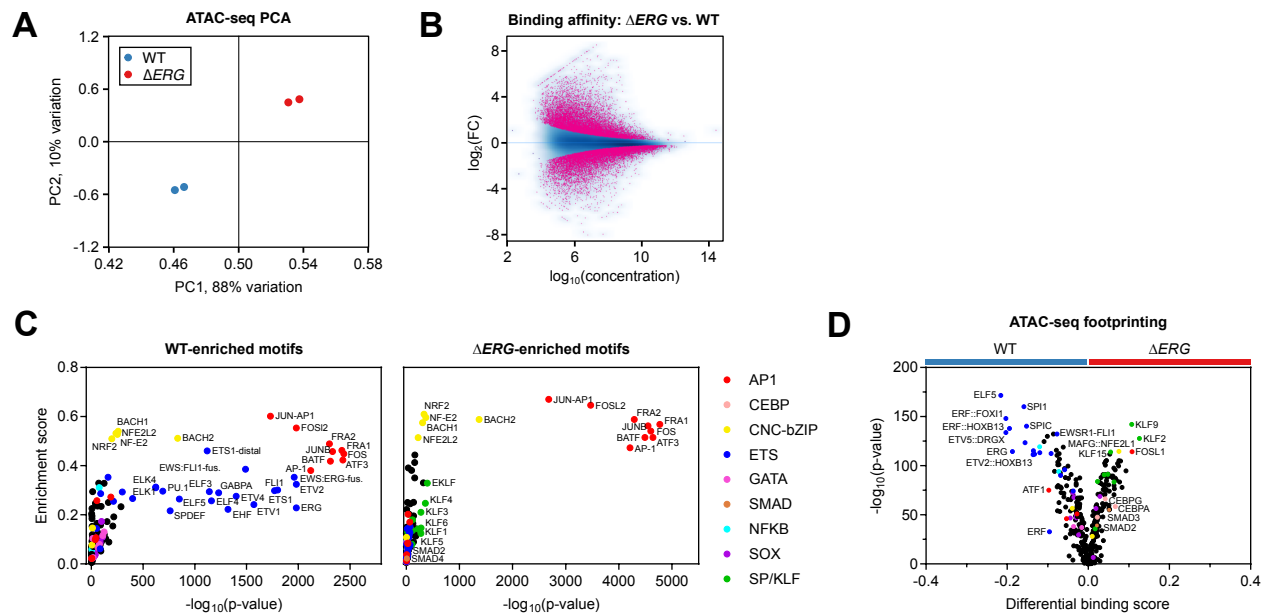


Fig. S1: Chromatin accessibility profiling of *ERG* knockout in human aortic endothelial cells. (A) Principal component analysis (PCA) of assay for transposase-accessible chromatin with sequencing (ATAC-seq) in telomerase-immortalized human aortic endothelial cells (teloHAECs) with CRISPR/Cas9-mediated deletion of *ERG* exon 6 (Δ ERG) versus wild-type cells (WT) ($n = 2$). (B) MA ($\log_2$ fold change versus average signal) plot depicting differentially accessible chromatin regions (DARs) in Δ ERG and WT teloHAECs ($p_{\text{adj}} < 0.05$). FC, fold change. (C) Motif enrichment analysis of DARs associated with Δ ERG and WT teloHAECs with motifs of interest indicated ($p_{\text{adj}} < 0.05$). (D) ATAC-seq footprinting analysis depicting motif differential binding scores for Δ ERG and WT teloHAECs with motifs of interest indicated ($p_{\text{adj}} < 0.05$).

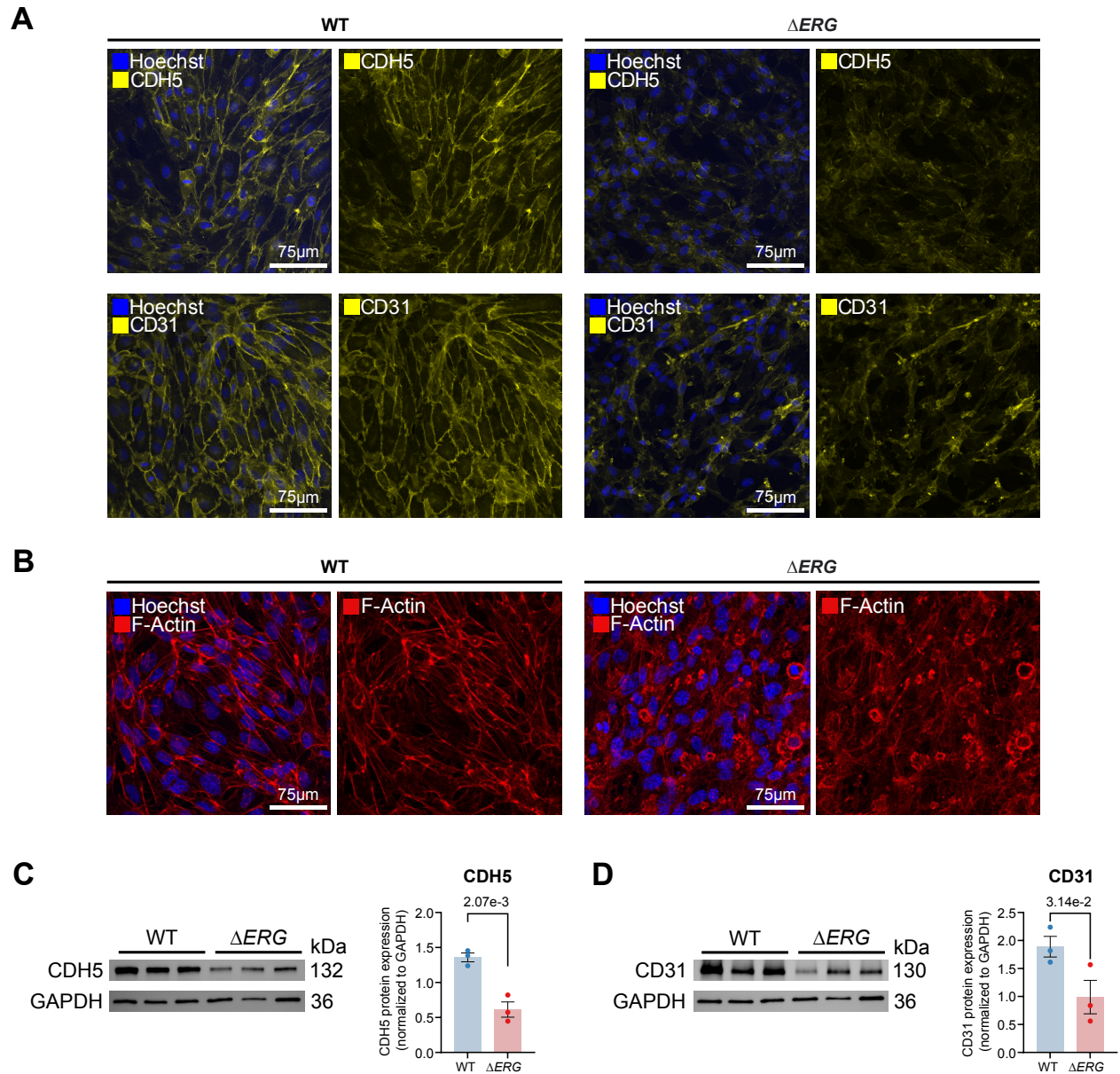


Fig. S2: Chronic loss of *ERG* promotes endothelial-to-mesenchymal transition, disrupts junctional arrangement, and increases migration of aortic endothelial cells. (A) Representative confocal microscopy images of *ERG* knockout (Δ ERG) and wild-type (WT) telomerase-immortalized human aortic endothelial cells (teloHAECs) stained with the junctional markers CDH5 and CD31. (B) Representative confocal microscopy images of Δ ERG and WT teloHAECs stained with F-actin. Representative western blot of CDH5 (C) and CD31 (D) with densitometry quantification of protein expression normalized to GAPDH. ($n = 3$; unpaired t-tests). Bar graphs are presented as mean $\pm$ standard error of the mean (SEM).

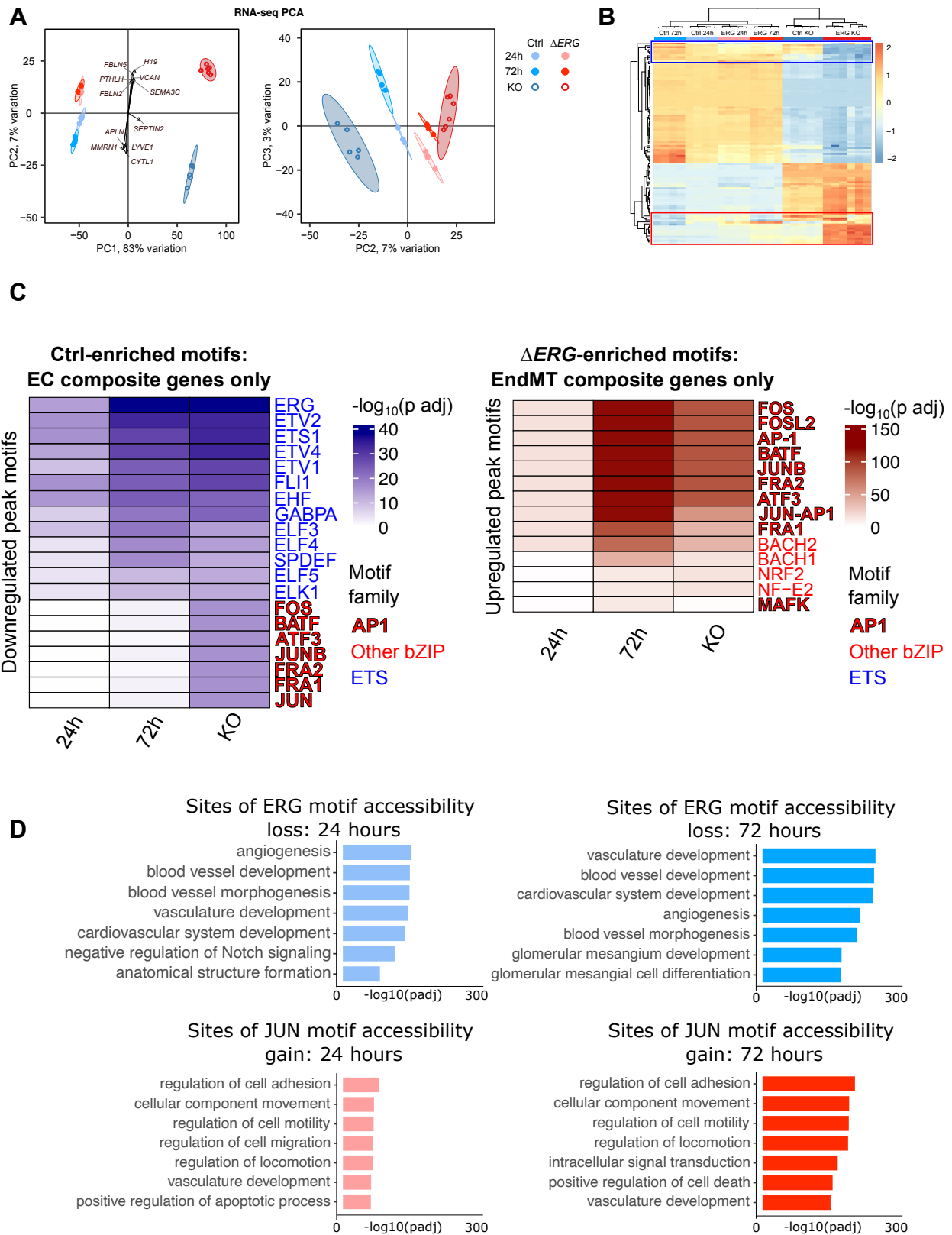


Fig. S3: Induction of endothelial-to-mesenchymal transition is accompanied by activation of the AP1 transcription factor family. (A) Principal component analysis (PCA) plots depicting

PC1/PC2 (left) and PC2/PC3 (right) of RNA-sequencing (RNA-seq) from telomerase-immortalized human aortic endothelial cells (teloHAECs) treated with control (Ctrl) or *ERG* small interfering RNA (siRNA) for 24 or 72 hours ($n = 4$) or featuring a CRISPR knockout (KO) of *ERG* ($n = 5-6$). Top genes contributing to PC1 and PC2 values are labelled. **(B)** Heatmap of z-score normalized differentially expressed (DE) genes plotted across *ERG* disruption treatments. Control (blue outline) and Δ *ERG*-associated transcriptome regions (red outline) are highlighted. **(C)** Control and Δ *ERG*-enriched motifs contributing to EC and EndMT composite gene expression. **(D)** Gene Ontology (GO) term enrichments called using GREAT for peaks that lose accessibility in *ERG* siRNA-treated teloHAECs relative to Ctrl siRNA-treated cells, and contain an ERG motif (top), or for peaks that gain accessibility and contain an AP1 (JUN) motif (bottom) at the specified time-point.

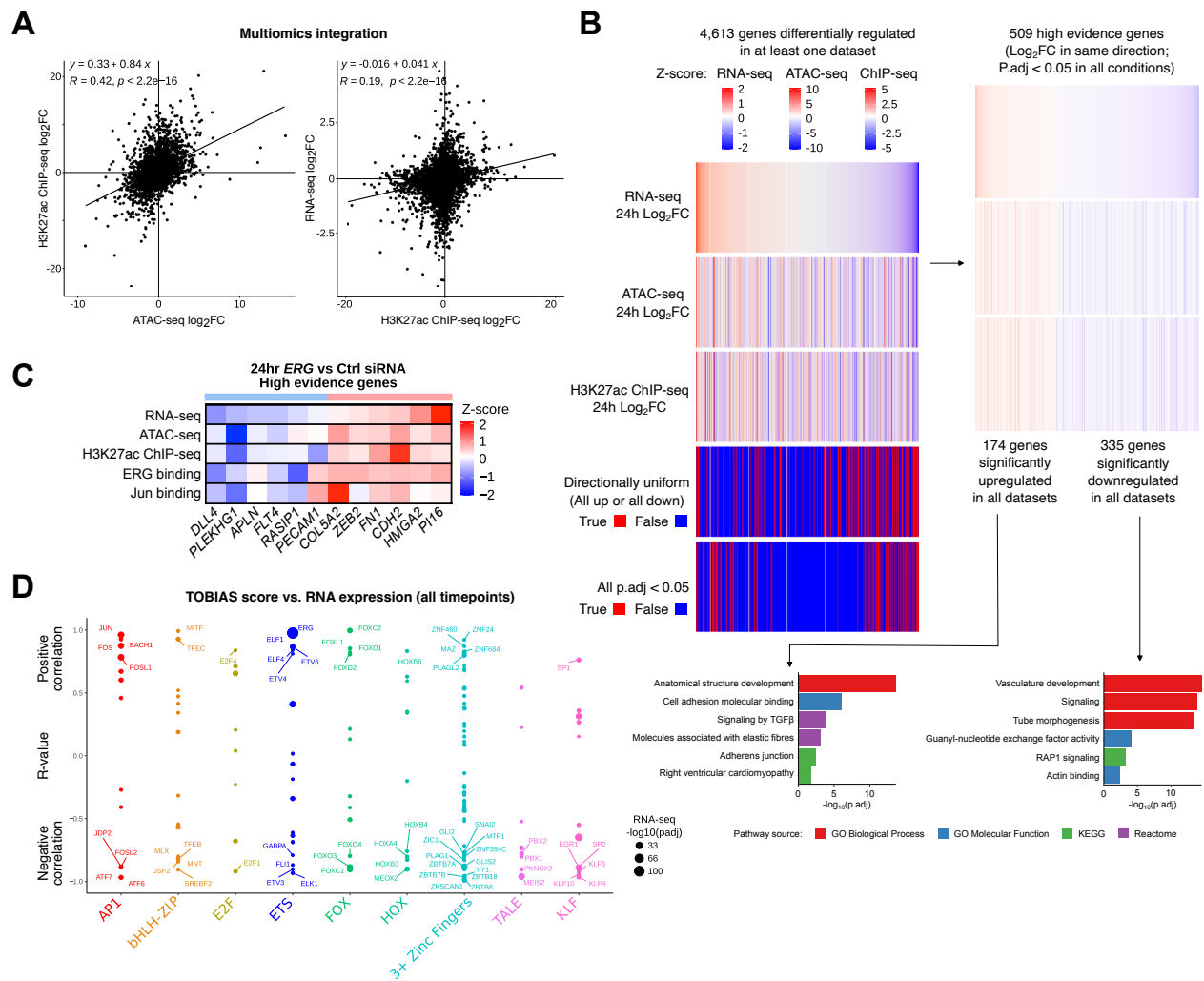


Fig. S4: Multiomic integration identifies conserved endothelial responses to loss of *ERG*. (A) Dot plots comparing fold changes (FC) for RNA-seq, assay for transposase-accessible chromatin with sequencing (ATAC-seq), and H3K27ac chromatin immunoprecipitation sequencing (ChIP-seq) in 24 hour *ERG* siRNA versus control siRNA-treated teloHAECs. Lines of best fit and associated R values are depicted. p-values are derived from the Pearson correlation. (B) Heatmaps displaying Z-score normalized fold changes for all genes that are differentially regulated in at least one 24 hour *ERG* siRNA versus control siRNA dataset (p.adj < 0.05). Additional binary heatmaps show if each gene is differentially regulated in all three datasets, and if each gene has the same fold change directionality in all three datasets (top left). Heatmaps for the subset of genes that are both directionally uniform and significant in all three conditions (top right). Gene Ontology (GO), Kyoto Encyclopedia of Genes and Genomes (KEGG), and Reactome pathway enrichments for genes that are upregulated (bottom left) or downregulated (bottom right) in all three conditions. (C) Heatmap displaying z-score normalized multiomics data for select endothelial (left, blue bar) or endothelial-to-mesenchymal transition (EndMT; right, blue bar) high evidence genes that are uniformly downregulated or upregulated respectively (p.adj < 0.05). (D) Dot plot depicting correlations between the global transcription factor footprinting score and RNA-seq expression of

that transcription factor across all conditions. Transcription factors are grouped by family and correlations (R-values) are shown for footprinting scores versus RNA-seq data.

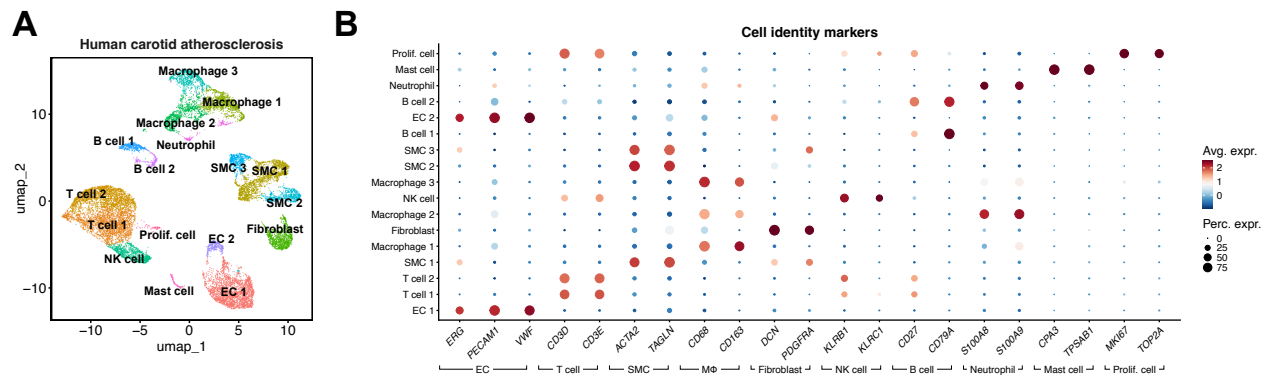


Fig. S5: Characterizing cell type composition of a publicly available human atherosclerosis single-cell RNA sequencing dataset. (A) Uniform manifold approximation and projection (UMAP) plot of cells obtained from human carotid atherosclerotic core and proximal adjacent regions. EC, endothelial cell; NK cell, natural killer cell; Prolif. cell, proliferating cell; SMC, smooth muscle cell. (B) Cell identity markers associated with cell clusters. MΦ, macrophage.

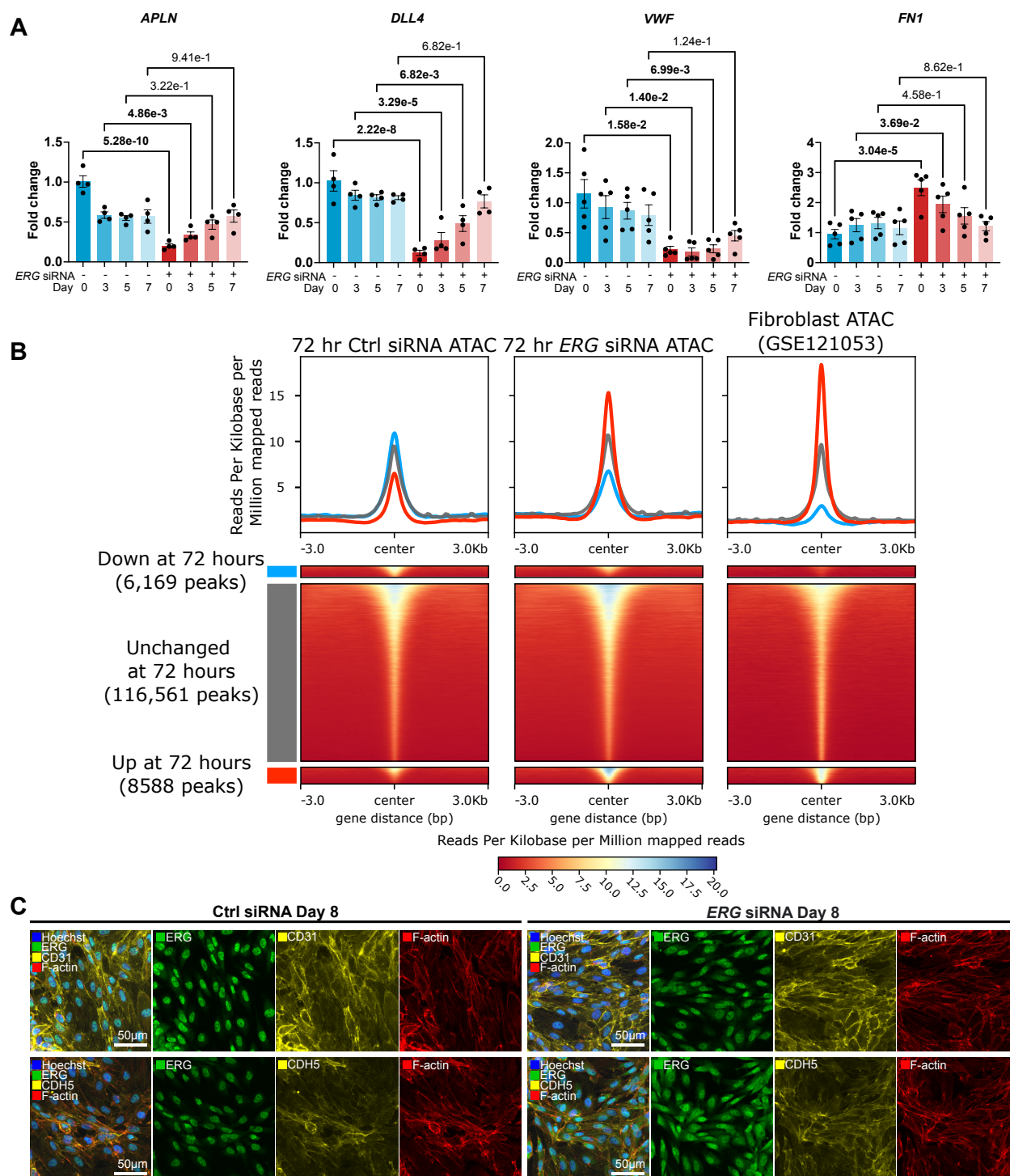


Fig. S6: Gene regulatory networks and endothelial function are restored upon ERG re-expression. (A) Quantitative PCR of endothelial markers *APLN*, *DLL4* (two-way ANOVA), and *VWF* (Welch's t-tests) and the mesenchymal marker *FN1* (two-way ANOVA) ($n = 5$). Significant p-values are denoted with bold text. (B) Heatmap (bottom) and summary plot (top) displaying aggregate reads at each peak for ATAC-seq peaks from control or *ERG* siRNA (72 hours) treated telHAECs ($n = 3$) along with human lung fibroblasts ($n = 5$). Peaks are grouped by

directionality and significance, with the blue group significantly lost in *ERG* siRNA-treated samples relative to controls ($p < 0.05$), the red group significantly gained in *ERG* siRNA-treated samples relative to controls ($p < 0.05$), and grey unchanged between the two conditions ($p > 0.05$). (C) Representative immunofluorescence staining of ERG (green), CD31 (yellow), CDH5 (yellow), F-actin (red) and Hoechst (blue) in teloHAECs that were transfected with control or *ERG* siRNA and after 72 hours were grown out for an additional 8 days. Barrier markers (CD31 and CDH5) and F-actin localization were similar between groups, suggestive of barrier recovery.