SUPPORTING INFORMATION

Probe	Gene	Average Expression	Log2FC	p_{obs}	p_{adj}
222787_s_at	***TMEM106B***	**7.95**	**0.86**	**4.1E-14**	**1.3E-09**
211122_s_at	***CXCL11***	**5.64**	**-0.82**	**3.8E-13**	**6.2E-09**
224549_x_at		**7.51**	**-0.78**	**5.3E-12**	**5.7E-08**
226675_s_at	***MALAT1***	**9.52**	**-0.74**	**6.8E-11**	**5.5E-07**
202687_s_at	***TNFSF10***	**6.77**	**-0.72**	**1.9E-10**	**1.2E-06**
224567_x_at	***MALAT1***	**10.97**	**-0.71**	**4.0E-10**	**2.0E-06**
219230_at	***TMEM100***	**8.05**	**0.71**	**4.3E-10**	**2.0E-06**
AFFX-r2-Bs-lys-5_at		**5.19**	**0.67**	**2.9E-09**	**1.2E-05**
205809_s_at	***WASL***	**6.58**	**-0.65**	**7.8E-09**	**2.8E-05**
1558378_a_at	***AHNAK2***	**6.01**	**-0.65**	**1.1E-08**	**3.5E-05**
201996_s_at	***SPEN***	**8.80**	**-0.65**	**1.2E-08**	**3.5E-05**
222344_at		**6.88**	**-0.64**	**2.0E-08**	**5.1E-05**
202688_at	***TNFSF10***	**7.35**	**-0.63**	**2.1E-08**	**5.1E-05**
201340_s_at	***ENC1***	**7.28**	**-0.63**	**2.4E-08**	**5.6E-05**
210163_at	***CXCL11***	**5.17**	**-0.62**	**5.2E-08**	**1.1E-04**
AFFX-r2-Bs-lys-M_at		**5.21**	**0.60**	**1.4E-07**	**2.8E-04**
209257_s_at	***SMC3***	**7.09**	**-0.59**	**1.5E-07**	**2.9E-04**
205051_s_at	***KIT***	**7.63**	**-0.59**	**1.6E-07**	**2.9E-04**
208621_s_at	***EZR***	**7.23**	**-0.59**	**2.0E-07**	**3.4E-04**
1558924_s_at	***CLIP1***	**5.44**	**-0.58**	**2.9E-07**	**4.6E-04**
204567_s_at	***ABCG1***	**8.09**	**-0.58**	**3.3E-07**	**0.001**
208624_s_at	***EIF4G1***	**8.57**	**-0.57**	**5.2E-07**	**0.001**
200835_s_at	***MAP4***	**9.01**	**-0.56**	**7.5E-07**	**0.001**
220037_s_at	***LYVE1***	**8.63**	**-0.56**	**7.8E-07**	**0.001**
1552526_at	*FAM71C*	5.23	0.55	1.2E-06	0.002
242877_at		4.71	0.55	1.3E-06	0.002
1568803_at		4.68	0.55	1.4E-06	0.002
204014_at	*DUSP4*	8.35	-0.54	1.5E-06	0.002
AFFX-ThrX-M_at		6.42	0.54	1.7E-06	0.002
208859_s_at	*ATRX*	6.64	-0.54	1.7E-06	0.002
201615_x_at	*CALD1*	7.53	-0.54	2.0E-06	0.002
205651_x_at	*RAPGEF4*	6.34	-0.54	2.1E-06	0.002
AFFX-LysX-3_at		6.75	0.53	2.5E-06	0.002
239579_at	*EPHX4*	4.99	-0.53	2.5E-06	0.002
1553185_at	*RASEF*	8.83	-0.53	2.8E-06	0.002
219387_at	*CCDC88A*	5.62	-0.53	2.8E-06	0.002
1555928_at		5.56	-0.53	2.9E-06	0.002
206665_s_at	*BCL2L1*	5.29	-0.52	4.0E-06	0.003
217028_at	*CXCR4*	9.49	-0.52	4.4E-06	0.004
201867_s_at	*TBL1X*	6.49	-0.52	4.7E-06	0.004
AFFX-r2-Bs-thr-M_s_at		8.04	0.51	5.8E-06	0.005

208900_s_at	*TOP1*	7.27	-0.51	6.0E-06	0.005
203032_s_at	*FH*	8.67	-0.51	6.2E-06	0.005
215043_s_at	*GUSBP3* *SMA5* *SMA4*	5.64	-0.51	7.5E-06	0.005
224563_at	*WASF2*	7.26	-0.51	7.6E-06	0.005
AFFX-r2-Bs-dap-3_at		10.03	0.50	8.9E-06	0.006
AFFX-PheX-5_at		6.21	0.50	9.2E-06	0.006
210935_s_at	*WDR1*	8.67	-0.50	9.3E-06	0.006
241926_s_at	*ERG*	9.45	-0.50	1.0E-05	0.007
208930_s_at	*ILF3*	8.27	-0.50	1.1E-05	0.007
236684_at	*CNOT9*	4.93	0.50	1.1E-05	0.007
1553673_at	*STK35*	6.01	0.50	1.2E-05	0.007
1557836_at	*ELMOD2*	6.48	0.49	1.5E-05	0.009
209183_s_at	*C10orf10*	9.47	-0.49	1.7E-05	0.010
1554761_a_at	*DNAAF5*	7.48	-0.49	1.8E-05	0.011
1554333_at	*DNAJA4*	5.81	-0.48	1.9E-05	0.011
236620_at	*RIF1*	6.89	-0.48	2.2E-05	0.013
1554710_at	*KCNMB1*	4.33	0.48	2.2E-05	0.013
229274_at	*GNAS*	6.23	-0.48	2.3E-05	0.013
216700_at	*TRIO*	6.60	0.48	2.5E-05	0.013
208879_x_at	*PRPF6*	7.60	-0.48	2.5E-05	0.013
206978_at	*CCR2*	5.10	0.48	2.5E-05	0.013
221683_s_at	*CEP290*	6.06	-0.47	2.8E-05	0.015
232063_x_at	*FARSB*	5.74	0.47	3.0E-05	0.015
230746_s_at		4.66	-0.47	3.1E-05	0.015
38241_at	*BTN3A3*	5.52	-0.47	3.3E-05	0.016
230040_at	*ADAMTS18*	9.36	-0.47	3.4E-05	0.016
1560642_at		4.26	-0.47	3.4E-05	0.016
239491_at	*CERS5*	4.93	0.47	3.8E-05	0.018
236966_at	*ARMC8*	6.08	0.47	3.8E-05	0.018
212650_at	*EHBP1*	6.26	-0.47	4.0E-05	0.018
242856_at	*SNHG24*	6.10	0.46	4.0E-05	0.018
AFFX-r2-Bs-lys-3_at		6.31	0.46	4.0E-05	0.018
211077_s_at	*TLK1*	6.51	-0.46	4.0E-05	0.018
212675_s_at	*CEP68*	8.17	-0.46	4.1E-05	0.018
209258_s_at	*SMC3*	6.25	-0.46	4.1E-05	0.018
AFFX-ThrX-3_at		7.97	0.46	4.3E-05	0.018
234442_at		6.13	0.46	4.5E-05	0.018
222340_at		4.47	0.46	4.5E-05	0.018
214329_x_at	*TNFSF10*	7.13	-0.46	4.5E-05	0.018
234758_at		3.96	-0.46	4.7E-05	0.019
231461_at	*KRT71*	5.53	0.46	4.7E-05	0.019
203347_s_at	*MTF2*	7.17	-0.46	4.8E-05	0.019

216953_s_at	*WT1*	6.17	0.46	5.1E-05	0.020
205952_at	*KCNK3*	4.79	0.46	5.1E-05	0.020
244026_at		5.21	0.46	5.4E-05	0.020
217320_at	*LOC100293211*	4.58	0.46	5.4E-05	0.020
1557910_at	*HSP90AB1*	11.64	-0.46	5.8E-05	0.021
AFFX-r2-Bs-thr-3_s_at		8.48	0.45	6.6E-05	0.024
227152_at	*KIAA1551*	6.32	-0.45	7.0E-05	0.025
1555926_a_at		5.23	-0.45	7.0E-05	0.025
219424_at	*EBI3*	5.52	-0.45	7.7E-05	0.027
201538_s_at	*DUSP3*	7.48	-0.45	7.9E-05	0.027
219754_at	*RBM41*	7.38	-0.45	7.9E-05	0.027
208325_s_at	*AKAP13*	6.26	-0.45	8.1E-05	0.028
223292_s_at	*MRPS15*	6.42	0.45	8.2E-05	0.028
232731_x_at	*RAMP2-AS1*	4.42	-0.45	8.4E-05	0.028
227939_s_at	*TRA2A*	4.31	0.44	9.0E-05	0.030
1558214_s_at	*CTNNA1*	7.16	-0.44	9.1E-05	0.030
1560255_at	*CELF2-AS1*	5.96	0.44	9.6E-05	0.031
231999_at	*ANKRD11*	8.13	-0.44	9.6E-05	0.031
1566030_at		4.33	0.44	1.0E-04	0.032
235730_at	*NUTM2B-AS1*	5.07	-0.44	1.0E-04	0.032
243235_at		5.12	0.44	1.1E-04	0.034
219730_at	*LOC100996782* *MED18*	6.49	0.44	1.1E-04	0.035
211767_at	*GINS4*	5.13	0.44	1.1E-04	0.035
1564494_s_at	*P4HB*	10.89	-0.44	1.1E-04	0.035
1564733_at		6.94	0.44	1.2E-04	0.035
244100_at		5.31	-0.44	1.2E-04	0.035
222877_at	*NRP2*	9.23	-0.44	1.2E-04	0.036
210875_s_at	*ZEB1*	9.41	-0.44	1.2E-04	0.036
212364_at	*MYO1B*	9.18	-0.43	1.2E-04	0.036
AFFX-r2-Bs-phe-5_at		6.32	0.43	1.3E-04	0.038
1569325_at	*ARPC5*	6.32	0.43	1.3E-04	0.038
236377_at	*TMEM132D*	5.21	0.43	1.4E-04	0.039
200920_s_at	*BTG1*	10.35	-0.43	1.4E-04	0.039
209821_at	*IL33*	9.56	-0.43	1.4E-04	0.039
207908_at	*KRT2*	6.03	0.43	1.4E-04	0.039
219059_s_at	*LYVE1*	9.78	-0.43	1.5E-04	0.039
243193_at		4.15	0.43	1.5E-04	0.039
212009_s_at	*STIP1*	9.36	-0.43	1.5E-04	0.039
209127_s_at	*SART3*	7.71	-0.43	1.5E-04	0.040
218723_s_at	*RGCC*	9.72	-0.43	1.5E-04	0.040
204595_s_at	*STC1*	7.68	-0.43	1.6E-04	0.041
221400_at	*MYO3A*	5.20	0.43	1.6E-04	0.041
1566082_at		4.83	0.43	1.6E-04	0.041

226623_at	*PHYHIPL*	5.62	0.43	1.6E-04	0.041
AFFX-PheX-M_at		6.68	0.43	1.6E-04	0.041
237300_at	*PSMA3*	5.89	0.43	1.7E-04	0.041
242930_at	*OSGEP*	5.05	0.43	1.7E-04	0.041
214119_s_at	*LOC101929368* *FKBP1A*	12.64	-0.43	1.7E-04	0.041
232178_at	*ZNF503*	6.49	0.43	1.7E-04	0.042
224254_x_at		8.29	-0.43	1.7E-04	0.042
238916_at	*LINC00938*	4.81	-0.42	1.8E-04	0.044
239571_at		6.28	-0.42	1.9E-04	0.045
229450_at	*IFIT3*	6.09	-0.42	1.9E-04	0.046
AFFX-r2-Bs-dap-M_at		9.26	0.42	1.9E-04	0.046
217019_at		7.34	-0.42	2.0E-04	0.047
207642_at	*HCRT*	5.77	0.42	2.0E-04	0.047
216598_s_at	*CCL2*	9.96	-0.42	2.0E-04	0.047
237227_at	*NEK10*	5.71	-0.42	2.0E-04	0.047
236071_at	*C9orf135-AS1*	4.47	0.42	2.1E-04	0.048
226901_at	*C17orf58*	9.57	-0.42	2.1E-04	0.048
240284_x_at	*LOC105369635*	5.24	0.42	2.1E-04	0.048
201679_at	*SRRT*	5.56	-0.42	2.2E-04	0.048
AFFX-DapX-3_at		9.47	0.42	2.2E-04	0.048
214718_at	*GATAD1*	8.88	-0.42	2.3E-04	0.049

Table S1. List of 147 probes/genes differentially expressed between siNC and si*ANRIL* transfedted HUVECs from the GeneChip microarray analysis. Fold changes between the two groups are shown in a log2 scale and *P* values were determined by two-way ANOVA.

Name	Sequence	Name	Sequence
ABCG1_F	GAGGGATTTGGGTCTGAACTGC	GAPDH_F	GTCTCCTCTGACTTCAACAGCG
ABCG1_R	TCTCACCAGCCGACTGTTCTGA	GAPDH_R	ACCACCCTGTTGCTGTAGCCAA
AHNAK2_F	TCCTGGTGGAAGCGAGATTCAG	KIT_F	CACCGAAGGAGGCACTTACACA
AHNAK2_R	ACCACCTGTGACACTGTAGCCA	KIT_R	TGCCATTCACGAGCCTGTCGTA
ANRIL_total_F	GCCTCATTCTGATTCAACAGC	LYVE1_F	GCCGACAGTTTGCAGCCTATTG
ANRIL_total_R	GATCTCCCCGGTTTTCTTCT	LYVE1_R	CCGAGTAGGTACTGTCACTGAC
ANRIL_DQ_F	CCACATCCCTTGGAGTAATGA	MAP4_F	CCTTGCTTCAGGCTTAGTGCCA
ANRIL_DQ_R	CCTTTTATCACCCAGCTTCG	MAP4_R	GCTTCTCAGGAGCCTTTGCATC
ANRIL_NR_F	AACCTGAGCAGCTGGGACTA	MTAP_F	GTCATAGTGACCACAGCTTGTGG
ANRIL_NR_R	TGTGTCCATAGCACCTTCCA	MTAP_R	CCTCTGGCACAAGAATGACTTCC
CDKN2A_F	CTCGTGCTGATGCTACTGAGGA	SMC3_F	ATGCGTGGAAGTCACTGCTGGA
CDKN2A_R	GGTCGGCGCAGTTGGGCTCC	SMC3_R	GCAGAAAAGTAACCTCTCCAGG
CDKN2B_F	ACGGAGTCAACCGTTTCGGGAG	SPEN_F	GATTCCTCTCCACACCTGACTTC
CDKN2B_R	GGTCGGGTGAGAGTGGCAGG	SPEN_R	TGTTGCCAGAGACGAAGTGGAG
CLIP1_F	AGAAGACGCTGCTGGACACAGA	TMEM100_F	ACAGTCCCTCTGGTCAGTGAGA
CLIP1_R	TGGCATCTTCCGCTGTTTGAGC	TMEM100_R	GGCGATGAAGACAACCACAGCA
CXCL11_F	AAGGACAACGATGCCTAAATCCC	TMEM106B_F	CCTACTTGTCAGGGAACAGGAAG
CXCL11_R	CAGATGCCCTTTTCCAGGACTTC	TMEM106B_R	AACACAGCCAATCCAGAAAGGAG
EIF4G1_F	GCCATTTCAGAGCCCAACTTCTC	TNFSF10_F	TGGCAACTCCGTCAGCTCGTTA
EIF4G1_R	CGGAAGTTCACAGTCACTGTTGG	TNFSF10_R	AGCTGCTACTCTCTGAGGACCT
ENC1_F	AGACGTGTGGAACAGCATCACC	WASL_F	AAAGTGGAGCAGAACAGTCGGC
ENC1_R	CATATTATCTCATCGAGTGATGGAG	WASL_R	GTTGGTGGTGTAGACTCTTGGC
EZR_F	ATCGAGGTGCAGCAGATGAAGG		
EZR_R	CGCAGCATCAACTCCTCCTTCT		

Table S2. List of primers for *ANRIL* and its top downstream gene candidates that were used in semiquantitative and quantitative RT-PCR analysis.

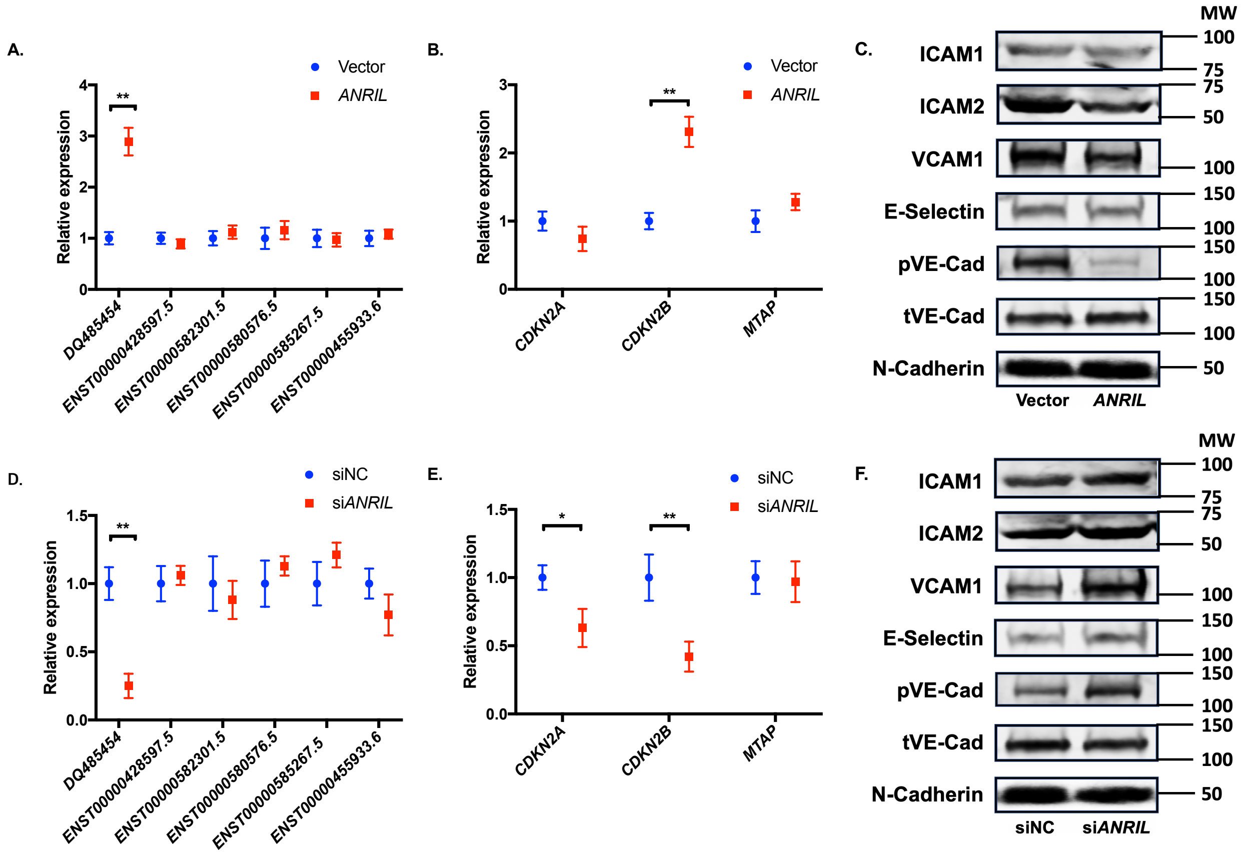

Figure S1. Effects of overexpression and knockdown of *ANRIL* (*DQ485454*) on expression of its neighboring genes and genes for endothelial cell adhesion molecules in HCAECs.
A: Specific overexpression of *ANRIL* transcript *DQ485454* in HCAECs transfected with the pcDNA3.1-*ANRIL* plasmid as determined by real-time qRT-PCR analysis. **B:** Effects of overexpression of *ANRIL* transcript *DQ485454* on expression of *CDKN2A*, *CDKN2B*, and *MTAP*. **C:** Effects of overexpression of *ANRIL* transcript *DQ485454* on expression of genes encoding EC adhesion molecules in HCAECs as determined Western blot analysis. **D:** Specific knockdown of *ANRIL* transcript *DQ485454* in HCAECs transfected with *ANRIL* siRNA (si*ANRIL*) as determined by real-time qRT-PCR analysis. **E:** Effects of knockdown of *ANRIL* transcript *DQ485454* on expression of *CDKN2A*, *CDKN2B*, and *MTAP*. **F:** Effects of knockdown of *ANRIL* transcript *DQ485454* on expression of genes encoding EC adhesion molecules in HCAECs as determined Western blot analysis. Western blot analysis was carried out using plasma membrane protein extracts isolated by biotinylation. **P*<0.05, ***P*<0.01, n=3/group. Only statistically significant values are marked with asterisk.

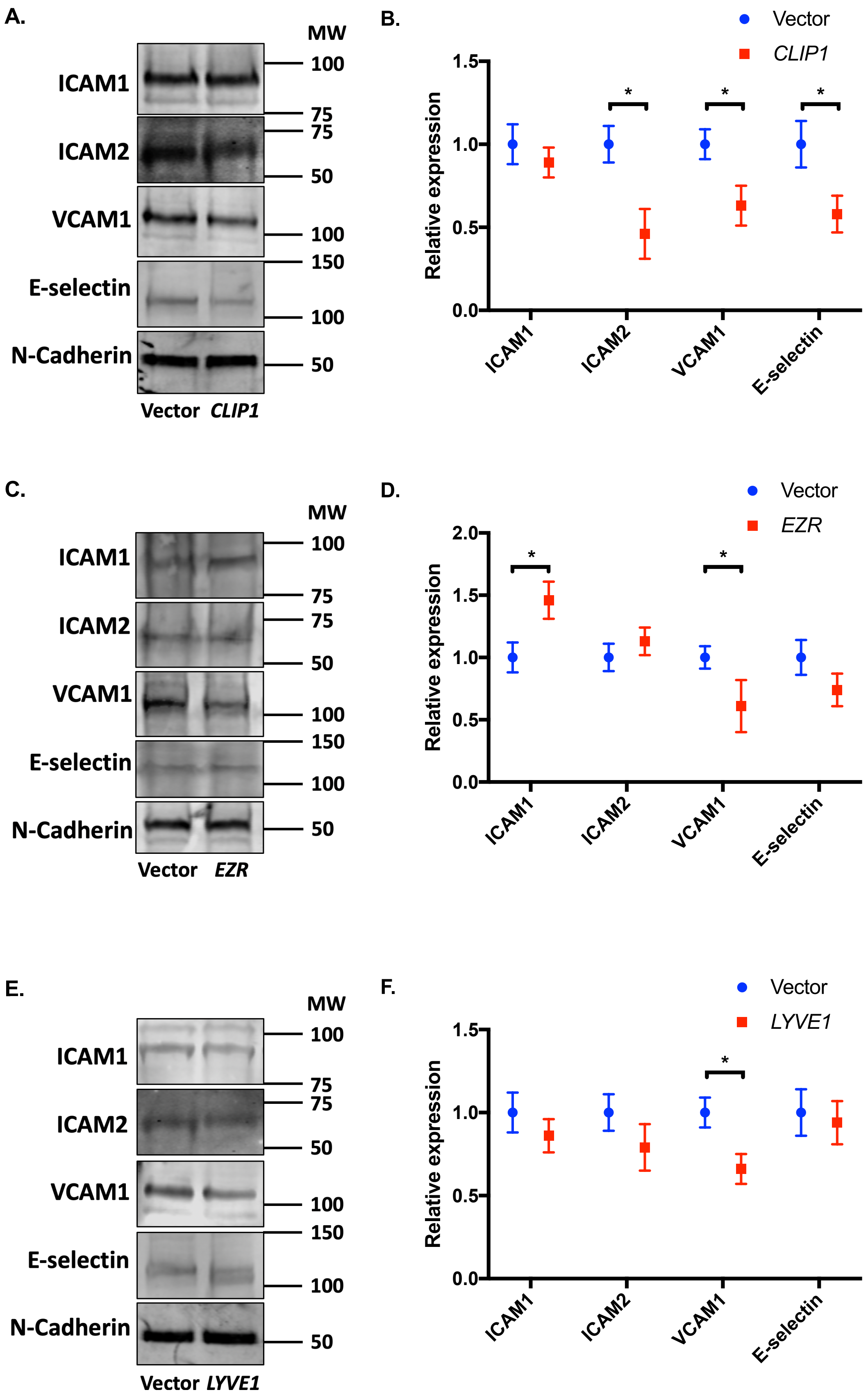
A.
MW
ICAM1
100
75
ICAM2
75
50
VCAM1
100
E-selectin
150
100
N-Cadherin
50
Vector
CLIP1
B.
Vector
CLIP1
Relative expression
1.5
1.0
0.5
0.0
*
*
*
ICAM1
ICAM2
VCAM1
E-selectin
C.
MW
ICAM1
100
75
ICAM2
75
50
VCAM1
100
E-selectin
150
100
N-Cadherin
50
Vector
EZR
D.
Vector
EZR
Relative expression
2.0
1.5
1.0
0.5
0.0
*
*
ICAM1
ICAM2
VCAM1
E-selectin
E.
MW
ICAM1
100
75
ICAM2
75
50
VCAM1
100
E-selectin
150
100
N-Cadherin
50
Vector
LYVE1
F.
Vector
LYVE1
Relative expression
1.5
1.0
0.5
0.0
*
ICAM1
ICAM2
VCAM1
E-selectin

Figure S2. Effects of overexpression of *CLIP1*, *EZR* and *LYVE1* on expression of genes encoding endothelial cell adhesion molecules.

A: Western blot analysis of cell adhesion proteins (ICAM-1, ICAM-2, VCAM-1, and E-selectin) from plasma membrane protein extracts of HCAECs transfected with pcDNA3.1 vector or pcDNA3.1-*CLIP1*. **B:** Western blot images in (**A**) were quantified and plotted. **C:** Western blot analysis of cell adhesion proteins (ICAM-1, ICAM-2, VCAM-1, and E-selectin) from plasma membrane protein extracts of HCAECs transfected with pcDNA3.1 vector or pcDNA3.1-*EZR*. **D:** Western blot images in (**C**) were quantified and plotted. **E:** Western blot analysis of cell adhesion proteins (ICAM-1, ICAM-2, VCAM-1, and E-selectin) from plasma membrane protein extracts of HCAECs transfected with pcDNA3.1 vector or pcDNA3.1-*LYVE1*. **F:** Western blot images in (**E**) were quantified and plotted. *$P<0.05$, n=3/group. N-Cadherin was used as loading control. Data were normalized to the baseline N-Cadherin expression, which was defined as 1.0. Only statistically significant values are marked with asterisk.

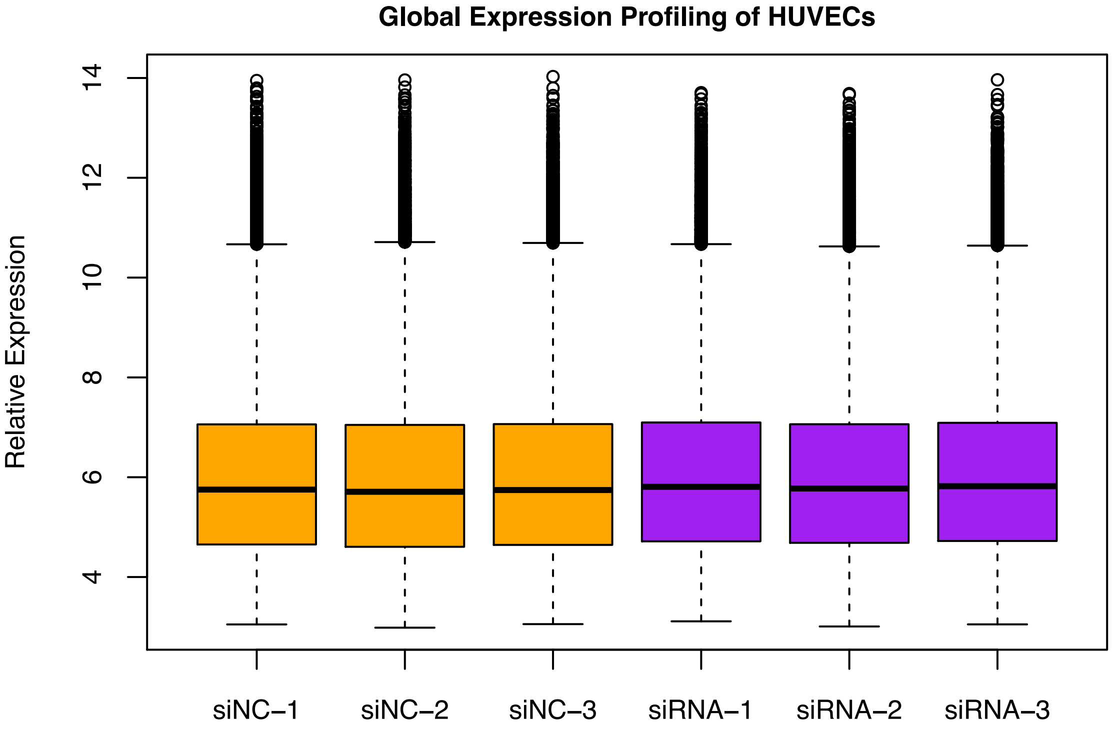

Figure S3. Genome-wide expression profiling of 6 RNA samples (3 siNC vs. 3 si*ANRIL*) from the GeneChip microarray analysis

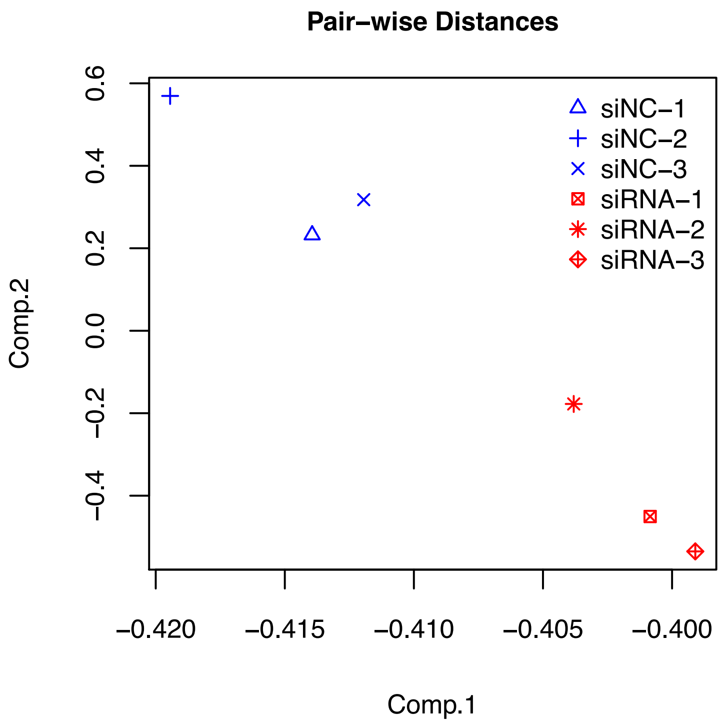

Figure S4. PCA plot of 6 samples from the GeneChip microarray analysis. X-axis and Y-axis represent the first two principal components derived using genome-wide expression data.