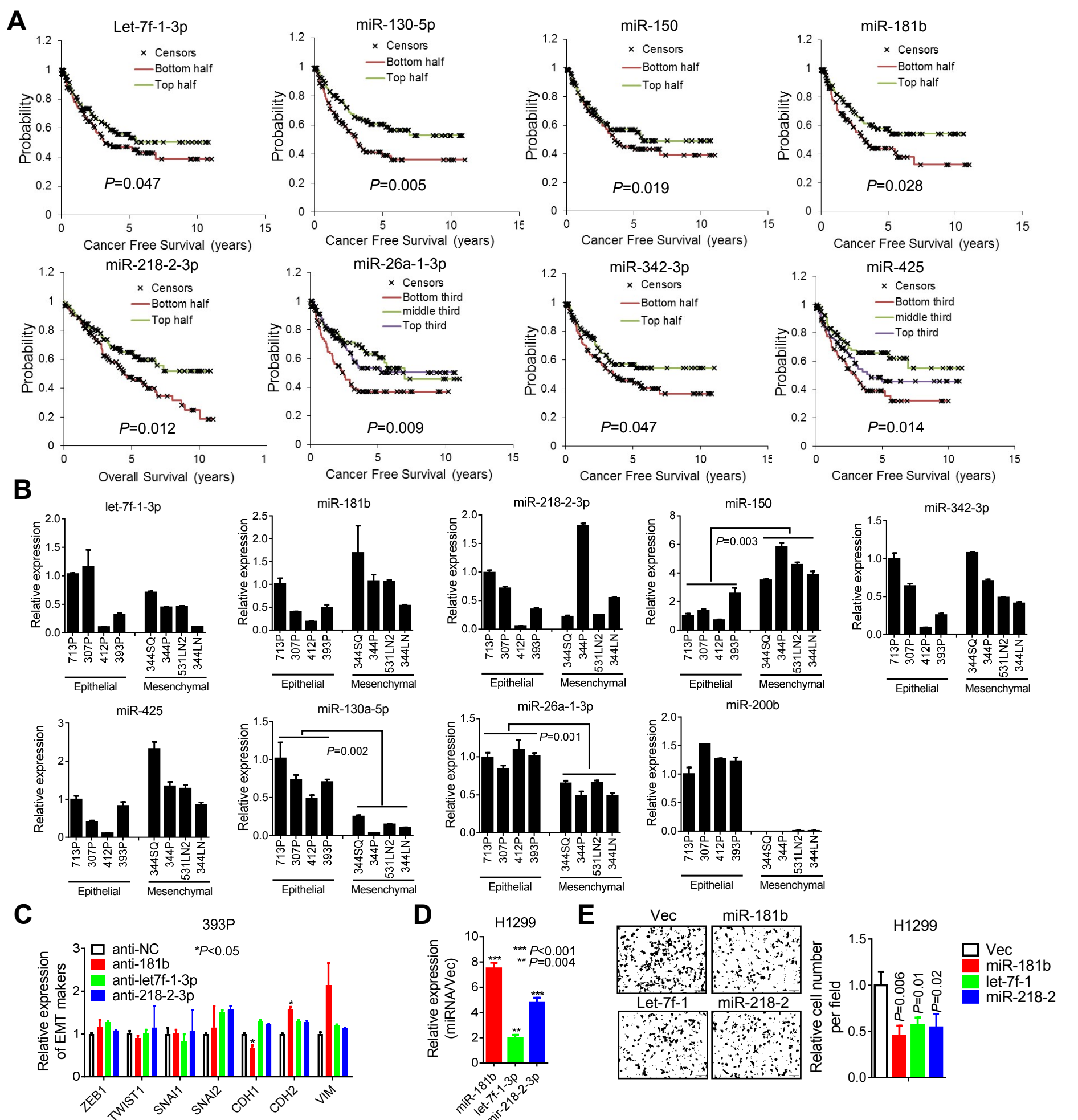
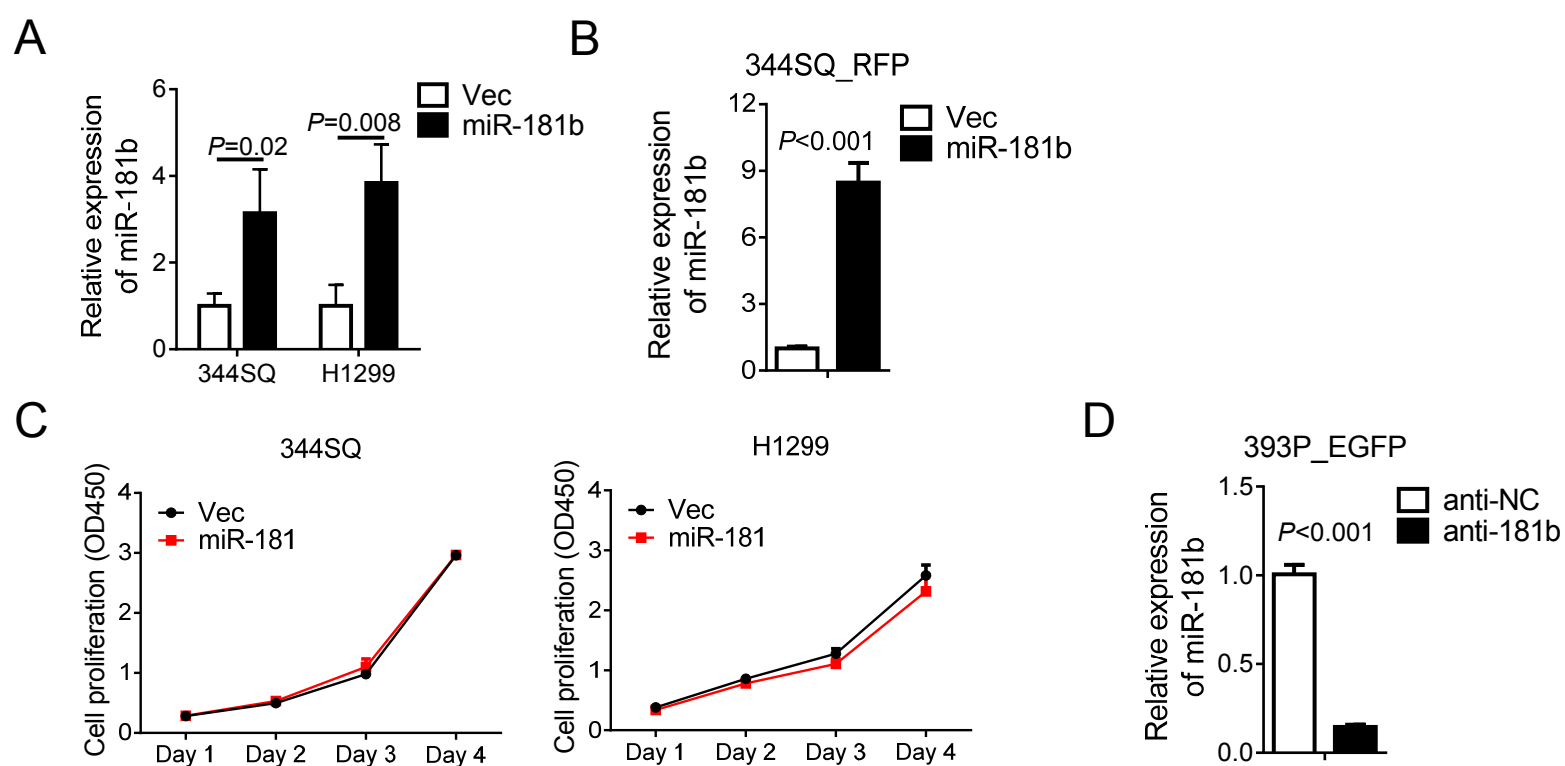
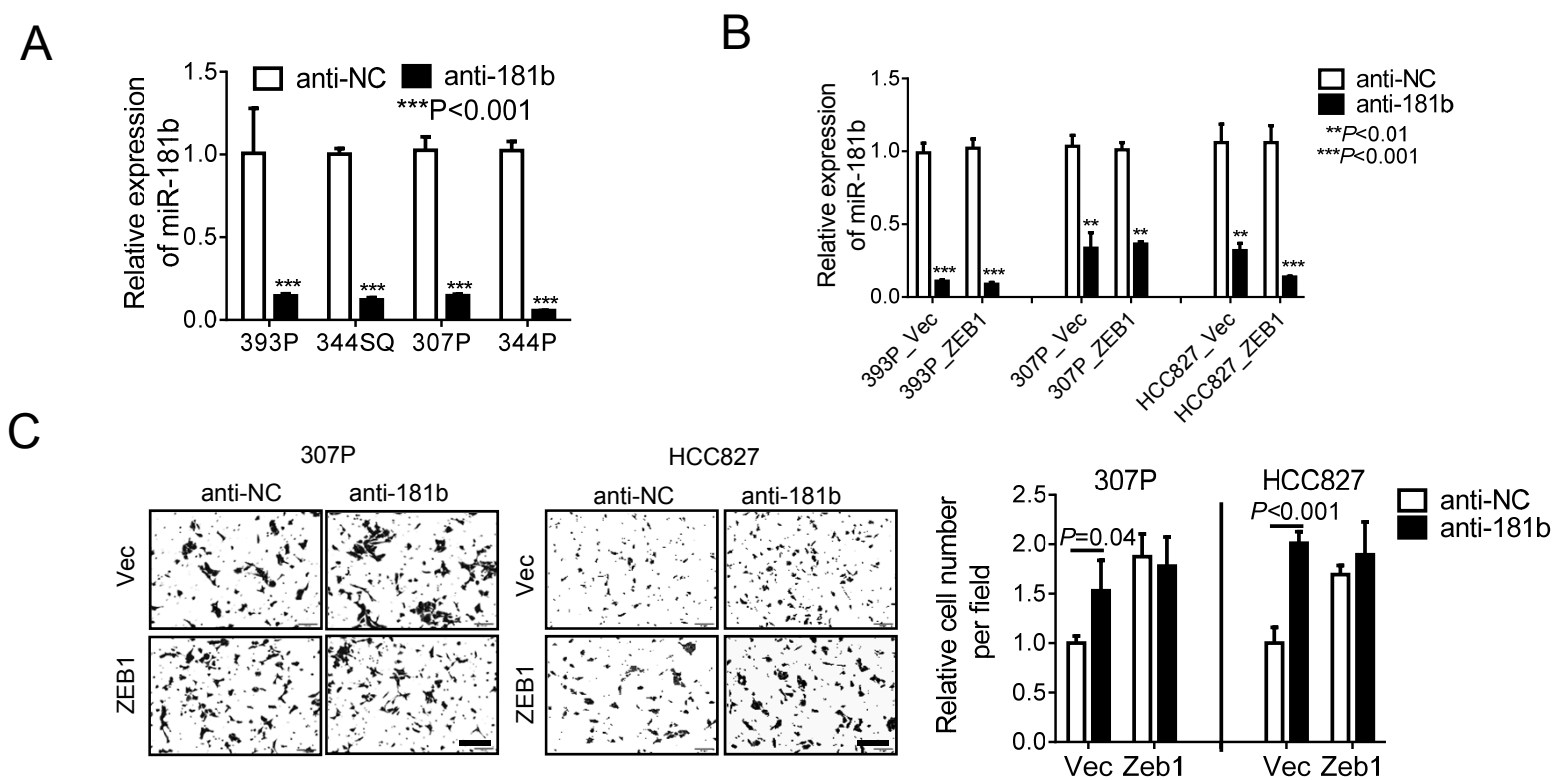




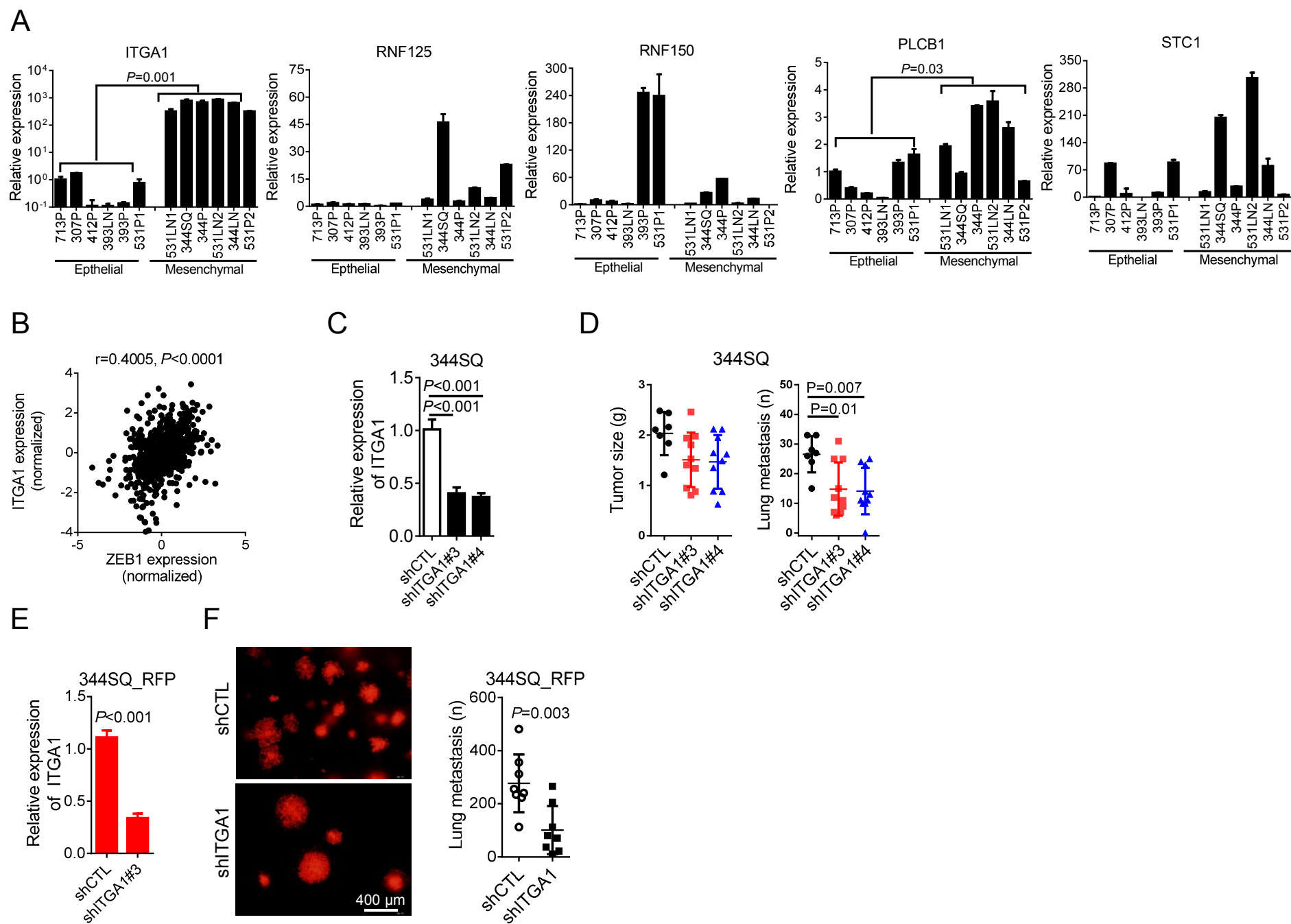
Supplemental Figure 1. miRNAs that are not downregulated by ZEB1 have metastasis suppressor activity. (A) Kaplan Meier plots showing the miR levels that are correlated positively with longer survival durations. (B) qPCR analysis of miR expression levels in KP cell lines classified as epithelial or mesenchymal. P values are indicated for those miRNAs that reach statistical significance. A ZEB1 target, miR-200b, was included as a positive control. (C) qPCR analysis of epithelial (CDH1) and mesenchymal (ZEB1, TWIST1, SNAI1, SNAI2, CDH2 and VIM) markers in 393P cells transfected with the indicated antagomirs or negative control (anti-NC). (D) qPCR assays to quantify ectopic miR expression in H1299 cells stably transfected with the corresponding miRNAs or empty vector. Results expressed relative to empty vector (Vec). (E) Boyden chamber assays of H1299 cells that express ectopic miRNAs or empty vector. Migratory cells were photographed (images) and counted (bar graphs). Results are expressed relative to empty vector transfectants. Scale bar: 200 μ m. Values are Mean $\pm$ SD. n=3. P values, 2-tailed Student's t-test and Dunnett's test for 2-group and > 2-group comparisons. Results were replicated (n $\geq$ 2 experiments).



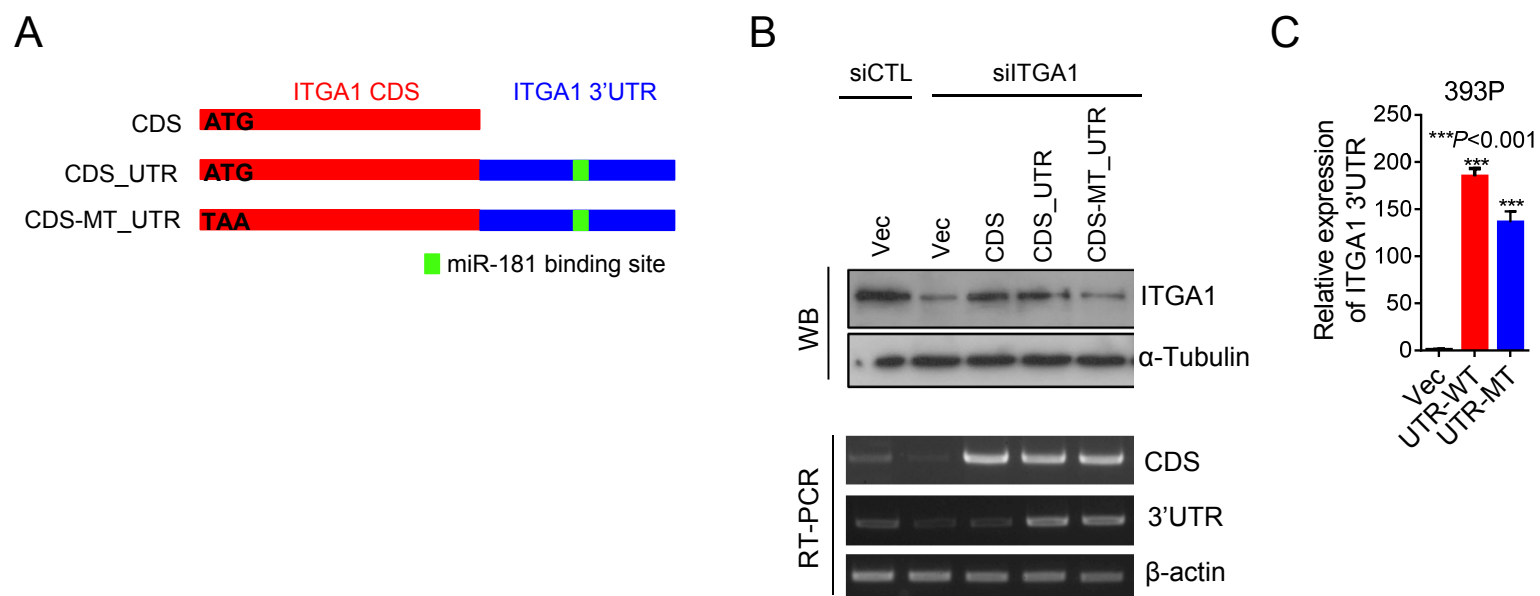
Supplemental Figure 2. Characterization of miR-181b transfectants. (A) Quantitative RT-PCR (qPCR) analysis of miR-181b levels in 344SQ and H1299 cells stably transfected with miR-181b or empty vector (Vec). (B) qPCR analysis of miR-181b levels in 344SQ_RFP cells transfected with miR-181b or empty vector (Vec). (C) Relative densities of 344SQ and H1299 transfectants in monolayer culture as assessed by the WST-1 method. $n=4$. (D) qPCR analysis of miR-181b levels in 393P_EGFP cells treated with antagomir-181b or negative control oligomers (anti-NC). Values are Mean $\pm$ SD. $n=3$, unless otherwise indicated. P values, 2-tailed Student's t-test. Results were replicated ($n \geq 2$ experiments).



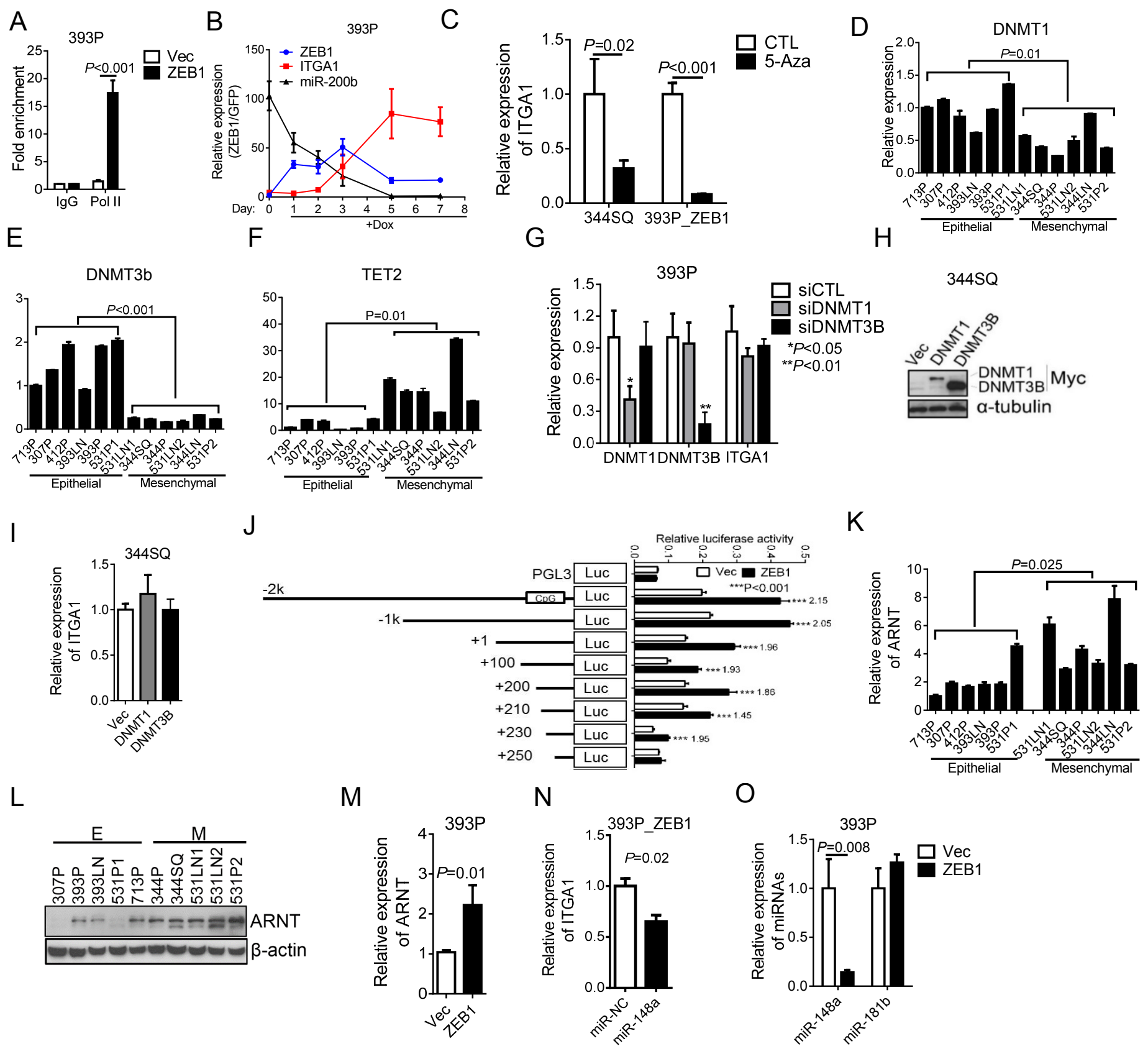
Supplemental Figure 3. AntagomiR-181b promotes the migration of lung cancer cells with low but not high endogenous ZEB1 levels. (A) Quantitative RT-PCR (qPCR) analysis of miR-181b levels in KP cells treated with antagomir-181b or negative control oligomers (anti-NC). **(B)** qPCR analysis of miR-181b levels in lung cancer cells stably transfected with ZEB1 or empty (Vec) expression vectors after treatment with antagomir-181b or anti-NC. **(C)** Boyden chamber assays of cells in **(B)**. Migratory cells were photographed (images) and counted (bar graphs). Results are expressed relative to negative controls (anti-NC). Scale bar: 200 μ m. Values are Mean $\pm$ SD. $n=3$. P values, 2-tailed Student's t-test. Results were replicated ($n \geq 2$ experiments).



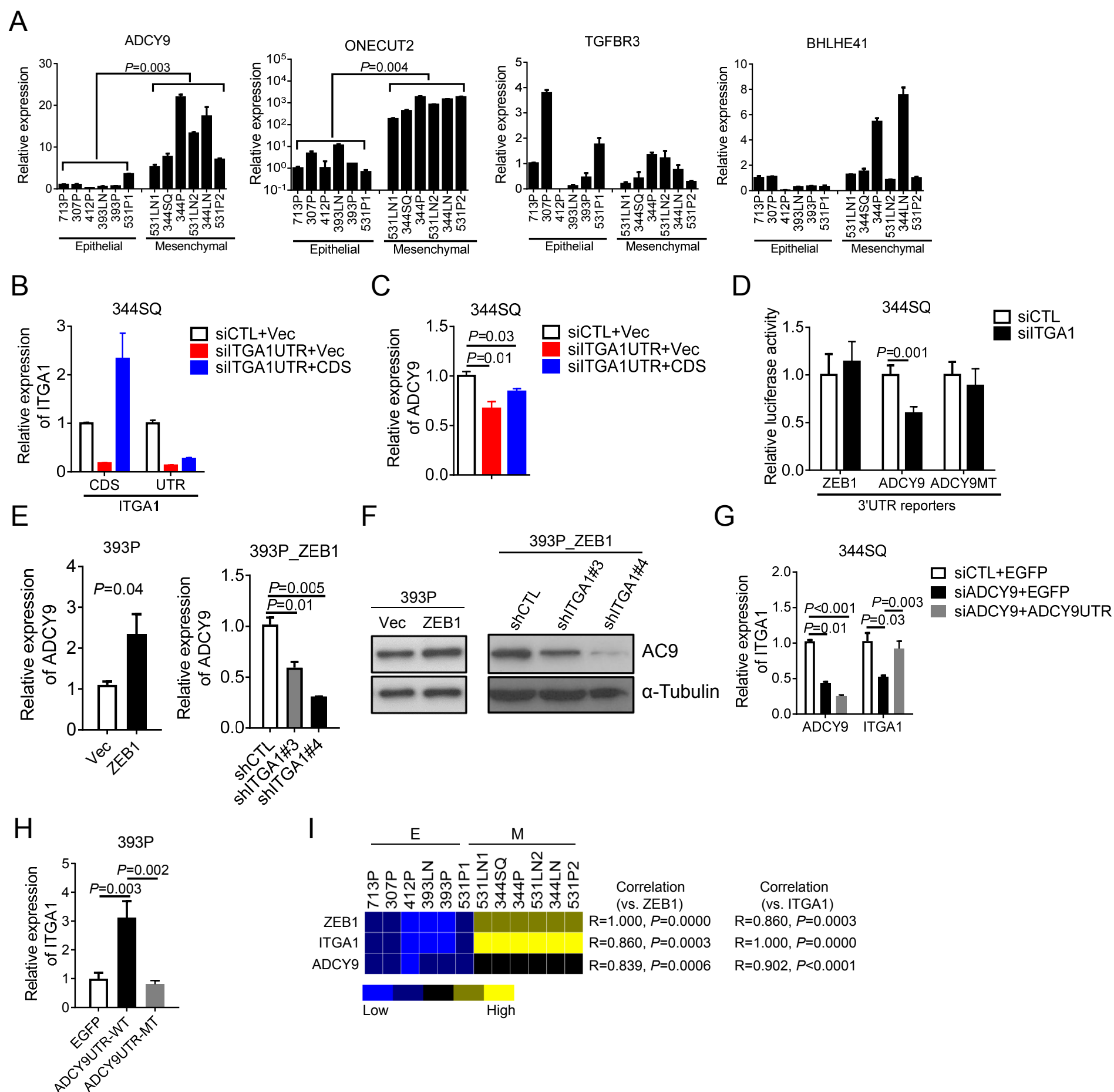
Supplemental Figure 4. ITGA1 promotes metastasis. (A) Quantitative RT-PCR (qPCR) analysis of predicted miR-181b targets that were the most highly upregulated by ectopic ZEB1 expression in 393P cells. P values are indicated for those miRs that are significantly different between epithelial and mesenchymal KP cells. (B) Scatter plot of normalized gene expression levels (ITGA1 versus ZEB1) in a compendium of 1,016 human lung adenocarcinomas in The Cancer Genome Atlas (dots). Correlation r-value by Pearson's. (C) qPCR analysis of ITGA1 mRNA in 344SQ cells stably transfected with scrambled control shRNA (shCTL) or 1 of 2 distinct ITGA1 shRNAs (shITGA1). Results expressed relative to shCTL. (D) Primary tumor weights and numbers of lung metastases in syngeneic mice injected subcutaneously with 344SQ cells stably transfected with 1 of 2 distinct ITGA1 shRNAs (shITGA1) or control shRNA (shCTL). (E) qPCR analysis of ITGA1 levels in 344SQ_RFP cells stably transfected with shITGA1 or shCTL. Results expressed relative to shCTL transfectants. (F) Fluorescence microscopic image of RFP-positive tumors on the lung surface. Scatter plot of lung metastasis numbers per mouse (dots) following tail vein injection. Values are Mean $\pm$ SD. n=3, unless otherwise indicated. P values, 2-tailed Student's t-test and Dunnett's test for 2-group and > 2-group comparisons. Results were replicated (n $\geq$ 2 experiments).



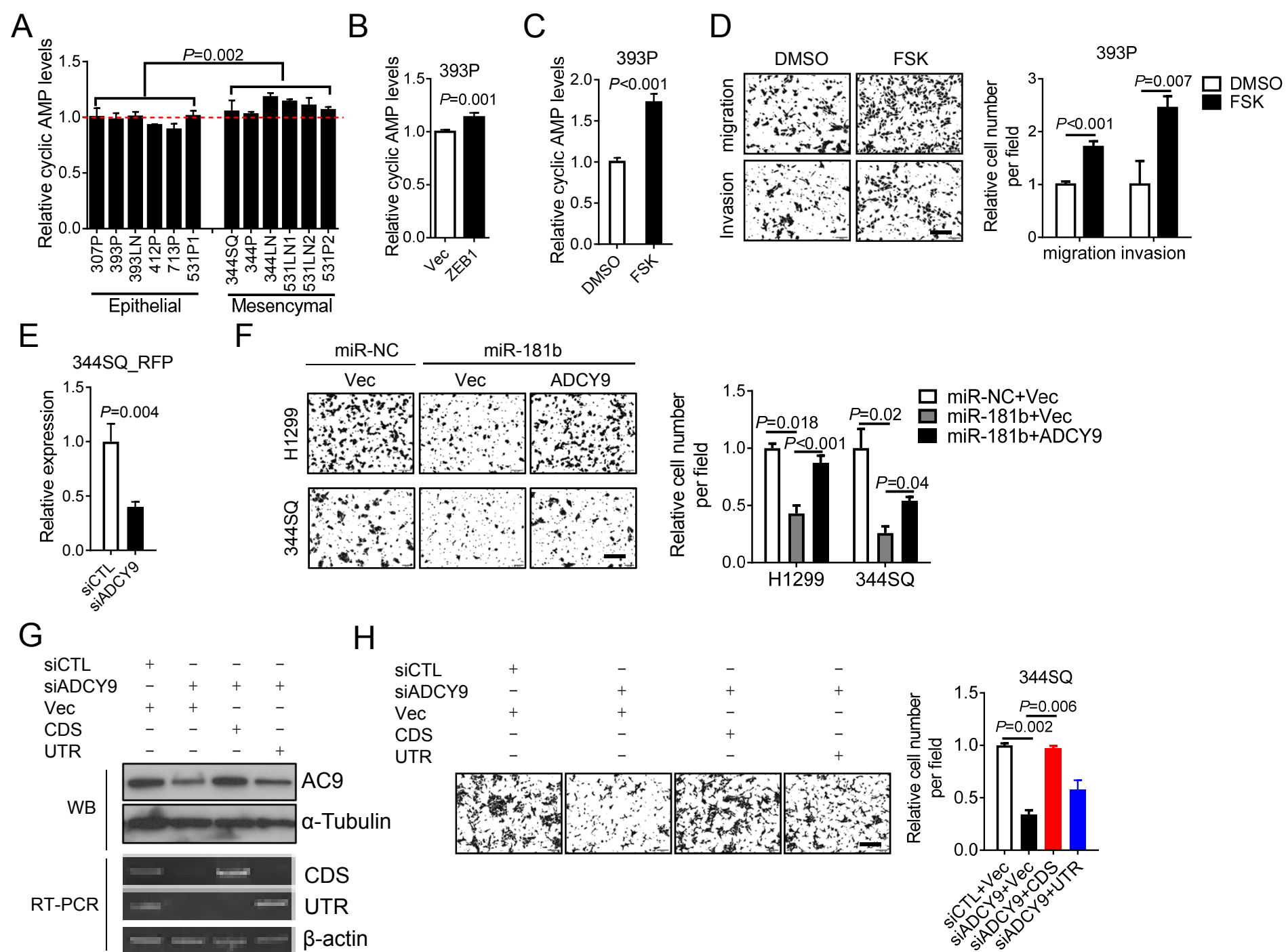
Supplemental Figure 5. Ectopic expression of ITGA1 3'UTR constructs. (A) Schematic illustration of constructs used in Figure 3E that express wild-type ITGA1 coding sequences with the 3'UTR (CDS_UTR) or without the 3'UTR (CDS) or that has a mutation (ATG to TAA) in the translation start codon (CDS-MT_UTR). (B) Western blot analysis (WB) to detect ectopic ITGA1 protein (top) and RT-PCR analysis (RT-PCR) to detect the ectopic CDS or 3'UTR RNAs. 344SQ_RFP cells were stably transfected with constructs in (A) and transiently transfected with scrambled control siRNA (siCTL) or an ITGA1 siRNA (siITGA1) that targets 3'UTR sequences to deplete endogenous ITGA1 mRNA but not the ectopic CDS or 3'UTR. α -tubulin and β -actin included as loading controls. (C) qPCR analysis of ectopic ITGA1 3'UTR expression in 393P cells stably transfected with vectors that express wild-type (UTR-WT) or miR-181b binding site-mutated 3'UTR (UTR-MT). Values are Mean $\pm$ SD. $n=3$. P values, Dunnett's test. Results were replicated ($n \geq 2$ experiments).



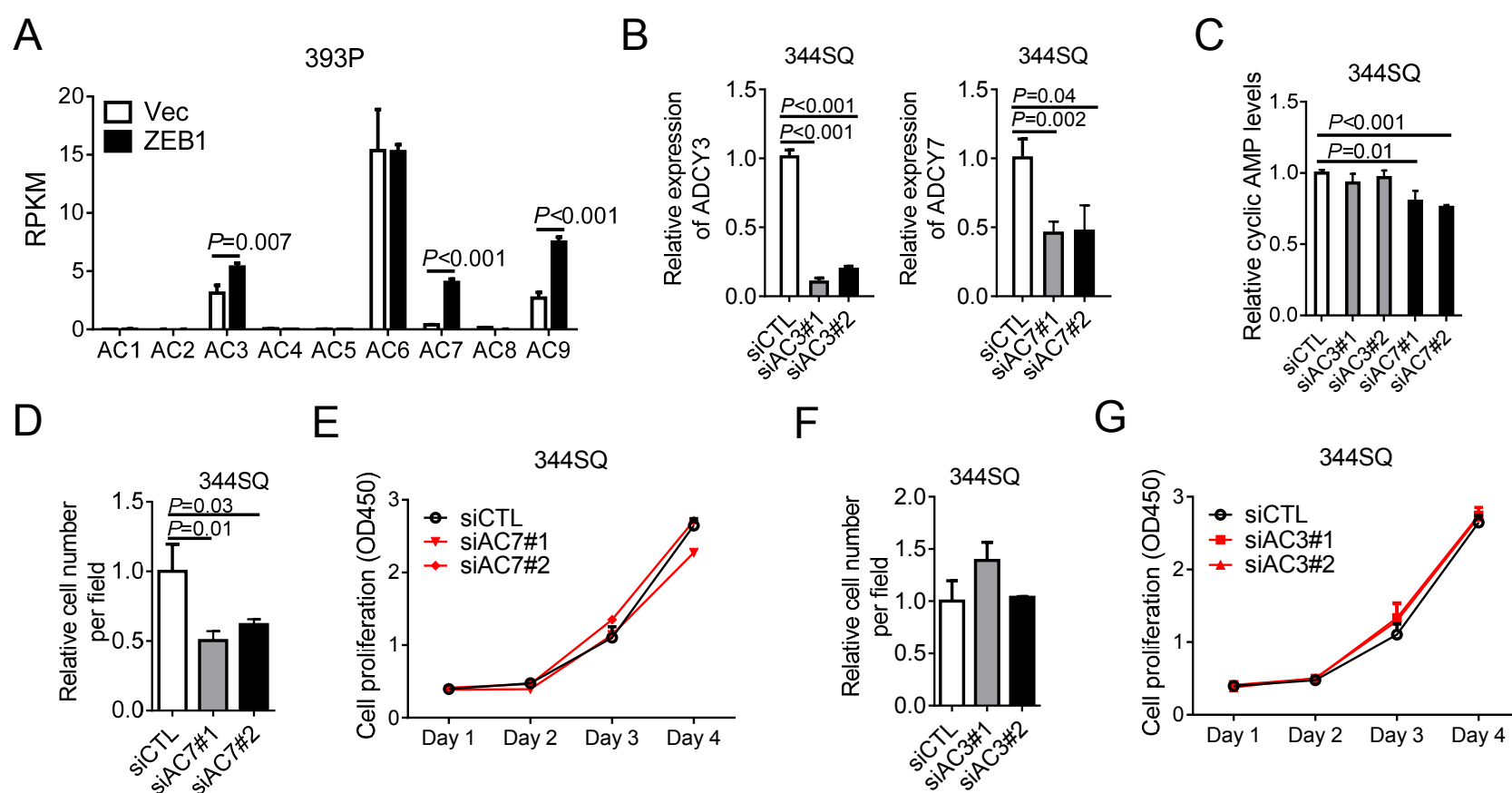
Supplemental Figure 6. Zeb1 upregulates ITGA1 expression through multiple intermediates. (A) RNA Pol II chromatin immunoprecipitation assays of the ITGA1 gene promoter in 393P_ZEB1 cells (ZEB1) and 393P_vector cells (Vec). Values are expressed relative to the IgG control. (B) Quantitative RT-PCR (qPCR) analysis of ITGA1 and ZEB1 levels before (t=0) and each day after the start of doxycycline treatment in 393P cells that express doxycycline-inducible ZEB1. A ZEB1 target, miR-200b, was included as a positive control. (C) Quantitative RT-PCR (qPCR) analysis of mRNA levels after treatment with vehicle (CTL) or 5-azacytidine (5-Aza). (D-F) qPCR analysis of mRNAs in KP cells classified as epithelial or mesenchymal. (G) qPCR analysis of mRNAs in 393P cells transiently transfected with siRNAs against DNMT1 (siDNMT1), DNMT3B (siDNMT3B), or scrambled control (siCTL). (H and I) Western blot analysis (E) and qPCR analysis of ITGA1 mRNA (F) in 344SQ cells transiently transfected with Myc-tagged DNMT1 or DNMT3B. Ectopic DNMT protein detected using an anti-Myc antibody. Anti- α -tubulin antibody included as a loading control. (J) Schema, luciferase reporters driven by ITGA1 promoter fragments. Bar graph, luciferase activities in 393P cells co-transfected with reporters and ZEB1 or empty (Vec) expression vector. (K) qPCR analysis of ARNT mRNA levels in KP cells classified as epithelial or mesenchymal. (L) Western blot analysis of ARNT protein levels in KP cells classified as epithelial (E) or mesenchymal (M). β -actin was used as a loading control. (M) qPCR analysis of ARNT mRNA levels in 393P_ZEB1 cells (ZEB1) and 393P_Vec cells (Vec). (N) qPCR analysis of ITGA1 mRNA levels in 393P_ZEB1 cells transiently transfected with miR-148a or non-coding control (miR-NC). (O) qPCR analysis of miRs in 393P_ZEB1 cells (ZEB1) and 393P_vector cells (Vec). Values are Mean $\pm$ SD. n=3, unless otherwise indicated. P values, 2-tailed Student's t-test and Dunnett's test for 2-group and > 2-group comparisons. Results were replicated (n $\geq$ 2 experiments).



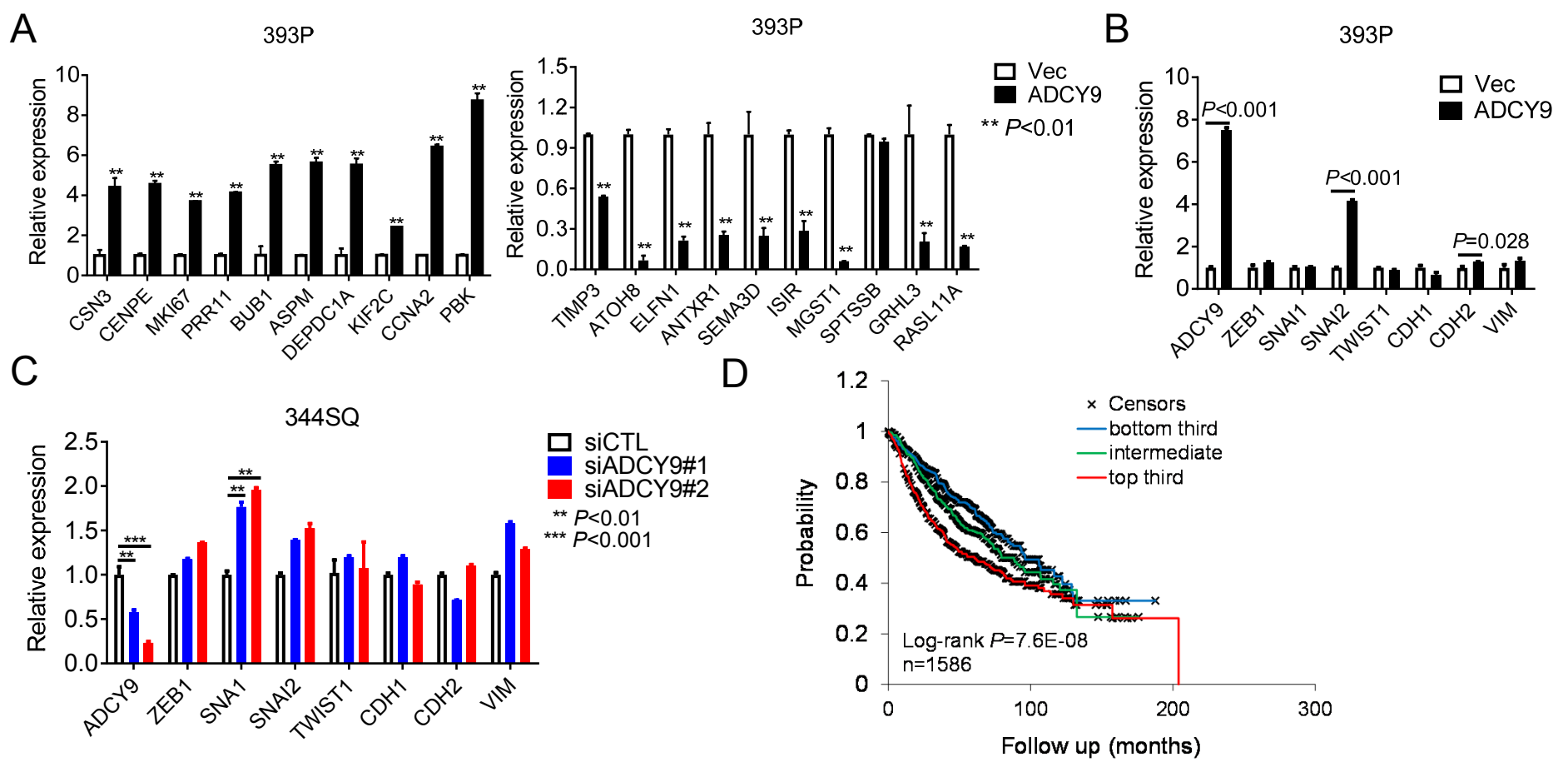
Supplemental Figure 7. ITGA1 and ADCY9 compete for binding to miR-181b. (A) Quantitative RT-PCR (qPCR) analysis of mRNAs. P values are indicated for those mRNAs that are significantly different between KP cell lines classified as epithelial or mesenchymal. (B and C) qPCR analysis of ITGA1 (B) and ADCY9 (C) mRNA levels in 344SQ cells co-transfected with siRNA against the 3'UTR of ITGA1 (siUTR) or control siRNA (siCTL) and a vector that expresses ITGA1 coding sequence (CDS) or nothing (Vec). (D) ITGA1 3'UTR reporter activities in 344SQ cells transiently co-transfected with ITGA1 siRNA (siITGA1) or control siRNA (siCTL) and the indicated 3'UTR reporter constructs. (E and F) ADCY9 mRNA (E) and AC9 protein (F) levels in 393P cell transfectants by qPCR and WB, respectively. (G) qPCR analysis of ADCY9 and ITGA1 mRNA levels in 344SQ cells co-transfected with scrambled siRNAs (siCTL) or ADCY9 siRNAs (siADCY9) and ADCY9 3'UTR (ADCY9UTR) or EGFP control expression vectors. (H) qPCR analysis of ITGA1 mRNA levels in 393P cells transfected with wild-type ADCY9 3'UTR (WT) or mutant ADCY9 3'UTR lacking miR-181b binding sites (MT) or EGFP expression vectors. (I) A heat map showing the expression pattern of ZEB1, ITGA1, and ADCY9 in KP cell lines classified as epithelial (E) or mesenchymal (M). Pearson correlation analysis was performed. Values are Mean $\pm$ SD. n=3. P values, 2-tailed Student's t-test and Dunnett's test for 2-group and > 2-group comparisons. Results were replicated (n $\geq$ 2 experiments).



Supplemental Figure 8. ADCY9 increases cyclic AMP production and promotes tumor cell migration and invasion. (A-C) Cyclic AMP levels in: (A) KP cell lines classified as mesenchymal or epithelial; (B) 393P_ZEB1 cells (ZEB1) and 393P_vector cells (Vec); (C) 393P cells treated with forskolin (FSK) or the vehicle dimethylsulfoxide (DMSO). (D) Boyden chamber assays of 393P cells treated with FSK or DMSO. Migratory cells were photographed (images) and counted (bar graphs). Results are expressed relative to controls. Scale bar: 200 μ m. (E) qPCR analysis of ADCY9 mRNA levels in 344SQ_RFP cells transfected with ADCY9 siRNA (siAC9) or scrambled siRNAs (siCTL). Results are expressed relative to siCTL transfectants. (F) Boyden chamber migration assays of 344SQ and H1299 cells co-transfected with miR-181b or control miR mimic and ADCY9 or empty (Vec) expression vector. Migratory cells were photographed (images) and counted (bar graphs). Results are expressed relative to controls. Scale bar: 200 μ m. (G) Western blot (WB) and RT-PCR analysis of 344SQ cells transfected with (+) or without (-) ADCY9 siRNA (siADCY9), scrambled siRNA (siCTL), ADCY9 coding sequence (CDS), ADCY9 3'UTR (UTR), or empty vector (Vec). (H) Boyden chamber assays of 344SQ cell transfectants from (G). Migratory cells were photographed (images) and counted (bar graphs). Results are expressed relative to controls. Scale bar: 200 μ m. Values are Mean $\pm$ SD. $n=3$, unless otherwise indicated. P values, 2-tailed Student's t-test and Dunnett's test for 2-group and > 2-group comparisons. Results were replicated ($n \geq 2$ experiments).



Supplemental Figure 9. Expression and biological roles of ADCY isoforms in KP cells. (A) Expression levels of ADCY (AC) mRNAs in 393P_Vector cells and 393P_ZEB1 cells determined by RNA-seq. Results expressed as reads per kilobase of transcript per million mapped reads (RPKM). (B) qPCR analysis of ADCY3 (left) and ADCY7 (right) mRNA levels in 344SQ cells transfected with ADCY3 siRNA (siAC3) or ADCY7 siRNA (siAC7) or siCTL. Results are expressed relative to siCTL transfectants. (C) Cyclic AMP levels in 344SQ cells transfected with siAC3, siAC7, or siCTL. (D) Boyden chamber assays of 344SQ cells transfected with siCTL or siAC7. Migratory cells were photographed (images) and counted (bar graphs). Results are expressed relative to siCTL transfectants. Scale bar: 200 μ m. (E) Relative densities of 344SQ cells transfected with siAC7 or siCTL in monolayer culture as assessed by the WST-1 method. $n=4$. (F) Boyden chamber assays of 344SQ cells transfected with siCTL or siAC3. Migratory cells were photographed (images) and counted (bar graphs). Results are expressed relative to siCTL transfectants. Scale bar: 200 μ m. (G) Relative densities of 344SQ cells transfected with siAC3 or siCTL in monolayer culture as assessed by the WST-1 method. $n=4$. Values are Mean $\pm$ SD. $n=3$, unless otherwise indicated. P values, 2-tailed Student's t-test and Dunnett's test for 2-group and > 2 -group comparisons. Results were replicated ($n \geq 2$ experiments).



Supplemental Figure 10. ADCY9 does not induce EMT but activates a poor-prognosis expression signature in lung cancer. (A) qPCR validation of genes found by Affymetrix profiling to be upregulated (left bar graph) or downregulated (right bar graph) by ectopic ADCY9 expression in 393P cells. (B and C) qPCR analysis of mRNA levels of markers of epithelial (CDH1) and mesenchymal (ZEB1, SNAI1, SNAI2, TWIST1, CDH2, VIM) differentiation in 393P_ADCY9 cells (AC9) and 393P_vector cells (Vec) (B) or 344SQ cells transfected with siCTL or 1 of 2 ADCY9 siRNAs (C). Results are expressed relative to Vec (B) and siCTL (C) transfectants. (D) Kaplan-Meier analysis of lung cancer patients, comparing the differences in risk between tumors with high (“top third”), intermediate, or low (“bottom third”) t-scores that reflect the degree of overlap with the 1,421-gene expression signature. Log rank test (Log rank p) evaluates differences between two arms. Values are Mean $\pm$ SD. $n = 3$, unless otherwise indicated. P values, 2-tailed Student’s t-test and Dunnett’s test for 2-group and > 2 -group comparisons. Results were replicated ($n \geq 2$ experiments).

Supplementary Table 1

Cancer	Correlation coefficient			P value		
	ADCY9 vs. ITGA1	ADCY9 vs. ZEB1	ITGA1 vs. ZEB1	ADCY9 vs. ITGA1	ADCY9 vs. ZEB1	ITGA1 vs. ZEB1
ACC	0.371300768	0.393727558	0.120483507	0.000754738	0.000330798	0.290205695
BLCA	0.453964941	0.485035176	0.754298922	3.90E-22	1.83E-25	3.35E-76
BRCA	0.163876597	0.299120903	0.768174823	4.93825E-08	4.53E-24	6.75E-214
CESC	0.018469113	0.042712944	0.582454101	0.748422031	0.458089572	5.23E-29
CHOL	0.124297352	-0.055910382	0.623011932	0.470127038	0.746031373	4.9452E-05
CRC	0.096102511	0.221989007	0.706858057	1.64E-02	2.15E-08	1.91E-95
DLBC	0.39525568	0.532669137	0.563380419	0.005428558	9.73E-05	3.06E-05
ESCA	0.207041952	0.264945076	0.734902611	0.004803331	2.78E-04	1.61E-32
GBM	0.226577313	0.206631372	0.210841649	0.003849629	0.008541669	0.007259847
HNSC	0.258010356	0.314444946	0.789367133	2.3614E-09	2.13E-13	7.75E-112
KICH	-0.079396631	0.040897766	0.33900585	0.526277488	0.744391673	0.005361976
KIRC	0.36086756	0.296517452	0.767771417	7.75E-18	2.80205E-12	9.90E-105
KIRP	0.086527109	-0.076459454	0.591369183	0.141589458	0.194172098	9.64E-29
LAML	0.037756318	-0.245705611	-0.016426209	0.621883606	0.001120336	0.830156207
LGG	0.225548888	0.043999326	0.197481779	2.24362E-07	0.318506449	6.19481E-06
LIHC	0.393447577	0.239384051	0.491857534	3.48E-15	3.11213E-06	5.37E-24
LUAD	0.107844485	0.280283311	0.557525511	0.0143421	9.45457E-11	2.13E-43
LUSC	0.295068055	0.324961737	0.703961405	1.60E-11	8.73E-14	3.59E-76
MESO	0.08540522	0.080209663	0.483101988	0.431560847	0.460200918	2.14E-06
OV	0.130306668	0.273563308	0.639833267	0.035021563	7.03E-06	1.43E-31
PAAD	0.323634817	0.335222617	0.814849085	1.05E-05	4.79E-06	1.54E-43
PCPG	0.091605695	0.296435866	0.155400442	0.222623977	5.60E-05	0.037784356
PRAD	0.59579456	0.547776047	0.823481832	4.45E-49	2.93E-40	6.19E-124
SARC	0.477786885	0.349290501	0.397418396	3.55E-16	7.60035E-09	3.12801E-11
SKCM	-0.21714274	-0.318660976	0.658592344	2.06726E-06	1.58E-12	1.19E-59
STAD	0.49119428	0.562750918	0.761153463	1.37E-26	4.90E-36	1.12E-79
TGCT	0.598214135	0.391715669	0.48182847	6.29E-16	7.16E-07	4.31E-10
THCA	0.43621786	0.305125625	0.797880951	8.82E-25	2.68E-12	3.32E-112
THYM	0.597308851	-0.227587608	-0.071254535	5.97E-13	0.012422848	0.439304599
UCEC	0.039590203	0.167767068	0.59395272	0.356277095	8.3025E-05	2.88E-53
UCS	0.103090071	0.503261857	0.186944163	0.445400028	6.60E-05	0.163789592
UVM	-0.149424309	-0.149217401	0.794379398	0.185869348	0.186486286	1.46E-18

Supplementary table 3

qPCR primers		
Gene	Forward (5'-3')	Reverse (5'-3')
Itga1 (mouse)	TGGCTTCTCACC GTTATCCTA	CACACAAGGCATTGATCTCTCT
ITGA1(human)	CCGAAGAGGTACTTGTTCGAGC	GGCTTCCGTGAATGCCCTCCTTT
Rpl32(mouse)	GGAGAAGGTTCAAGGGCCAG	TGCTCCCATAACCGATGTTTG
RPL32 (human)	CCTTGTGAAGCCCAAGATCG	TGCCGGATGAAC TTCTTGGT
Zeb1 (mouse)	GCTCAGCCAGGAACCCGAG	TGGGCACCCTCTGCCACACA
Dnmt1 (mouse)	GGACAAGGAGAATGCCATGAAGC	TTACTCCGTCCAGTGCCACCAA
Dnmt3a (mouse)	CGCAAAGCCATCTACGAAGTCC	GCTTGTCTGCACTTCCACAGC
Dnmt3b (mouse)	CGCACAACCAATGACTCTGCTG	GGTGACTTCAGAAGCCATCCGT
Tet1 (mouse)	TCACAACATGCACAACGGA	GGTTGGCCCATTGACTTG
Tet2 (mouse)	ACCTGGCTACTGTCTATTGCTCC	TGCAGTGACTCCTGAGAATGGC
Tet3 (mouse)	GCAGAAGGAGAACTGAGCAC	CTTAAAGGAGCTAAAGTGGTTCTGAG
Arnt (mouse)	CTCACGAAGGTCGTTTCACTGTC	CCACAAGTGAGGTTCTCCTTCC
Fgd4 (mouse)	CCTCAAAGTAGCAGCTCGGAAC	GAGCCAACCAAGCTGAATCTGG
Sema4g (mouse)	TTCATGGAGCGTGAGGAAGGCT	TGGCAGATGAGACGAGCCTTCA
Pkdc (mouse)	AGCTGTTGCAGACTTCCTGGGA	CCGTTCACTAGCACAACTGCC
Thrb (mouse)	ACCACTATCGCTGCATCACCTG	ACTGGTTGCGGGTGACTTTGTC
Nmnat2 (mouse)	TGTCAAGTCGGCACCGTCTCAT	ATCAGGTCTCGATGGTGTCTCA
Evi2a(mouse)	CTTCTGGACAGCAAGCATCACC	TGAGGCAAGGAGTTGTTGACCG
Plcl2(mouse)	GGAACGGAACTACAGAAGGCAG	GTGGATCTGCTTCAGGTTCTCC
Onecut2(mouse)	TTCCAGCGCATGTCTGCCTTAC	GAAGATGGCGAAGAGTGTTCGG
Trim2(mouse)	CACGAACCTCATGGATGTGCTG	GGTCTCACAGGACTGGCAGTAA
Vcan (mouse)	GGACCAAGTTCACCCCTGACAT	CTTCACTGCAAGGTTCTCTTCT
Sipa1l2(mouse)	GACGTGATTGGCTGGACTTCAG	GTCATTTCCACAGTCTCGCAGC
Adcy9(mouse)	GCAAAATGGCTGTCAAGACGAGC	CTGGCTGTAGTGAGCTTCTCC
Mfsd6(mouse)	TGAGCTGAGGACTTCTGCACAG	TGCCAATCCCTCGAAAGTTGC
Megf9(mouse)	GGTGCAGAGAAATGCCTAGAAGG	GCACTGATGTGGTCAAAGAGGC
Zfhx4(mouse)	AGCCTTGACAGCAGAGGGTTCT	GCTCCTTTGCTGGCTTCTGTTT
Hoxb4(mouse)	CTGGATGCGCAAAGTTCACGTG	CGCTCAGGTAGCGATTGTAGTG
Itsn1(mouse)	TGCTCCTTTGCCAGTGACCTCT	TCTGGCTTCTCGTTTGAGCTGC
Pax9(mouse)	ATCCGCTCCATCACCGACCAAG	CCTTCTCCAATCCATTCACTGCG
Dock4(mouse)	GATAGGAGAGGTGGATGGCAAG	CGCCTTGAGATGCAGATCGTAG
Mb21d2(mouse)	GGAAATACGACGACGAGAGCG	GAGAGCAACAGATACTCGTTGGC
Fos (mouse)	GGGAATGGTGAAGACCGTGTCA	GCAGCCATCTTATTCGGTTCCC
Asah2(mouse)	GTGACAACGACAAGAGCACCTG	GCCTTCTGATAGATGATCCGTCC
Nsun3(mouse)	CTGTCTCGTCGGACTCTCAGA	TCAGCCTTGGAAGCGTGCATG
G6pc3(mouse)	CCTTCATTGCTGAGTGGCTCAAC	CCTGGACCAGTCTCACAAGAAG
Dip2c(mouse)	CAGATAGAGGACAATGACCAGGC	CCGACAGTTGAGCAGAGGTAC
Cnksr3(mouse)	ATGGATGCCTCCCTGAAGAAGG	GTGTCCTCTGTAGCCGAAACTC
Iqgap2(mouse)	CGCCAGGAATATCTGCACAGAC	CTTCCTTGCTGTCAACATTCGG
Tmed8(mouse)	ATAACCGTGCAGGTGAGTCTC	AGAACTCCTGGAGCCTCTCTCT
Bhlhe41(mouse)	GGCATTGGAGAAAGCAGTAGTC	AGTGGAAACGCATCCAAGTCGGC
Adcy3 (mouse)	CCTCTGAGGATGAGCACGAACT	GAGTAGCGTGTTCATCTCTGG
Adcy7 (mouse)	GACGAGATGCTGTCAAGCATTG	CACGCTCAAAGCCCTTCTCCAA
Rnf150 (mouse)	GCTCCAACACAACGAGACCATC	CCTTTCAGCAGGCTCACTATC
Rnf125 (mouse)	TGTCAGCGGGAAGTGGATGAAG	CAGGTCGTGAATGGCAAAGTGG
stc1 (mouse)	AGGAGGACTGCTACAGCAAGCT	TCCAGAAGGCTTCGGACAAGTC
Plcb1 (mouse)	CGCTGAGGAAGAGCCTGTCTATT	GTCTTGAACGCACACTCTGCGA
Csn3 (mouse)	CTACTTCTGCTTAGTCTCCAGC	GGTTGGAATGGCGGTGTATCC
Aspm (mouse)	GCAAAGGAAGTTGCGGATGCTG	TAGTGCTTCAACCTCAGAAACCG

Bub1 (mouse)	TGCCACAGTGTGGACCAGAAAC	GACAGTTGGTGATGGTGCCT
Prr11 (mouse)	ACCAGAGGAACGCACTCCACTA	CTACCTGGACTTTTCTCAGCAGC
Mki67 (mouse)	GAGGAGAAACGCCAACCAAGAG	TTTGTCTCGGTGGCGTTATCC
Cenpe (mouse)	AGGATCATGCCACCAGAGAAGAC	GCTGTGTCTCTTGGAGTTTCTGG
Pbk (mouse)	CTCAGAGTGTCTTTGCACATGGC	CATCCAATGGCAGAGAGACTCC
Ccna2 (mouse)	TTGTAGGCACGGCTGCTATGCT	GGTGTCTCCATTCTCAGAACCTG
Kif2c (mouse)	CTGTGCCTACAACTCTCGCAAG	TGCTCTTCTGCCTCCTCACTGA
Depdc1a (mouse)	AGCTCGGAGAGTCTAGTACCAC	CCTCTCTAAGTGAGGTTGCAGC
Timp3 (mouse)	AGGATGCCTTCTGCAACTCCGA	GTGTAGACCAGAGTGCCAAAGG
Antxr1 (mouse)	CGGATTGCAGACAGTAAGGACC	GGATGGTTCAGCCGCCAGAATT
Sema3d (mouse)	TAGACACGCACAACCTGGAGTC	GCTGTTCCAGAGTAGAGGTGCT
Islr (mouse)	CCAATGTGACCACACTGAGCCT	AATAGCCACCGAGCGGATCTCA
Elfn1 (mouse)	ATCGTTCACCGTGTCCAAGCTG	GCTGGTAGAGACCACGCAGTAT
Atoh8 (mouse)	CAACGGAGATCAAAGCCCTGCA	CTTCTGCCCATAGGAGTAGCAC
Mgst1 (mouse)	TGCGACCGCATTCCAGAGGATA	TCCACCTTCTCGTCAGTGCGAA
Sptssb (mouse)	TGCTGTCATGGAGCCTTGGGAA	ATTCCCAAGCCAGGCGGATGTG
Grhl3 (mouse)	GTCCAGCACATTGAAGAGGTGG	TGCGAGGAGAAGTCTGTGCTCA
Rasl11a (mouse)	GATTCATCGGCGACTACGAACC	CGGAGTGTCTGGATCTGTAGG
ChIP PCR primers		
Pol II ChIP primers	AAGATCGCCCTCTCAGTGAA	CTGTCCGAGACATGGACAAA
ARNT ChIP primers (+200)	CCATCTGGGATCTGAGAAGC	GACGCCTGGGGACCAT
ARNT ChIP primers (+1k)	GTGGCACCCCTTCTCTACTTT	CCTGGTCACTCATGATCCC
DNA methylation related primers		
BSP primers	TTTAGTGAAAGGTAGATGTTTTTTTAAG	TACTAATTCRTAAACAAAACTAACAAAA
miRNA qPCR RT primers		
miR-148a-RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACACAAAG	
U6-RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACAAAATATG	
miR-181a-RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACACTCAC	
miR-181b-RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACACCCAC	
miR-218-5p-RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACACATGG	
miR-342-3p-RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACACGGGT	
let-7f-1-3p-RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACGGGAAG	
miR-150-5p-RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACCACTGG	
miR-425-3p-RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACGGCGGA	
miR-26a-1-3p-RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACCGTGCA	
mir-130a-3p-RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACATGCC	
miRNA qPCR primers	Forward (5'-3')	Reverse (5'-3')
U6	GCGCGTCGTGAAGCGTTC	GTGCAGGGTCCGAGGT
miR-148a	CGCGTCAGTGCACCTACAGAAC	GTGCAGGGTCCGAGGT
miR-181a	CATTCAACGCTGTGCGGTG	GTGCAGGGTCCGAGGT
miR-181b	AACATTCAATTGCTGTGCGGTGG	GTGCAGGGTCCGAGGT
miR-218-5p-rltm	CGCGTTGTGCTTGATCTAAC	GTGCAGGGTCCGAGGT
miR-342-3p-rltm	CGTCTCACACAGAAATCGCA	GTGCAGGGTCCGAGGT
let-7f-1-3p-rltm	GCGCGCTATACAATCTATTGC	GTGCAGGGTCCGAGGT
miR-150-5p-rltm	CGTCTCCAACCCCTTGTC	GTGCAGGGTCCGAGGT
miR-425-3p-rltm	CGATCGGAATGTGCGTG	GTGCAGGGTCCGAGGT

miR-26a-1-3p-rltm	CGCGCCTATTCTTGTTACTT	GTGCAGGGTCCGAGGT
mir-130a-3p-rltm	GCGCCAGTGCAATGTTAA	GTGCAGGGTCCGAGGT
Clone primers		
Primers for promoter cloning (PGL3-Basic)		
Pitga1-1k	CGACGCGTGTGGCACCCCTTCCTACTTTG	CCGCTCGAGGACGCCTGGGGACCATTG
Pitga1-2k	CGACGCGTTGATGTTGGAGCAGTAGCTGAG	CCGCTCGAGGACGCCTGGGGACCATTG
Pitga1+1	GGGGTACCGGATTTGGTTCGTGAAGC	CCGCTCGAGGACGCCTGGGGACCATTG
Pitga1+100	GGGGTACCCCGCGAAGTTGGCTT	CCGCTCGAGGACGCCTGGGGACCATTG
Pitga1+200	GGGGTACCATCCATCTGGGATCTGAGAAGC	CCGCTCGAGGACGCCTGGGGACCATTG
Pitga1+210	GGGGTACCGATCTGAGAAGCGTGGAGC	CCGCTCGAGGACGCCTGGGGACCATTG
Pitga1+230	GGGGTACCGCTTAGCAGCATTTCGACC	CCGCTCGAGGACGCCTGGGGACCATTG
Pitga1+250	GGGGTACCAACACAGGAAATTACTCTCCACC	CCGCTCGAGGACGCCTGGGGACCATTG
Pitga1-Sp1mt	GTTTTGGTCGAATGCTGCTAATTTTTCTCCACGCTTCTCAGATCC	GGATCTGAGAAGCGTGGAGAAAAATTAGCAGCATTCTG ACCAAAAC
Pitga1-Arntmt	GTGGAGCGGGCTTAGCAATATTGGACCAAAACACAGGAAATTACTCTTC	GAAGAGTAATTTCTGTGTTTTGGTCCAATATTGCTA AGCCCGCTCCAC
Pitga1-Runx1mt	GGGCTTAGCAGCATTTCGAGGACGACACAGGAAATTACTCTCCACC	GGTGGGAAGAGTAATTTCTGTGTCTCCTCGAATGCT GCTAAGCCC
Primers for 3'UTR cloning (pCI-neo)		
Itga1	GCTCTAGATTGGATTCTTCAAAAGGCCACTAAAG	AAGGAAAAAGCGGCCGCTGGCCAAACGGCTCTTCC
Itga1 148aMT	GCAGTTGAGCTTAAATTCTATGTAGAATAGCCTGACTAGATGGAGTCCTTATT TAAACATGAG	CTCATGTTTAAATAAGGACTCCATCTAGTCAGGCTAT TCTACATAGAATTTAAGCTCAACTGC
Itga1 181bMT	CAGATTGCTCCATTTCAATTACAATACTAAATGTACGGTATCATCGTGTGTG A	TCACACACGATGATACCGTACATTTAGTTATTGTAAT TGAAATGGAGCAATCTG
Adcy9	AAGGAAAAAGCGGCCGCTTTCCTGGTAAACTTCACTGTATAGC	AAGGAAAAAGCGGCCGCGACTGCAGCCCAGGTGA
Adcy9 181bMT1	TGTGACAATACCTCTTGCTTCTAAACATTCGTTCCTGTACAATGCCACAGAT T	AATCTGTGGCATTGTACAGGAACAGAATGTTTAGAAG CAAGAGGTATTGTCACA
Adcy9 181bMT2	GGCAGGAAGCAATACTTCAGAATTCATTCTGTGTAAATAGTTGCTTTGCATTG C	GCAATGCAAGCACTATTTACACAGAATGAATTCTG AAGTATTGCTTCTCTGCC
Primers for gene expression (pLVX-puro)		
Itga1 (mouse)	CCGCTCGAGATGGTCCCCAGGCGTC	GCTCTAGATCATTTCTCCATTTTCTTCTTTAGTG
Adcy9 (mouse)	CCGCTCGAGATGCAGTTACCTCTGTACCTGAGC	GCTCTAGATTAAGCGTAATCTGGAACATCGTATGGGT ACACACTCTTTGAGACATTGAGCTT
mir-218-2	CCGCTCGAGACCTTGTCCTCTTTGCTG	GCTCTAGAGTGGATACTCGAAGCACGG
let-7f-1	CCGCTCGAGCATTGCTTATGCTATGCATGC	GGAATTCCTAAAGGCCTGGTCTTAG
miR-181b	CCGCTCGAGAAGCTCTGGGCTGGAGGA	GCTCTAGATTGAATAAACAAACCTGAAAGTTCAG
miR-181c	CCGCTCGAGTTTACATTATGGTTTGATTGTGCTG	GCTCTAGATTATTTCCCAATCCAATCAGC
Primers for gene expression (pEGFP-C3)		
Itga1 CDS	CCGCTCGAGATGGTCCCCAGGCGTC	GCTCTAGATCATTTCTCCATTTTCTTCTTTAGTG
Itga1 NC	CCGCTCGAGTAGGTCCCCAGGCGTC	GCTCTAGATCATTTCTCCATTTTCTTCTTTAGTG
Itga1 UTR	CCGCTCGAGATGGTCCCCAGGCGTC	GCTCTAGATCATTTCTCCATTTTCTTCTTTAGTG
ADCY9 UTR	CCGCTCGAGCTTTCCTGGTAACTTCACTGTATAGC	GGAATTCGACTGCAGCCCAGGTGA
Primers for invitro trancription (pGEM-T)		
Itga1	TAATACGACTCACTATAGCTGGCTTCTCACCGTTATCC	AGGCATACAAGGGCCCCAC
Adcy9	TAATACGACTCACTATAGGGCCCTGCTTTCTGGC	GAAGAAATAATCTTTCATCAGGCTG