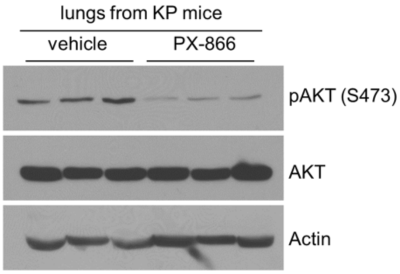
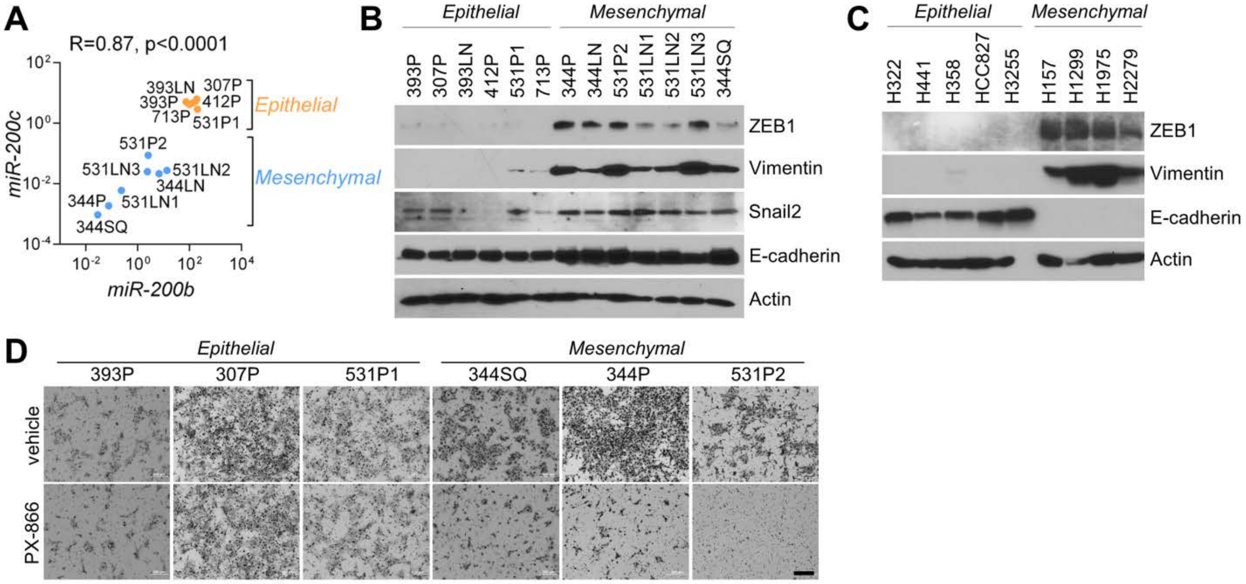
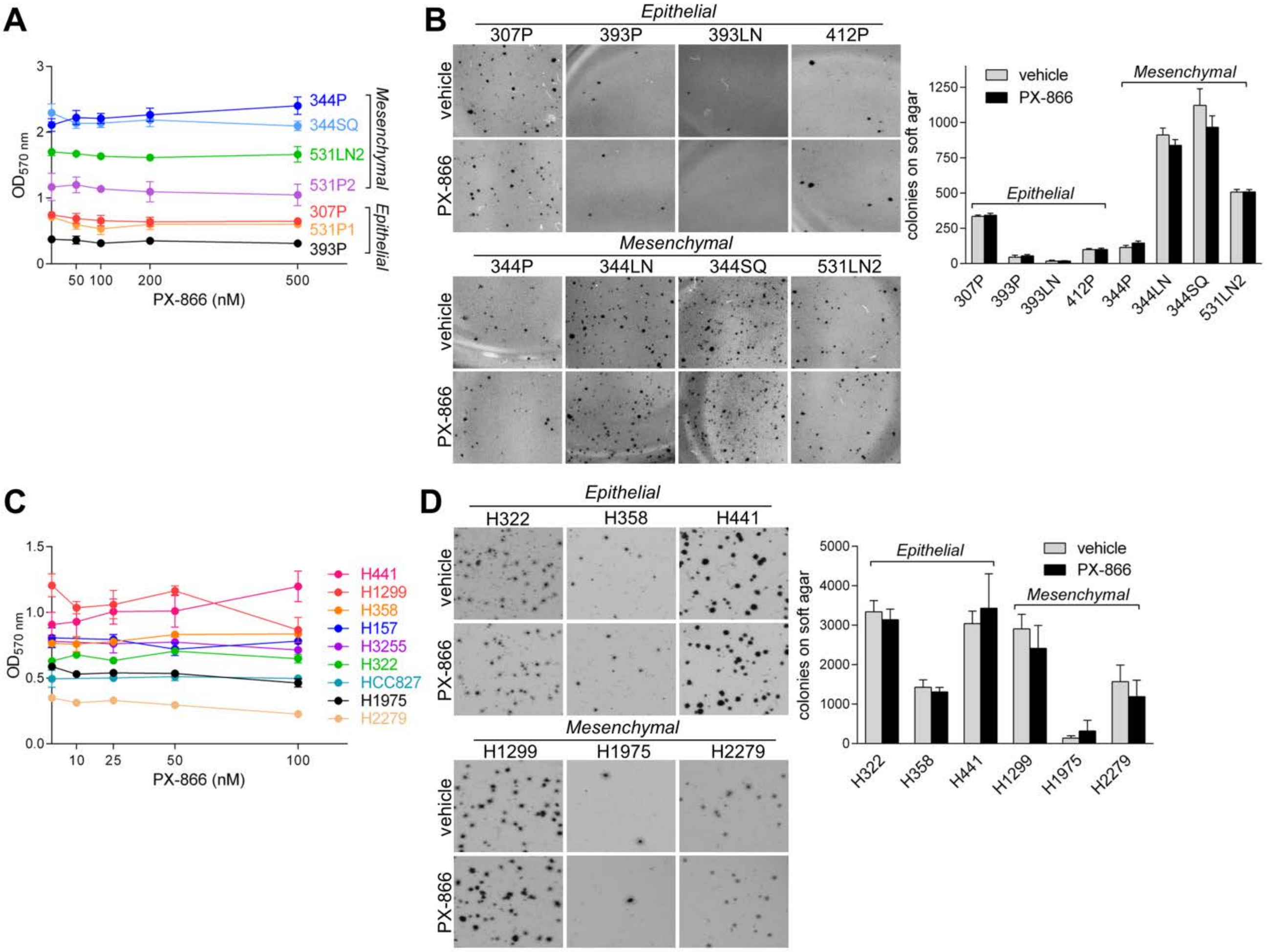


Supplemental Figure 1
PX-866 inhibits PI3K signaling. Western blot analysis using phospho-specific (p) and total AKT antibodies. Controls include blotting for actin.

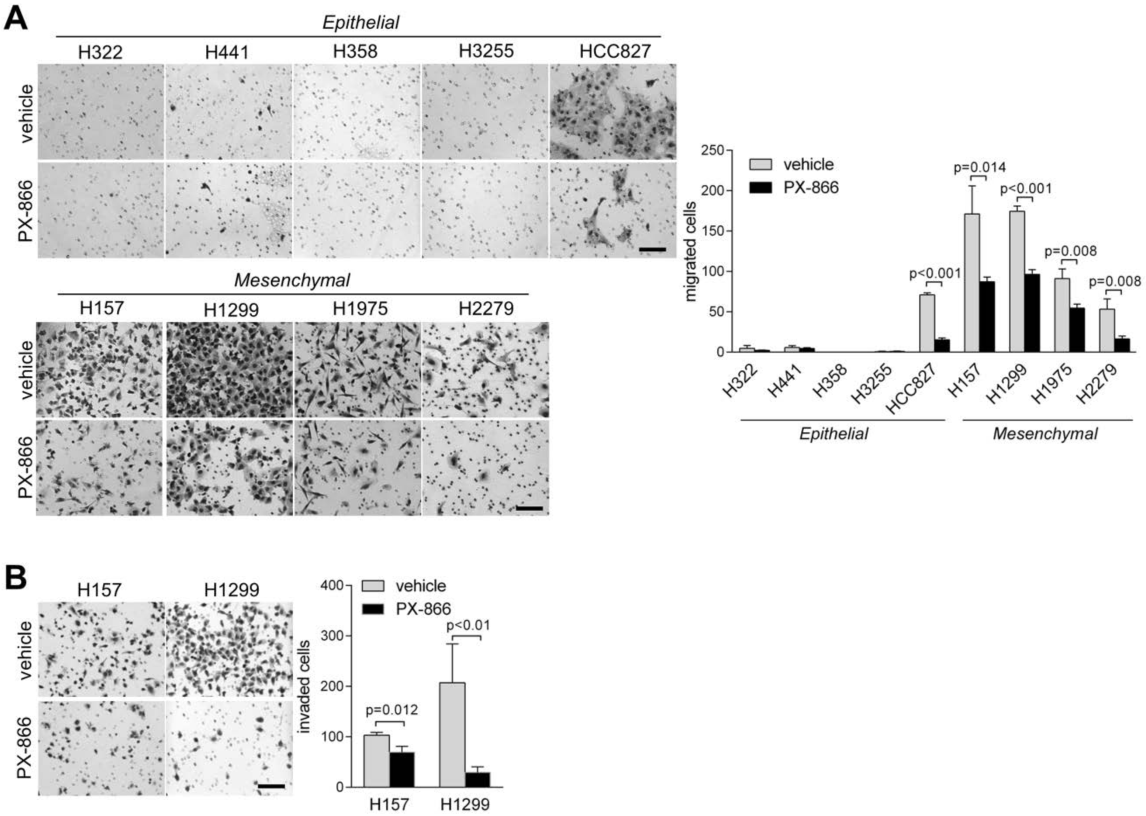


Supplemental Figure 2
Mesenchymal murine lung adenocarcinoma cells are sensitive to PX-866. (**A**) qPCR assays. Log-scale cluster plots of normalized miR-200c and miR-200b levels in KP cell lines. N=13, mean±SD from triplicate samples; R and P, one-tailed Spearman's rank correlation test. Brackets indicate cell lines deemed to be epithelial or mesenchymal on the basis of the expression levels of corresponding differentiation markers. (**B, C**) Western blot analysis of KP (B) and human lung cancer cell lines (C). Controls include blotting for actin. (**D**) Invasion assays. Invasive cells in Boyden chambers were photographed after 24 hrs of incubation in each condition. Controls include vehicle treatment. Bar size, 100 µm. Quantified result (bar graph) is shown in Figure 1D.



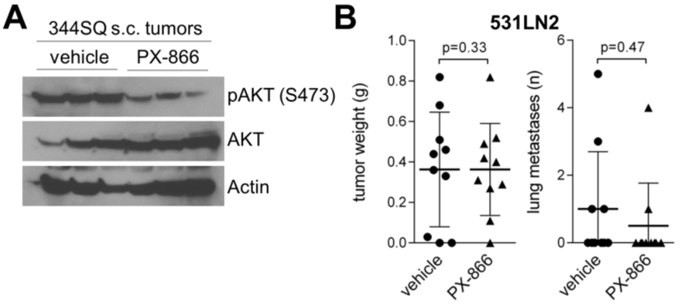
Supplemental Figure 3

PX-866 has no effects on cellular proliferation. (**A, C**) Relative cell density. Epithelial and mesenchymal KP cells (A) and human lung cancer cells (C) were plated in monolayer culture, treated for 3 days with the indicated doses of PX-866 or vehicle, and subjected to MTT assays ($OD_{570\ nm}$). Mean±SD from triplicate samples. Vehicle treatment designated by PX-866 dose = 0. (**B, D**) Soft agar colony formation. Epithelial and mesenchymal KP cells (B) and human lung cancer cells (D) were cultured in soft agar and treated for 14 days with PX-866 or vehicle; the resulting colonies were photographed (images; magnification: 4X) and counted (bar graph). Values represent mean±SD from triplicate wells.



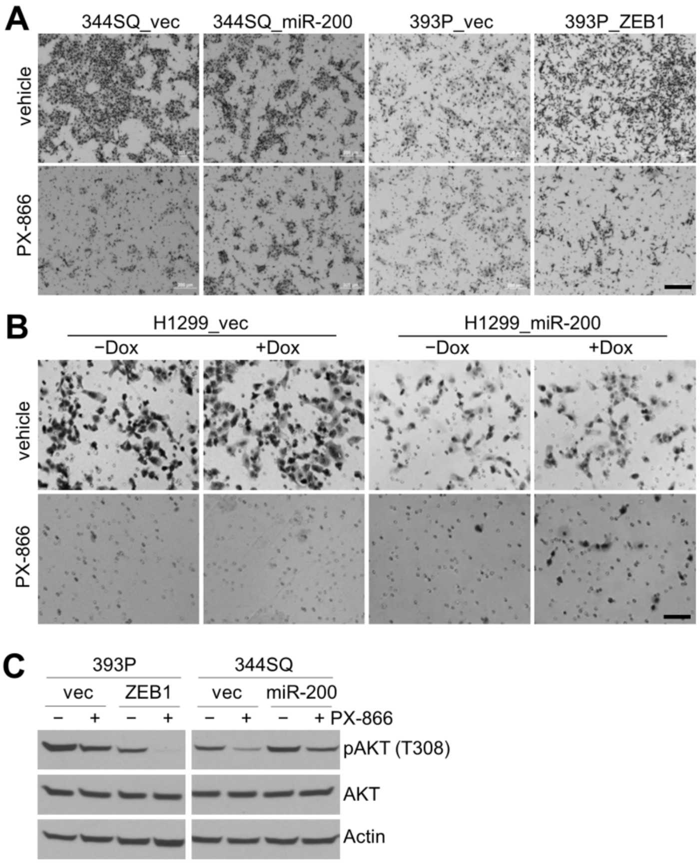
Supplemental Figure 4

Mesenchymal human lung adenocarcinoma cells are sensitive to PX-866. (**A**) Migration assays. Migratory epithelial and mesenchymal human lung cancer cells treated with vehicle or PX-866 were photographed (images) and quantified (bar graph) after 24 hrs of incubation in Boyden chambers. Results represent mean±SD from triplicate samples. (**B**) Invasion assays. Invasive H157 and H1299 cells treated with vehicle or PX-866 were photographed (images) and quantified (bar graph) after 24 hrs of incubation in Boyden chambers. Results represent mean±SD from triplicate samples. Bar size, 100 µm.

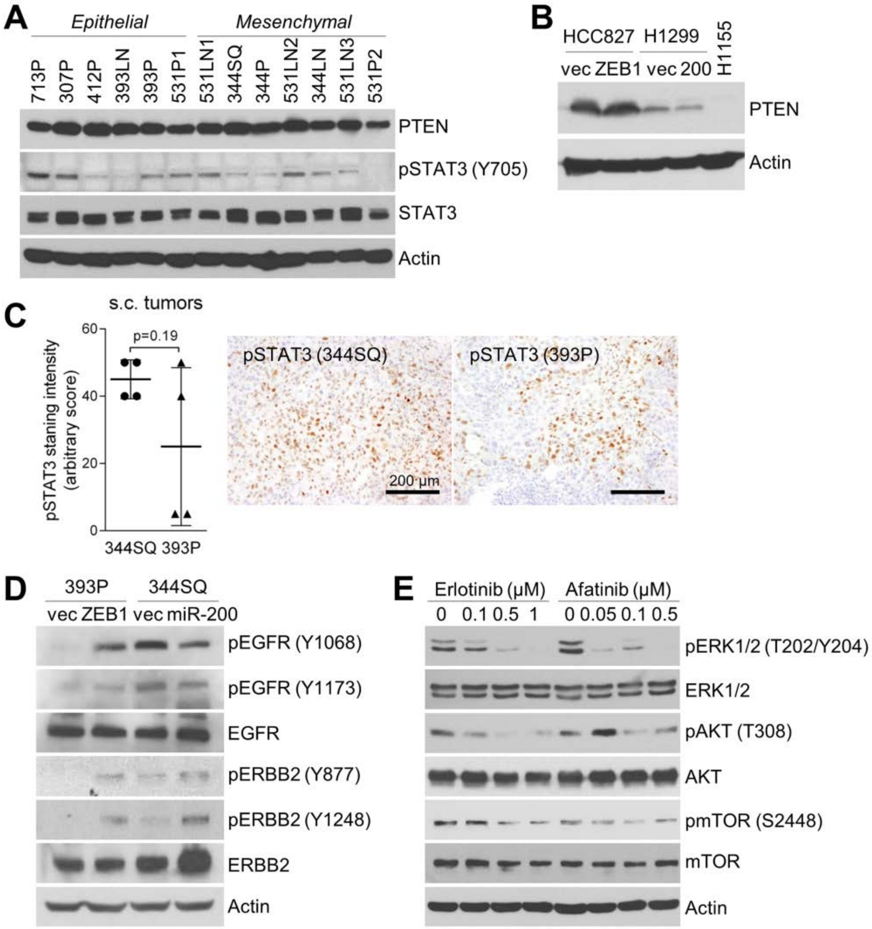


Supplemental Figure 5

PX-866 decreases AKT phosphorylation in 344SQ tumors and has no effect on established 531LN2 tumors. (**A**) Western blot analysis of 344SQ tumors using phospho-specific (p) and total AKT antibodies. Controls include blotting for actin. (**B**) Scatter plots of primary tumor weight (g) and numbers (n) of visible lung metastases in syngeneic mice injected with 531LN2 cells (10 mice per cohort). Treatment with PX-866 or vehicle was started one week after tumor cell injection. Mean±SD was calculated for each cohort.

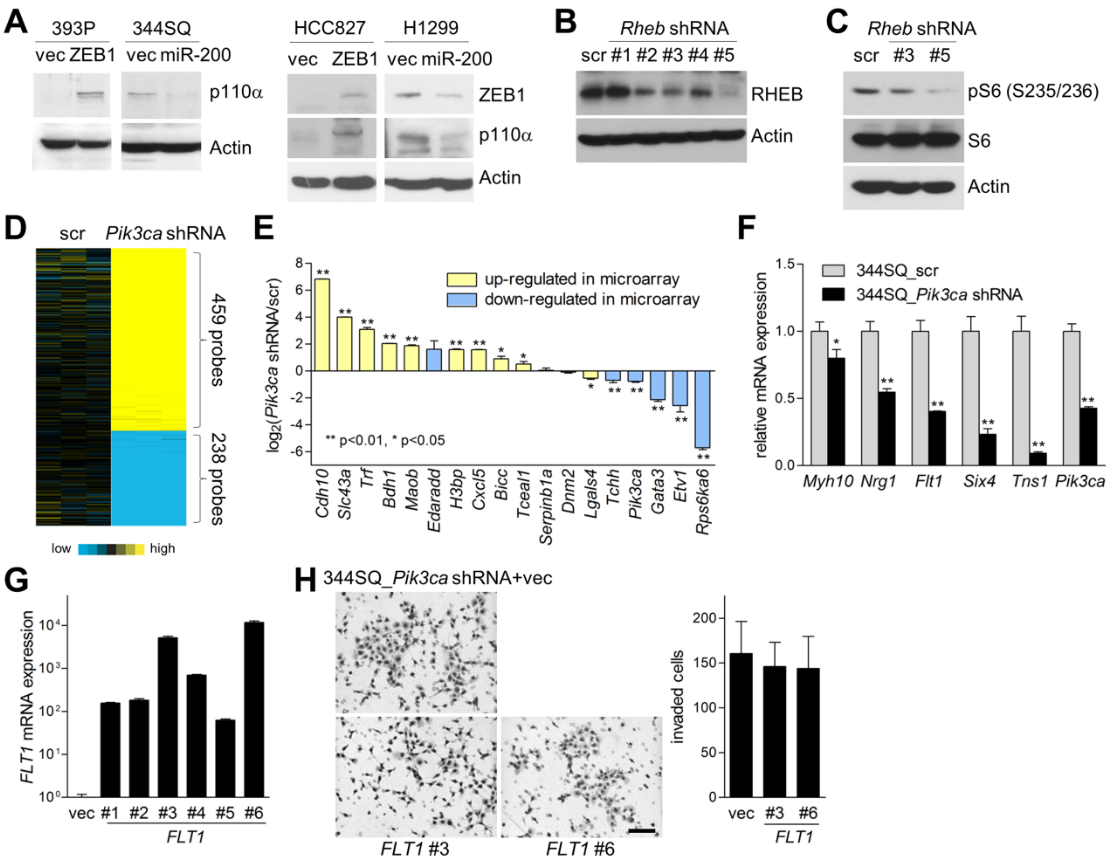


Supplemental Figure 6
Mesenchymal lung adenocarcinoma cells are sensitive to PX-866. (**A, B**) Invasion assays. Invasive KP cells (A) and H1299 cells (B) were photographed after 24 hrs of incubation in the presence or absence (vehicle) of PX-866. H1299 cells were treated with (+) or without (-) doxycycline (Dox, 1 µg/ml) to induce expression of the miR-200b/a/429 construct. Bar size, 100 µm. Quantified results (bar graphs) are shown in Figure 1, G and H, respectively. (**C**) Western blot analysis using phospho-specific (p) and total AKT antibodies. Controls include blotting for actin.



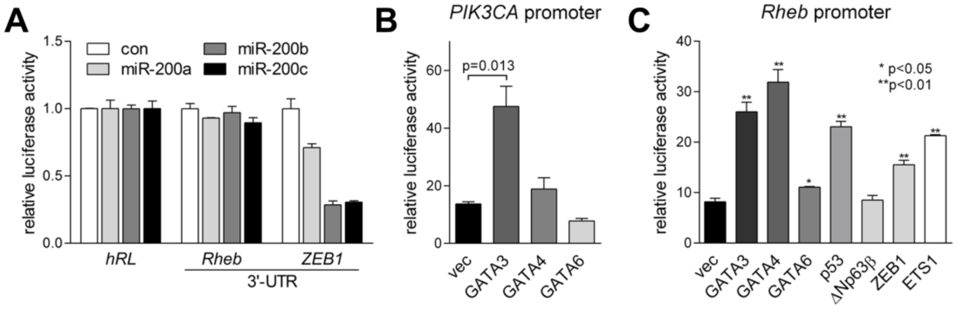
Supplemental Figure 7

p110a activation by ZEB1 is independent of PTEN and STAT3. (**A**) Western blot analysis of PTEN, phospho-STAT3, and total STAT3 in KP cells. Actin was used as a loading control. (**B**) Western blot analysis of PTEN in human lung cancer cells. Lysate from H1155 PTEN-null cells was loaded as negative control. (**C**) Scatter plot of phospho-STAT3 staining intensity in primary tumors of 344SQ and 393P KP cells injected into syngeneic, immunocompetent mice. Representative positive cells (brown) were photographed (images). Bar size, 200 µm. (**D, E**) Western blot analysis using phospho-specific (p) and total protein antibodies. Controls include blotting for actin.



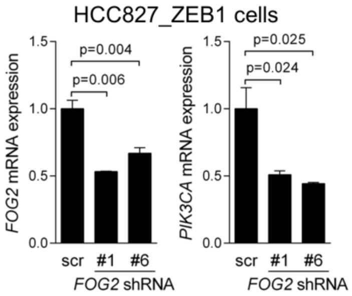
Supplemental Figure 8

p110a has multiple candidate pro-invasive mediators. (**A**) Western blot analysis of KP cells (393P and 344SQ) and human lung cancer cells (HCC827 and H1299) that express ectopic ZEB1, miR-200b/a/429 (miR-200), or empty vector (vec). Controls include empty vector transfectants and blotting for actin. (**B, C**) Western blot analysis of 344SQ cells stably transfected with *Rheb*-specific (#1-5) or scrambled (scr) shRNAs. Controls include scrambled shRNA transfectants and blotting for actin. (**D**) Heat map depiction of 697 Affymetrix probe sets up- or downregulated in 344SQ_*Pik3ca* shRNA cells, with 344SQ_scrambled shRNA cells (scr) as the reference. Scale bar at bottom. (**E, F**) qPCR analysis to confirm the differential expression of genes from arrays listed in Supplemental Table 1 and depicted in panel D. qPCR analyses of top up- or downregulated genes (E, color-coding designates up- or downregulation in the arrays) and candidate pro-invasive genes (F). Values were normalized on the basis of L32 ribosomal protein mRNA levels and represent the mean±SD from triplicate samples. *p<0.05, **p<0.01. (**G**) *FLT1* qPCR assay of 344SQ cells stably co-transfected with *Pik3ca* shRNA and *FLT1* cDNA (clones #1-6) or a control empty vector (vec). Mean±SD from triplicate samples. (**H**) Invasion assay. Invasive 344SQ_*Pik3ca* shRNA_*FLT1* cells (clones #3 and #6) and 344SQ_*Pik3ca* shRNA_vector cells (vec) were photographed (images) and quantified (bar graph) after 24 hrs of incubation in Boyden chambers. Bar size, 100 µm. Results represent mean±SD from triplicate samples.



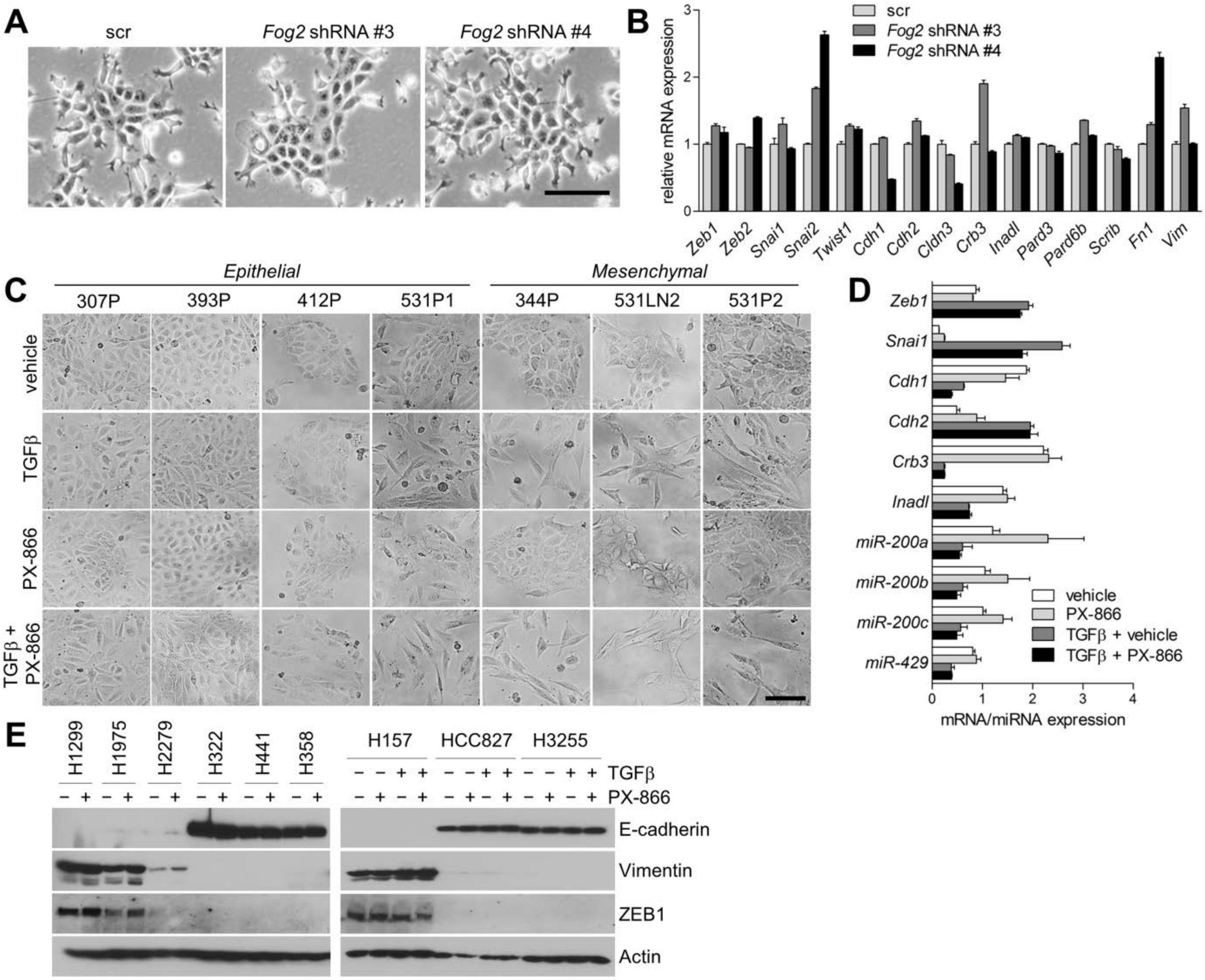
Supplemental Figure 9

GATA3 activates the *PIK3CA* and *RheB* promoters. (A) *Rheb* 3'-UTR reporter assays. Results were normalized using a dual firefly/Renilla luciferase system. *ZEB1* 3'-UTR (ZEB1) was used as a positive control. Mean±SD from triplicate samples. (B, C) Transient co-transfection assays using reporters containing *PIK3CA* or *RheB* promoters and vectors expressing the indicated transcription factors. Results were normalized using a dual firefly/Renilla luciferase system. Mean±SD from triplicate samples.



Supplemental Figure 10

FOG2 is upstream of p110a. qPCR assays of HCC827_ZEB1 cells stably transfected with *FOG2* shRNAs (clones #1 and #6) or a scrambled shRNA (scr). qPCR values were normalized on the basis of ribosomal protein L32 mRNA levels and represent mean±SD from triplicate samples.



Supplemental Figure 11

FOG2 is not required for ZEB1-induced EMT. (**A**) Phase-contrast microscopic images of 344SQ_*Fog2* shRNA cells (shRNA #3 and #4) and 344SQ_scr shRNA cells (scr) in monolayer culture. Bar size, 100 µm. (**B**) qPCR analysis of EMT marker expression in cells from panel A. Values normalized on the basis of ribosomal protein L32 mRNA levels, averaged from triplicate samples (mean±SD), and expressed relative to 344SQ_scr transfectants, which were set at 1.0. (**C**) Phase-contrast microscopic images of epithelial and mesenchymal KP cells after 3 days in culture with TGFβ (1 ng/ml) and/or PX-866 (50 nM). Bar size, 100 µm. Controls include vehicle treatment. (**D**) qPCR analysis of EMT marker expression in 344SQ cells treated as in panel C. Controls include vehicle treatment. Values normalized on the basis of ribosomal protein L32 mRNA (for mRNAs) or snoRNA-135 (for miR-200 family), averaged from triplicate samples (mean±SD), and expressed relative to vehicle-treated cells, which were set at 1.0. (**E**) Western blot analysis of E-cadherin, vimentin, and ZEB1 in human lung cancer cells after 3 days in culture with TGFβ (1 ng/ml) and/or PX-866 (50 nM). Actin was used as a loading control.

Supplemental Table 1. Differentially expressed genes in 344SQ_*Pik3ca* shRNA vs. 344SQ_scr.

Gene Symbol	Gene Title	Entrez Gene	fold change (Pik3ca shRNA/scr)	p-value
Trf	transferrin	22041	125.86468445	0.00000450
Slc43a3	solute carrier family 43, member 3	58207	43.21027214	0.00003669
Cdh10	cadherin 10	320873	30.68561962	0.00004926
Cxcl5	chemokine (C-X-C motif) ligand 5	20311	28.69858071	0.00000585
Bicc1	bicaudal C homolog 1 (Drosophila)	83675	24.33340585	0.00001115
Hebp1	heme binding protein 1	15199	24.20531778	0.00005687
Bdh1	3-hydroxybutyrate dehydrogenase, type 1	71911	23.80070740	0.00079079
Lgals4	lectin, galactose binding, soluble 4	16855	23.11556285	0.00000294
Tceal1	transcription elongation factor A (SII)-like 1	237052	21.86727819	0.00023400
Maob	monoamine oxidase B	109731	19.95580336	0.00075550
Gsta1	glutathione S-transferase, alpha 1 (Ya)	14857	19.10126004	0.00000534
D830012I24Rik	RIKEN cDNA D830012I24 gene	320070	18.13049434	0.00000722
Nid1	nidogen 1	18073	17.11119202	0.00000004
Sim2	single-minded homolog 2 (Drosophila)	20465	16.66998620	0.00003063
Sema4a	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	20351	16.41689365	0.00001846
Calml4	calmodulin-like 4	75600	16.38854194	0.00002022
Cdx2	caudal type homeo box 2	12591	16.18681805	0.00518484
Gm566	gene model 566, (NCBI)	229672	15.84656976	0.00000430
Serpinh1	serine (or cysteine) peptidase inhibitor, clade H, member 1	12406	15.54163945	0.00001317
Sim2	single-minded homolog 2 (Drosophila)	20465	15.04022310	0.00038424
Casd1	CAS1 domain containing 1	213819	14.04176117	0.00000399
Tff2	trefoil factor 2 (spasmolytic protein 1)	21785	13.39053709	0.00000396
Timp3	tissue inhibitor of metalloproteinase 3	21859	13.23249470	0.00062990
Jak1	Janus kinase 1	16451	12.89566025	0.00070161
Jak1	Janus kinase 1	16451	12.50766830	0.00297062
1700112E06Rik	RIKEN cDNA 1700112E06 gene	76633	12.20972059	0.00043753
Lepr	leptin receptor	16847	11.87053466	0.00156298
Pgf	placental growth factor	18654	11.63429459	0.00070764
Bicc1	bicaudal C homolog 1 (Drosophila)	83675	11.46988128	0.00002030
Nid1	nidogen 1	18073	11.40220099	0.00107531
Itga1	integrin alpha 1	109700	11.31039915	0.00618837
Muc1	mucin 1, transmembrane	17829	11.19472948	0.00076631
Centd3	centaurin, delta 3	106952	11.17340567	0.00001927
Cdh17	cadherin 17	12557	10.68385663	0.00000292
BC020077	cDNA sequence BC020077	230500	10.46023069	0.00004929
Lgals2	lectin, galactose-binding, soluble 2	107753	10.32012359	0.00771737
Thbd	thrombomodulin	21824	9.87538092	0.00005900
Dsg2	desmoglein 2	13511	9.87456726	0.00000077
Vegfc	vascular endothelial growth factor C	22341	9.40403763	0.00668621
Dsg2	desmoglein 2	13511	9.35817754	0.00290452
Lepr	leptin receptor	16847	9.32405722	0.00834251
Cblc	Casitas B-lineage lymphoma c	80794	9.32026831	0.00051344
Sardh	sarcosine dehydrogenase	192166	9.04181241	0.00514306
Apob	apolipoprotein B	238055	8.86890939	0.00000938

Cdx2	caudal type homeo box 2	12591	8.82034316	0.00004434
Myo5c	myosin VC	208943	8.81182166	0.00010650
Klhl1	kelch-like 1 (Drosophila)	93688	8.74654744	0.00042853
AW107722	expressed sequence AW107722	106391	8.61293516	0.00017324
Muc4	mucin 4	74074	8.38335584	0.00081045
Pamci	peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor	237504	8.28690065	0.00019809
E130304F04Rik	RIKEN cDNA E130304F04 gene	245269	8.22806171	0.00110011
Vip	vasoactive intestinal polypeptide	22353	8.20609729	0.00861428
5830433M19Rik	RIKEN cDNA 5830433M19 gene	67770	8.18023236	0.00008241
Sema4a	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	20351	7.98712827	0.00004775
Ly6e	lymphocyte antigen 6 complex, locus E	17069	7.89816731	0.00016727
Tusc1	tumor suppressor candidate 1	69136	7.86937900	0.00292758
1810011O10Rik	RIKEN cDNA 1810011O10 gene	69068	7.77383563	0.00001954
Jun	Jun oncogene	16476	7.76095168	0.00127435
Crebbp	CREB binding protein	12914	7.69211520	0.00040474
Clic6	chloride intracellular channel 6	209195	7.64964358	0.00001881
Lgals6	lectin, galactose binding, soluble 6	16857	7.63250964	0.00665693
Crisp1	cysteine-rich secretory protein 1	11571	7.60530213	0.00074172
1810011O10Rik	RIKEN cDNA 1810011O10 gene	69068	7.53836346	0.00000261
5230400M03Rik	RIKEN cDNA 5230400M03 gene	329406	7.38779333	0.00125955
Zfp533	zinc finger protein 533	241494	7.35503877	0.00298529
Cfb	complement factor B	14962	7.31247496	0.00000859
Grip1	glutamate receptor interacting protein 1	74053	7.27370283	0.00000089
Serpinh1	serine (or cysteine) peptidase inhibitor, clade H, member 1	12406	7.23678786	0.00000381
Avil	advillin	11567	7.23242694	0.00000408
Guca2a	guanylate cyclase activator 2a (guanylin)	14915	7.16927455	0.00678104
Ift74	intraflagellar transport 74 homolog (Chlamydomonas)	67694	7.16132316	0.00006311
Prpmp5	proline-rich protein MP5	381832	7.06764006	0.00001026
2310061G22Rik	RIKEN cDNA 2310061G22 gene	70407	7.02851815	0.00037131
Centd3	centaurin, delta 3	106952	6.97709606	0.00982829
Ptpn22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	19260	6.87728366	0.00003336
Dsg2	Desmoglein 2	13511	6.77989547	0.00864124
Tas2r108	taste receptor, type 2, member 108	57253	6.69259992	0.00779416
6230424C14Rik	RIKEN cDNA 6230424C14 gene	67786	6.63547483	0.00000107
Cdkn2b	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	12579	6.60899104	0.00000521
Sox11	SRY-box containing gene 11	20666	6.46680387	0.00009709
Mtap	methylthioadenosine phosphorylase	66902	6.38992568	0.00006039
Gsta4	glutathione S-transferase, alpha 4	14860	6.38829388	0.00000055
Mtap	methylthioadenosine phosphorylase	66902	6.38417822	0.00030533
Hook1	hook homolog 1 (Drosophila)	77963	6.37263796	0.00310345
1700016G05Rik	RIKEN cDNA 1700016G05 gene	67690	6.30598860	0.00002038
Gjb1	gap junction membrane channel protein beta 1	14618	6.25604816	0.00047032
Cdkn2a	cyclin-dependent kinase inhibitor 2A	12578	6.22329809	0.00000235
B230218O03	hypothetical protein B230218O03	329333	6.19951294	0.00606758

Hmgcll1	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1	208982	6.15310484	0.00022132
Slc39a4	solute carrier family 39 (zinc transporter), member 4	72027	6.14945263	0.00002098
Krt20	keratin 20	66809	6.13897127	0.00001788
Gnai1	guanine nucleotide binding protein, alpha inhibiting 1	14677	6.03345332	0.00004322
Cotl1	coactosin-like 1 (Dictyostelium)	72042	6.01060573	0.00000025
B130021B11Rik	RIKEN cDNA B130021B11 gene	320860	5.98140702	0.00593181
Sox11	SRY-box containing gene 11	20666	5.95028229	0.00095891
Tgfb3	transforming growth factor, beta 3	21809	5.80267647	0.00015151
Ly6a	lymphocyte antigen 6 complex, locus A	110454	5.79696859	0.00003635
Gm266	gene model 266, (NCBI)	212539	5.73556178	0.00756277
Nfia	nuclear factor I/A	18027	5.72135529	0.00014550
Flnc	filamin C, gamma (actin binding protein 280)	68794	5.59445606	0.00149424
Dsg2	desmoglein 2	13511	5.57857126	0.00000055
Scarf2	scavenger receptor class F, member 2	224024	5.52982242	0.00002396
Bicc1	bicaudal C homolog 1 (Drosophila)	83675	5.44751838	0.00001260
6230424C14Rik	RIKEN cDNA 6230424C14 gene	67786	5.43615388	0.00000296
Mapk13	mitogen activated protein kinase 13	26415	5.41778780	0.00002837
Rbmx	RNA binding motif protein, X chromosome	19655	5.40188160	0.00612367
Ptpn6	protein tyrosine phosphatase, non-receptor type 6	15170	5.34407207	0.00602266
Mtac2d1	membrane targeting (tandem) C2 domain containing 1	74413	5.31715583	0.00111853
LOC624112	hypothetical protein LOC624112	624112	5.21632107	0.00003351
Trmu	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	72026	5.21350143	0.00038839
H6pd	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	100198	5.16065078	0.00000138
Abcg2	ATP-binding cassette, sub-family G (WHITE), member 2	26357	5.14771928	0.00000503
Dtna	dystrobrevin alpha	13527	5.10474673	0.00030476
Sdsl	serine dehydratase-like	257635	5.09919052	0.00035339
Nfia	nuclear factor I/A	18027	5.09154731	0.00529736
Ehhadh	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	74147	5.07149546	0.00546861
Hsd17b2	hydroxysteroid (17-beta) dehydrogenase 2	15486	5.03165440	0.00464970
Enpep	glutamyl aminopeptidase	13809	4.95959466	0.00081054
Adam32	a disintegrin and metallopeptidase domain 32	353188	4.89337004	0.00449338
Cyp2c65	cytochrome P450, family 2, subfamily c, polypeptide 65	72303	4.83613178	0.00158919
Leprot	leptin receptor overlapping transcript	230514	4.80395899	0.00000419
Ugt1a2	UDP glucuronosyltransferase 1 family, polypeptide A2	22236	4.78176172	0.00006368
Timp3	tissue inhibitor of metalloproteinase 3	21859	4.77643566	0.00030513
Sox6	SRY-box containing gene 6	20679	4.75849751	0.00017351
C77405	expressed sequence C77405	98108	4.70987710	0.00113265
Phf14	PHD finger protein 14	75725	4.70511415	0.00670990
Jak1	Janus kinase 1	16451	4.68085347	0.00042033
Plaa	phospholipase A2, activating protein	18786	4.67669902	0.00108299

Slco3a1	solute carrier organic anion transporter family, member 3a1	108116	4.61210140	0.00023410
Itgb3bp	integrin beta 3 binding protein (beta3-endonexin)	67733	4.56850111	0.00000789
1700022F17Rik	RIKEN cDNA 1700022F17 gene	69421	4.54170627	0.00525169
Atp8b1	ATPase, class I, type 8B, member 1	54670	4.52970836	0.00008990
Cmtm3	CKLF-like MARVEL transmembrane domain containing 3	68119	4.52564743	0.00031466
Gpr56	G protein-coupled receptor 56	14766	4.52337637	0.00004718
Mycn	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	18109	4.51132604	0.00000476
Leprot	leptin receptor overlapping transcript	230514	4.50042132	0.00003590
Clca1	chloride channel calcium activated 1	12722	4.48142450	0.00000086
3110009O07Rik	RIKEN cDNA 3110009O07 gene	73077	4.47310958	0.00623204
Cstad	CSA-conditional, T cell activation-dependent protein	78617	4.46377774	0.00023150
Clca1	chloride channel calcium activated 1	12722	4.45976045	0.00000169
AW112010	expressed sequence AW112010	107350	4.44454089	0.00011405
C030038J10Rik	RIKEN cDNA C030038J10 gene	243385	4.41359967	0.00939025
C81600	expressed sequence C81600	97655	4.38153241	0.00716741
Jam4	junction adhesion molecule 4	72058	4.37216548	0.00008338
8430434A19Rik	RIKEN cDNA 8430434A19 gene	71556	4.36414411	0.00287874
9630041N07Rik	RIKEN cDNA 9630041N07 gene	214779	4.35482915	0.00666071
Pcbp3	poly(rC) binding protein 3	59093	4.33939380	0.00149991
Bcr	breakpoint cluster region homolog	110279	4.32663762	0.00592223
Cotl1	coactosin-like 1 (Dictyostelium)	72042	4.31438184	0.00000889
Gstt3	glutathione S-transferase, theta 3	103140	4.31372120	0.00074299
Gcat	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	26912	4.30559796	0.00522309
Plaa	phospholipase A2, activating protein	18786	4.30035153	0.00001009
Lgals2	lectin, galactose-binding, soluble 2	107753	4.28772950	0.00005039
1200009I06Rik	RIKEN cDNA 1200009I06 gene	74190	4.28666227	0.00031982
Apoa1	apolipoprotein A-I	11806	4.28444735	0.00864326
LOC672274	similar to Transcription factor SOX-4	672274	4.28203256	0.00092023
Cdh10	cadherin 10	320873	4.23642789	0.00062030
C1r	complement component 1, r subcomponent	50909	4.22115039	0.00349687
Apoc2	apolipoprotein C-II	11813	4.18422997	0.00005835
Gm1960	gene model 1960, (NCBI)	330122	4.15789905	0.00337119
Fblim1	filamin binding LIM protein 1	74202	4.08139199	0.00000417
Mtac2d1	membrane targeting (tandem) C2 domain containing 1	74413	4.06285184	0.00865686
Leprot	leptin receptor overlapping transcript	230514	4.04644743	0.00014320
Klhl1	kelch-like 1 (Drosophila)	93688	4.04120583	0.00019393
Aim1l	absent in melanoma 1-like	230806	4.02980653	0.00024190
LOC632764	similar to melanoma antigen	632764	4.02739367	0.00014079
Coro7	coronin 7	78885	4.01457938	0.00839548
Cdc2l6	Cell division cycle 2-like 6 (CDK8-like)	78334	3.99369073	0.00027732
Mettl7b	methyltransferase like 7B	71664	3.94838157	0.00063265
Anks3	ankyrin repeat and sterile alpha motif domain containing 3	72615	3.92872703	0.00071430
Clca1	chloride channel calcium activated 1	12722	3.92308477	0.00022926
Lsamp	Limbic system-associated membrane protein	268890	3.90301569	0.00246501
Dtna	dystrobrevin alpha	13527	3.86161342	0.00112679

4930578N16Rik	RIKEN cDNA 4930578N16 gene	75051	3.84429692	0.00276241
Sema3a	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	20346	3.82684780	0.00013248
Plac8	placenta-specific 8	231507	3.80917456	0.00000047
Scn5a	sodium channel, voltage-gated, type V, alpha	20271	3.79360617	0.00422885
Ajap1	Adherens junction associated protein 1	230959	3.78494392	0.00395533
Mtap	methylthioadenosine phosphorylase	66902	3.74338248	0.00000538
Cotl1	Coactosin-like 1 (Dictyostelium)	72042	3.72019993	0.00002478
Tspan12	tetraspanin 12	269831	3.69795077	0.00011137
Sgpp2	sphingosine-1-phosphate phosphotase 2	433323	3.68542556	0.00069674
Krt23	keratin 23	94179	3.64717874	0.00005894
Nrk	Nik related kinase	27206	3.64078800	0.00005547
Psmb8	proteosome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7)	16913	3.62015577	0.00011112
2810405K02Rik	RIKEN cDNA 2810405K02 gene	66469	3.58366481	0.00029338
Akap2	A kinase (PRKA) anchor protein 2	11641	3.57828122	0.00002335
5031426D15Rik	RIKEN cDNA 5031426D15 gene	68144	3.57800728	0.00518676
Dcc	Deleted in colorectal carcinoma	13176	3.57510537	0.00786443
3110045C21Rik	RIKEN cDNA 3110045C21 gene	67303	3.57424388	0.00198698
Zfp292	Zinc finger protein 292	30046	3.49377037	0.00196182
Centd3	centaurin, delta 3	106952	3.48920584	0.00154095
Ddc	dopa decarboxylase	13195	3.44664539	0.00009352
Pla2r1	phospholipase A2 receptor 1	18779	3.44323789	0.00168060
Ptgs1	prostaglandin-endoperoxide synthase 1	19224	3.44001650	0.00357388
Ctse	cathepsin E	13034	3.42495638	0.00000086
Bdh1	3-hydroxybutyrate dehydrogenase, type 1	71911	3.42314322	0.00420822
Med12l	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)-like	329650	3.41178937	0.00553100
St5	suppression of tumorigenicity 5	76954	3.40386955	0.00643955
Fmnl2	formin-like 2	71409	3.40124163	0.00001303
Usp31	ubiquitin specific peptidase 31	76179	3.39381981	0.00019388
Eps8l3	ESP8-like 3	99662	3.38078518	0.00028202
Fabp5	fatty acid binding protein 5, epidermal	16592	3.35259539	0.00002475
Pnma1	paraneoplastic antigen MA1	70481	3.33431167	0.00084795
D0H4S114	DNA segment, human D4S114	27528	3.32409646	0.00202502
Foxred2	FAD-dependent oxidoreductase domain containing 2	239554	3.31798108	0.00054604
1110036O03Rik	RIKEN cDNA 1110036O03 gene	66180	3.31326905	0.00028062
Mmp13	matrix metallopeptidase 13	17386	3.31142186	0.00001117
Atp9a	ATPase, class II, type 9A	11981	3.31043358	0.00418006
C030045D06Rik	RIKEN cDNA C030045D06 gene	109294	3.28724701	0.00112677
Sox11	SRY-box containing gene 11	20666	3.28688950	0.00607835
Ccbe1	collagen and calcium binding EGF domains 1	320924	3.25827496	0.00263780
Nol3	nucleolar protein 3 (apoptosis repressor with CARD domain)	78688	3.25712971	0.00034042
Ak3l1	adenylate kinase 3 alpha-like 1	11639	3.24764034	0.00022489
4631408O11Rik	RIKEN cDNA 4631408O11 gene	66693	3.23210773	0.00168112
Dlgh3	discs, large homolog 3 (Drosophila)	53310	3.21138859	0.00118673
Tmtc2	transmembrane and tetratricopeptide repeat containing 2	278279	3.20160221	0.00051178
Fbxo39	F-box protein 39	327959	3.19717173	0.00360102

Ugt1a2	UDP glucuronosyltransferase 1 family, polypeptide A2	22236	3.17949678	0.00000688
Fut4	fucosyltransferase 4	14345	3.17721651	0.00052048
Tceal8	transcription elongation factor A (SII)-like 8	66684	3.16599626	0.00038184
Plagl2	pleiomorphic adenoma gene-like 2	54711	3.16516209	0.00059723
9230117N10Rik	RIKEN cDNA 9230117N10 gene	77125	3.14618803	0.00000293
Fcgr3	Fc receptor, IgG, low affinity III	14131	3.14612112	0.00025040
Crisp3	cysteine-rich secretory protein 3	11572	3.14427171	0.00741923
Pnma2	paraneoplastic antigen MA2	239157	3.10706423	0.00011322
Cysltr1	cysteinyl leukotriene receptor 1	58861	3.10365562	0.00121147
Egfr	epidermal growth factor receptor	13649	3.09137904	0.00000413
Wbp11	WW domain binding protein 11	60321	3.08172037	0.00499993
Irf6	interferon regulatory factor 6	54139	3.07034567	0.00072782
Ccnd3	Cyclin D3	12445	3.05826587	0.00404725
Fabp5	fatty acid binding protein 5, epidermal	16592	3.05755067	0.00000129
Lhfp	lipoma HMGIC fusion partner	108927	3.04545579	0.00001410
Dock9	Dedicator of cytokinesis 9	105445	3.04047591	0.00489756
Itga1	integrin alpha 1	109700	3.02553262	0.00004077
Ugt1a2	UDP glucuronosyltransferase 1 family, polypeptide A2	22236	3.02489971	0.00005775
Sepp1	selenoprotein P, plasma, 1	20363	3.00292342	0.00129287
Ptger4	prostaglandin E receptor 4 (subtype EP4)	19219	3.00147655	0.00647944
Rprml	reprimo-like	104582	2.99499724	0.00802963
6330407J23Rik	RIKEN cDNA 6330407J23 gene	67412	2.98891515	0.00549379
Smarca1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	93761	2.98528056	0.00000019
Slc44a3	solute carrier family 44, member 3	213603	2.98415424	0.00304789
Pdgfd	Platelet-derived growth factor, D polypeptide	71785	2.95516664	0.00197290
Sema3a	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	20346	2.95215833	0.00004215
4632417K18Rik	RIKEN cDNA 4632417K18 gene	107373	2.94350740	0.00002513
Mtap9	microtubule-associated protein 9	213582	2.93716086	0.00568843
Dio3as	deiodinase, iodothyronine type III, antisense	353504	2.93392853	0.00003258
Pilra	paired immunoglobin-like type 2 receptor alpha	231805	2.93171375	0.00148276
Nfia	nuclear factor I/A	18027	2.92239356	0.00004949
Gm550	gene model 550, (NCBI)	225852	2.91588182	0.00997329
Gpd1	glycerol-3-phosphate dehydrogenase 1 (soluble)	14555	2.91013486	0.00029293
4930452B06Rik	RIKEN cDNA 4930452B06 gene	74430	2.89852209	0.00050179
Lphn3	Latrophilin 3	319387	2.89523564	0.00002945
Ptprj	protein tyrosine phosphatase, receptor type, J	105005	2.89487118	0.00015560
4931407K02Rik	RIKEN cDNA 4931407K02 gene	77627	2.88062056	0.00545433
Naprt1	nicotinate phosphoribosyltransferase domain containing 1	223646	2.87251847	0.00091835
Zfpm1	zinc finger protein, multitype 1	22761	2.87197707	0.00095806
Clec2d	C-type lectin domain family 2, member d	93694	2.87001264	0.00068433
Hs6st2	heparan sulfate 6-O-sulfotransferase 2	50786	2.86753523	0.00002122
Il1r1	interleukin 1 receptor, type I	16177	2.86713841	0.00163297
Ugt2b35	UDP glucuronosyltransferase 2 family, polypeptide B35	243085	2.85356848	0.00098770
Bdnf	brain derived neurotrophic factor	12064	2.84791540	0.00080934

Sema4b	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	20352	2.83481871	0.00031909
Slco4a1	solute carrier organic anion transporter family, member 4a1	108115	2.82965754	0.00001521
Scel	sciellin	64929	2.81112979	0.00001878
A930005I04Rik	RIKEN cDNA A930005I04 gene	403174	2.80749180	0.00411389
Trim34	Tripartite motif protein 34	94094	2.80483143	0.00077419
Magi1	membrane associated guanylate kinase, WW and PDZ domain containing 1	14924	2.80416760	0.00634200
Spata13	spermatogenesis associated 13	219140	2.80158830	0.00001078
Igfbp5	insulin-like growth factor binding protein 5	16011	2.80028960	0.00035536
Ifi203	interferon activated gene 203	15950	2.77086623	0.00112168
BC062109	cDNA sequence BC062109	231503	2.76760991	0.00002896
D12Ertd647e	DNA segment, Chr 12, ERATO Doi 647, expressed	52668	2.75904287	0.00024211
LOC432995	hypothetical gene supported by BC047216	432995	2.74759878	0.00164041
Slco4a1	solute carrier organic anion transporter family, member 4a1	108115	2.73995631	0.00658716
Spock2	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2	94214	2.73801977	0.00614169
C1qdc2	C1q domain containing 2	67389	2.72559387	0.00027966
Ak3l1	adenylate kinase 3 alpha-like 1	11639	2.71612719	0.00019466
Mysm1	myb-like, SWIRM and MPN domains 1	320713	2.69300187	0.00062600
Clic6	chloride intracellular channel 6	209195	2.68800377	0.00030313
Nrk	Nik related kinase	27206	2.68453512	0.00056290
Sugt1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	67955	2.68323648	0.00345979
Dtna	dystrobrevin alpha	13527	2.66752826	0.00062083
Egfr	epidermal growth factor receptor	13649	2.66740254	0.00043861
Dos	downstream of Stk11	216164	2.65101969	0.00591516
Slc12a1	solute carrier family 12, member 1	20495	2.63006025	0.00017316
Akr1c14	aldo-keto reductase family 1, member C14	105387	2.62818614	0.00056336
Ddah2	dimethylarginine dimethylaminohydrolase 2	51793	2.62744549	0.00136983
2310016A09Rik	RIKEN cDNA 2310016A09 gene	69574	2.61810135	0.00996844
Cysltr1	cysteinyl leukotriene receptor 1	58861	2.60305934	0.00324877
9130007G19Rik	RIKEN cDNA 9130007G19 gene	74550	2.59095253	0.00226794
2310033F14Rik	RIKEN cDNA 2310033F14 gene	69555	2.59069995	0.00021890
Anks4b	ankyrin repeat and sterile alpha motif domain containing 4B	72074	2.57882780	0.00063326
Anks1b	ankyrin repeat and sterile alpha motif domain containing 1B	544718	2.57414381	0.00032053
Folr4	folate receptor 4 (delta)	64931	2.56802109	0.00093694
Iigp2	interferon inducible GTPase 2	54396	2.56213660	0.00066703
Lphn3	latrophilin 3	319387	2.55033101	0.00010207
2010001H14Rik	RIKEN cDNA 2010001H14 gene	69824	2.54420137	0.00160564
Etohi1	ethanol induced 1	13999	2.54246642	0.00085400
2010300C02Rik	RIKEN cDNA 2010300C02 gene	639555	2.53489467	0.00021027
C1qdc2	C1q domain containing 2	67389	2.53441910	0.00040106
6620401M08Rik	RIKEN cDNA 6620401M08 gene	75744	2.53219552	0.00008963
4930452B06Rik	RIKEN cDNA 4930452B06 gene	74430	2.52763398	0.00255108
S100a8	S100 calcium binding protein A8 (calgranulin A)	20201	2.52369792	0.00637608
Porcn	porcupine homolog (Drosophila)	53627	2.52345846	0.00014989

Gstm1	glutathione S-transferase, mu 1	14862	2.52186621	0.00001075
4930402H24Rik	RIKEN cDNA 4930402H24 gene	228602	2.52039552	0.00104776
Pkib	protein kinase inhibitor beta, cAMP dependent, testis specific	18768	2.50900737	0.00612002
Plat	plasminogen activator, tissue	18791	2.50159117	0.00019743
Hnf4a	hepatic nuclear factor 4, alpha	15378	2.50142131	0.00012124
Ttr	transthyretin	22139	2.49521219	0.00335812
Gbp7	guanylate binding protein 7	229900	2.48974315	0.00261320
Fbn2	fibrillin 2	14119	2.48673936	0.00588084
Gls2	glutaminase 2 (liver, mitochondrial)	216456	2.48369750	0.00144113
Lcp1	lymphocyte cytosolic protein 1	18826	2.48325750	0.00030785
Fzd4	frizzled homolog 4 (Drosophila)	14366	2.48235927	0.00167656
Dpysl3	dihydropyrimidinase-like 3	22240	2.47830483	0.00154802
Ier5	immediate early response 5	15939	2.47673188	0.00445393
Cyp4v3	cytochrome P450, family 4, subfamily v, polypeptide 3	102294	2.46639066	0.00354506
Jag1	jagged 1	16449	2.44697183	0.00556601
Itih2	inter-alpha trypsin inhibitor, heavy chain 2	16425	2.44234701	0.00025459
Atp9a	ATPase, class II, type 9A	11981	2.43902472	0.00170491
Aqp1	aquaporin 1	11826	2.43269094	0.00389078
Fscn1	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)	14086	2.42421754	0.00490275
Spata13	spermatogenesis associated 13	219140	2.42329994	0.00018508
Gnai1	guanine nucleotide binding protein, alpha inhibiting 1	14677	2.41594555	0.00305227
Kcnab1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	16497	2.40549262	0.00127015
Nostrin	nitric oxide synthase trafficker	329416	2.40246845	0.00221111
Cotl1	coactosin-like 1 (Dictyostelium)	72042	2.40143649	0.00000029
Dpysl3	dihydropyrimidinase-like 3	22240	2.40035943	0.00014181
Anxa13	annexin A13	69787	2.38840067	0.00070006
Serpinb2	serine (or cysteine) peptidase inhibitor, clade B, member 2	18788	2.38379613	0.00044095
Akap2	A kinase (PRKA) anchor protein 2	11641	2.37897638	0.00006649
Paqr5	progestin and adipoQ receptor family member V	74090	2.37812148	0.00280626
Pilrb1	paired immunoglobin-like type 2 receptor beta 1	170741	2.37468475	0.00032890
Id2	inhibitor of DNA binding 2	15902	2.36527860	0.00001254
Apoa1	apolipoprotein A-I	11806	2.36384276	0.00548135
Zfp597	zinc finger protein 597	71063	2.35241803	0.00010381
Ifi47	interferon gamma inducible protein 47	15953	2.34587746	0.00319744
Rdm1	RAD52 motif 1	66599	2.34158340	0.00003674
Itga2	integrin alpha 2	16398	2.32823379	0.00031836
Egln3	EGL nine homolog 3 (C. elegans)	112407	2.32472406	0.00106395
Pbxip1	pre-B-cell leukemia transcription factor interacting protein 1	229534	2.32442620	0.00332986
A330021E22Rik	RIKEN cDNA A330021E22 gene	207686	2.32309455	0.00001819
Ivl	involucrin	16447	2.32111620	0.00449461
5430421B17	hypothetical protein 5430421B17	330593	2.31719262	0.00001148
Mrpl21	mitochondrial ribosomal protein L21	353242	2.31030910	0.00148533
Mtap	methylthioadenosine phosphorylase	66902	2.30912579	0.00000433
Fzd10	frizzled homolog 10 (Drosophila)	93897	2.30626392	0.00448776
Arhgdib	Rho, GDP dissociation inhibitor (GDI) beta	11857	2.30008215	0.00384688

BC046404	cDNA sequence BC046404	192976	2.29083079	0.00046753
Pik3ap1	phosphoinositide-3-kinase adaptor protein 1	83490	2.28741416	0.00002076
Ecm1	extracellular matrix protein 1	13601	2.28430987	0.00038402
Ptgds2	prostaglandin D2 synthase 2, hematopoietic	54486	2.28161026	0.00343867
Cdcp1	CUB domain containing protein 1	109332	2.27776164	0.00002155
Tmtc2	transmembrane and tetratricopeptide repeat containing 2	278279	2.26966201	0.00146107
Ifi203	interferon activated gene 203	15950	2.26837601	0.00004275
Cryab	crystallin, alpha B	12955	2.26692962	0.00971532
Ghr	growth hormone receptor	14600	2.26261661	0.00046224
Samd9l	sterile alpha motif domain containing 9-like	209086	2.25440806	0.00002007
Dpyd	dihydropyrimidine dehydrogenase	99586	2.25153948	0.00198415
Ifih1	interferon induced with helicase C domain 1	71586	2.24981563	0.00233321
Evpl	Envoplakin	14027	2.24121183	0.00840708
Gbp2	guanylate nucleotide binding protein 2	14469	2.23617529	0.00472055
BC024814	cDNA sequence BC024814	239706	2.23592411	0.00023630
Rnf128	ring finger protein 128	66889	2.23262677	0.00085191
Depdc7	DEP domain containing 7	211896	2.22948070	0.00003399
Spint1	serine protease inhibitor, Kunitz type 1	20732	2.22873654	0.00041353
Gstm1	glutathione S-transferase, mu 1	14862	2.22228593	0.00012402
Gbp1	guanylate nucleotide binding protein 1	14468	2.22092031	0.00014180
Gbp1	guanylate nucleotide binding protein 1	14468	2.22092031	0.00014180
Fzd4	frizzled homolog 4 (Drosophila)	14366	2.21654517	0.00156998
Fbln1	fibulin 1	14114	2.21622423	0.00045549
2310045A20Rik	RIKEN cDNA 2310045A20 gene	231238	2.21602144	0.00494674
Ghr	growth hormone receptor	14600	2.21477724	0.00135119
Hnf4a	hepatic nuclear factor 4, alpha	15378	2.20890125	0.00006098
Jag1	jagged 1	16449	2.20838863	0.00003838
Abcc4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	239273	2.20691217	0.00004038
Zfp386	zinc finger protein 386 (Kruppel-like)	56220	2.20618529	0.00027265
Angptl4	angiopoietin-like 4	57875	2.19494182	0.00191920
St3gal6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	54613	2.18362827	0.00000789
Gsta2	glutathione S-transferase, alpha 2 (Yc2)	14858	2.17669035	0.00021244
1810019J16Rik	RIKEN cDNA 1810019J16 gene	69073	2.16944898	0.00061619
Sdcbp2	syndecan binding protein (syntenin) 2	228765	2.16914317	0.00009493
Erbb4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	13869	2.16782744	0.00577862
Ppp1r13b	Protein phosphatase 1, regulatory (inhibitor) subunit 13B	21981	2.16430611	0.00050184
Hnt	neurotrimin	235106	2.16119802	0.00013308
Gpr120	G protein-coupled receptor 120	107221	2.16016808	0.00205374
Anxa10	annexin A10	26359	2.15767597	0.00090525
Sh3kbp1	SH3-domain kinase binding protein 1	58194	2.15132481	0.00018135
Zfp386	zinc finger protein 386 (Kruppel-like)	56220	2.14877454	0.00154415
Styk1	serine/threonine/tyrosine kinase 1	243659	2.13906607	0.00021072
Rps6ka5	ribosomal protein S6 kinase, polypeptide 5	73086	2.12825996	0.00009997
Gstm1	glutathione S-transferase, mu 1	14862	2.12293700	0.00000626
8430427H17Rik	RIKEN cDNA 8430427H17 gene	329540	2.12245541	0.00018656
Ryr1	ryanodine receptor 1, skeletal muscle	20190	2.11217204	0.00344642
Zfpm1	zinc finger protein, multitype 1	22761	2.11179870	0.00000594
1110061N23Rik	RIKEN cDNA 1110061N23 gene	68846	2.10551409	0.00157052

Cotl1	coactosin-like 1 (Dictyostelium)	72042	2.10167506	0.00018368
Ifi203	interferon activated gene 203	15950	2.09985144	0.00072913
Ugt2b34	UDP glucuronosyltransferase 2 family, polypeptide B34	100727	2.09910402	0.00560649
Zdhhc12	zinc finger, DHHC domain containing 12	66220	2.09719626	0.00545698
Cotl1	coactosin-like 1 (Dictyostelium)	72042	2.08888482	0.00000220
Crebbp	CREB binding protein	12914	2.08769510	0.00003642
Npc2	Niemann Pick type C2	67963	2.08542755	0.00014639
Gpc2	glypican 2 (cerebroglycan)	71951	2.08386802	0.00030097
Ugt2a3	UDP glucuronosyltransferase 2 family, polypeptide A3	72094	2.08282249	0.00542124
4930589M24Rik	RIKEN cDNA 4930589M24 gene	75906	2.08073394	0.00634602
Zfp597	zinc finger protein 597	71063	2.07833524	0.00518002
Gsn	Gelsolin	227753	2.06982383	0.00476050
Mtus1	mitochondrial tumor suppressor 1	102103	2.06929845	0.00021820
Mmp10	matrix metallopeptidase 10	17384	2.06784225	0.00039229
Col18a1	procollagen, type XVIII, alpha 1	12822	2.06731013	0.00054843
Gpm6b	glycoprotein m6b	14758	2.06660995	0.00000762
Elk1	ELK1, member of ETS oncogene family	13712	2.06596146	0.00895192
Lphn3	latrophilin 3	319387	2.05894881	0.00474030
Crebbp	CREB binding protein	12914	2.05805150	0.00964333
Carhsp1	calcium regulated heat stable protein 1	52502	2.05652881	0.00022209
Dnajc17	DnaJ (Hsp40) homolog, subfamily C, member 17	69408	2.05451000	0.00090703
Tbc1d2b	TBC1 domain family, member 2B	67016	2.04957925	0.00314224
Coro7	coronin 7	78885	2.04914043	0.00160521
Pldn	pallidin	18457	2.04772577	0.00048722
3100002L24Rik	RIKEN cDNA 3100002L24 gene	627901	2.04678889	0.00001849
Fcmd	Fukuyama type congenital muscular dystrophy homolog (human)	246179	2.04612134	0.00012287
Epas1	Endothelial PAS domain protein 1	13819	2.04517756	0.00152011
Gca	grancalcin	227960	2.04471686	0.00000696
Krtcap3	keratinocyte associated protein 3	69815	2.04224941	0.00003003
Cyp2s1	cytochrome P450, family 2, subfamily s, polypeptide 1	74134	2.04015154	0.00016534
AI449310	expressed sequence AI449310	101584	2.03953542	0.00205711
Zfp263	zinc finger protein 263	74120	2.03820003	0.00001781
Fez2	fasciculation and elongation protein zeta 2 (zygin II)	225020	2.03467224	0.00000208
Tns4	tensin 4	217169	2.02934956	0.00024472
Nedd10	neural precursor cell expressed, developmentally down-regulated gene 10	17998	2.02643810	0.00027731
Vasn	vasorin	246154	2.02463767	0.00060846
6820424L24Rik	RIKEN cDNA 6820424L24 gene	100515	2.02266361	0.00128722
Ocln	occludin	18260	2.02119544	0.00037189
Ocln	occludin	18260	2.02119544	0.00037189
Olfml2b	olfactomedin-like 2B	320078	2.01320641	0.00133109
B230120H23Rik	RIKEN cDNA B230120H23 gene	65964	2.00813249	0.00001376
Rnf128	ring finger protein 128	66889	2.00552078	0.00030234
Angpt2	angiopoietin 2	11601	2.00378670	0.00017949
Tnfrsf22	tumor necrosis factor receptor superfamily, member 22	79202	2.00265093	0.00205707
Sdpr	serum deprivation response	20324	2.00165943	0.00018535

Col25a1	procollagen, type XXV, alpha 1	77018	2.00078062	0.00820052
1700006H03Rik	RIKEN cDNA 1700006H03 gene	74174	0.49925466	0.00157554
2900078I11Rik	RIKEN cDNA 2900078I11 gene	73004	0.49878732	0.00944883
Oxct1	3-oxoacid CoA transferase 1	67041	0.49643304	0.00618405
Slc7a5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	20539	0.49482519	0.00023238
Hk3	hexokinase 3	212032	0.49452323	0.00117195
C030002B11Rik	RIKEN cDNA C030002B11 gene	78540	0.49407794	0.00218967
Nob1	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)	67619	0.49379010	0.00002469
Pspc1	paraspeckle protein 1	66645	0.49074385	0.00007505
Pik3ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	18706	0.48679294	0.00001693
Trim2	tripartite motif protein 2	80890	0.48644820	0.00002329
Trim2	tripartite motif protein 2	80890	0.48488280	0.00002726
Itgb5	integrin beta 5	16419	0.48319649	0.00888734
Rhoq	ras homolog gene family, member Q	104215	0.48251230	0.00005577
Arhgdig	Rho GDP dissociation inhibitor (GDI) gamma	14570	0.48232763	0.00013490
Abi1	abl-interactor 1	11308	0.48194542	0.00385545
Dach2	dachshund 2 (Drosophila)	93837	0.48190924	0.00556503
Adh7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	11529	0.48080975	0.00000899
4931420C21Rik	RIKEN cDNA 4931420C21 gene	234353	0.48022039	0.00526229
4931420C21Rik	RIKEN cDNA 4931420C21 gene	234353	0.48022039	0.00526229
Rgs3	regulator of G-protein signaling 3	436235	0.47904501	0.00021998
Shc4	SHC (Src homology 2 domain containing) family, member 4	271849	0.47862378	0.00502518
Bmp2k	BMP2 inducible kinase	140780	0.47804399	0.00019078
Ankrd37	ankyrin repeat domain 37	654824	0.47781125	0.00001452
Pik3ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	18706	0.47703854	0.00001851
Pik3ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	18706	0.47703854	0.00001851
D1Ertd471e	DNA segment, Chr 1, ERATO Doi 471, expressed	27877	0.47450105	0.00046441
Pcdhb22	protocadherin beta 22	93893	0.47230026	0.00057340
Cd1d1	CD1d1 antigen	12479	0.47146112	0.00006541
Ppargc1a	Peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	19017	0.46973218	0.00263327
LOC665521	similar to PRAME family member 8	665521	0.46953992	0.00250412
Tnrc15	trinucleotide repeat containing 15	227331	0.46946743	0.00034354
2510009E07Rik	RIKEN cDNA 2510009E07 gene	72190	0.46902430	0.00000642
Zfp37	zinc finger protein 37	22696	0.46829373	0.00017986
Serpinb9	serine (or cysteine) peptidase inhibitor, clade B, member 9	20723	0.46794618	0.00001794
Col4a4	procollagen, type IV, alpha 4	12829	0.46729174	0.00194585
Rhox5	reproductive homeobox 5	18617	0.46625123	0.00001688
9030613N10Rik	RIKEN cDNA 9030613N10 gene	71569	0.46474002	0.00398436
Chst1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	76969	0.46471010	0.00137868
Nfat5	Nuclear factor of activated T-cells 5	54446	0.46449903	0.00298953
Cib2	calcium and integrin binding family member 2	56506	0.46141364	0.00078311
Myh10	myosin, heavy polypeptide 10, non-muscle	77579	0.45932965	0.00005640

Pes1	pescadillo homolog 1, containing BRCT domain (zebrafish)	64934	0.45817196	0.00272856
1200015M12Rik	RIKEN cDNA 1200015M12 gene	319202	0.45582329	0.00022504
B230209C24Rik	RIKEN cDNA B230209C24 gene	320705	0.45509730	0.00097247
Tmprss6	transmembrane serine protease 6	71753	0.45451253	0.00497734
Rab6b	RAB6B, member RAS oncogene family	270192	0.45168635	0.00053723
Clic5	chloride intracellular channel 5	224796	0.44755632	0.00525286
4930515G13Rik	RIKEN cDNA 4930515G13 gene	75098	0.44667483	0.00135607
3110043J09Rik	RIKEN cDNA 3110043J09 gene	73167	0.44535329	0.00310115
Vamp5	vesicle-associated membrane protein 5	53620	0.44520160	0.00017042
Eif1a	eukaryotic translation initiation factor 1A	13664	0.44506753	0.00027649
Gnn	Grp94 neighboring nucleotidase variant 4	103220	0.44459397	0.00116419
Acpl2	acid phosphatase-like 2	235534	0.44411538	0.00022570
Mreg	melanoregulin	381269	0.44023848	0.00689362
Mta3	metastasis associated 3	116871	0.43839164	0.00003964
Cldn6	claudin 6	54419	0.43637441	0.00150070
4931432M23Rik	RIKEN cDNA 4931432M23 gene	636530	0.43402503	0.00688713
Six4	sine oculis-related homeobox 4 homolog (Drosophila)	20474	0.43293356	0.00025028
LOC639910	hypothetical protein LOC639910	639910	0.43211146	0.00118799
Serpinb9	serine (or cysteine) peptidase inhibitor, clade B, member 9	20723	0.43083618	0.00149265
Pdzx	PDZ domain containing, X chromosome	54634	0.43026771	0.00695428
Epb4.1l2	Erythrocyte protein band 4.1-like 2	13822	0.42976575	0.00176990
Abtb2	ankyrin repeat and BTB (POZ) domain containing 2	99382	0.42612301	0.00027598
Igsf4d	Immunoglobulin superfamily, member 4	239857	0.42517784	0.00731031
1110007C02Rik	RIKEN cDNA 1110007C02 gene	71784	0.42285135	0.00027807
Six4	sine oculis-related homeobox 4 homolog (Drosophila)	20474	0.42135143	0.00209953
Dach2	dachshund 2 (Drosophila)	93837	0.42018111	0.00036341
Fzd6	frizzled homolog 6 (Drosophila)	14368	0.41976199	0.00017226
Siah1a	seven in absentia 1A	20437	0.41967183	0.00169157
Ppargc1a	Peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	19017	0.41847344	0.00136128
Foxf1a	forkhead box F1a	15227	0.41722667	0.00738758
Mbnl3	muscleblind-like 3 (Drosophila)	171170	0.41677189	0.00242873
Bdp1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	544971	0.41463614	0.00521542
Bdh2	3-hydroxybutyrate dehydrogenase, type 2	69772	0.41398964	0.00139044
1700029I01Rik	RIKEN cDNA 1700029I01 gene	666532	0.41043618	0.00052580
D430039N05Rik	RIKEN cDNA D430039N05 gene	241520	0.40859908	0.00705093
Npr2	natriuretic peptide receptor 2	230103	0.40819390	0.00132631
AI836737	expressed sequence AI836737	103288	0.40704104	0.00030992
Rab3c	RAB3C, member RAS oncogene family	67295	0.40656113	0.00194674
Xrcc2	X-ray repair complementing defective repair in Chinese hamster cells 2	57434	0.40574879	0.00747229
Egr2	early growth response 2	13654	0.40408505	0.00112704
Megf10	multiple EGF-like-domains 10	70417	0.40203123	0.00271166
Col4a5	procollagen, type IV, alpha 5	12830	0.40164861	0.00000279
Reck	reversion-inducing-cysteine-rich protein with kazal motifs	53614	0.40058751	0.00619758
Zdhhc23	zinc finger, DHHC domain containing 23	332175	0.40032112	0.00276372

Fabp6	fatty acid binding protein 6, ileal (gastrotropin)	16204	0.40015501	0.00181978
Smoc2	SPARC related modular calcium binding 2	64074	0.39789640	0.00153879
Lrrc8e	leucine rich repeat containing 8 family, member E	72267	0.39750103	0.00555593
Hip1	huntingtin interacting protein 1	215114	0.39686936	0.00023012
Rragd	Ras-related GTP binding D	52187	0.39569119	0.00085177
Dst	dystonin	13518	0.39336433	0.00904668
Rgs3	regulator of G-protein signaling 3	50780	0.39178267	0.00003406
LOC629147	similar to Cortexin-1	629147	0.39114205	0.00510403
Insm1	insulinoma-associated 1	53626	0.38965973	0.00024783
Insm1	insulinoma-associated 1	53626	0.38668120	0.00010097
Sphk1	sphingosine kinase 1	20698	0.38604916	0.00024485
1700012I11Rik	RIKEN cDNA 1700012I11 gene	69334	0.38475169	0.00233769
Atp10d	ATPase, Class V, type 10D	231287	0.38250006	0.00001167
Speg	SPEG complex locus	11790	0.38218648	0.00317010
Hectd2	HECT domain containing 2	226098	0.38052823	0.00319468
Anxa8	annexin A8	11752	0.38028743	0.00043570
Zfp365	zinc finger protein 365	216049	0.37458210	0.00375260
Ang4	angiogenin, ribonuclease A family, member 4	219033	0.37045748	0.00663712
Nrg1	neuregulin 1	211323	0.36711919	0.00033842
Taf9b	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor	407786	0.36571051	0.00291380
Zfp142	zinc finger protein 142	77264	0.36439084	0.00724923
Tacc1	transforming, acidic coiled-coil containing protein 1	320165	0.36243789	0.00004680
Pdgfrl	platelet-derived growth factor receptor-like	68797	0.36084406	0.00008615
Gzme	granzyme E	14942	0.35980474	0.00058515
Pde4b	phosphodiesterase 4B, cAMP specific	18578	0.35940368	0.00260801
Ccdc109b	coiled-coil domain containing 109B	66815	0.35916504	0.00024899
Glrb	glycine receptor, beta subunit	14658	0.35845853	0.00751013
Dub1	deubiquitinating enzyme 1	13531	0.35775723	0.00001397
1700006H03Rik	RIKEN cDNA 1700006H03 gene	74174	0.35748845	0.00341377
Abhd3	abhydrolase domain containing 3	106861	0.35702796	0.00254158
Slc10a4	solute carrier family 10 (sodium/bile acid cotransporter family), member 4	231290	0.34879273	0.00146322
Shox2	short stature homeobox 2	20429	0.34519583	0.00015645
Tns1	tensin 1	21961	0.34464936	0.00264979
B230342M21Rik	RIKEN cDNA B230342M21 gene	100637	0.34199079	0.00028973
Atf7ip2	activating transcription factor 7 interacting protein 2	75329	0.34170291	0.00048107
A130040M12Rik	RIKEN cDNA A130040M12 gene	319269	0.34124029	0.00049750
Tacc1	transforming, acidic coiled-coil containing protein 1	320165	0.33987640	0.00105592
D3Bwg0562e	DNA segment, Chr 3, Brigham & Women's Genetics 0562 expressed	229791	0.33595164	0.00294568
Csn3	casein kappa	12994	0.33535919	0.00004504
9630013A20Rik	RIKEN cDNA 9630013A20 gene	319903	0.33198950	0.00688991
Klf12	Kruppel-like factor 12	16597	0.33193292	0.00062639
Rhbg	Rhesus blood group-associated B glycoprotein	58176	0.32503833	0.00217033
2310043L02Rik	RIKEN cDNA 2310043L02 gene	69664	0.32487891	0.00004089
3110009F21Rik	RIKEN cDNA 3110009F21 gene	67280	0.32295945	0.00043170
Ltbp1	latent transforming growth factor beta binding protein 1	268977	0.32072779	0.00039107

Tmprss5	transmembrane protease, serine 5 (spinesin)	80893	0.31944223	0.00149975
4930554P06Rik	RIKEN cDNA 4930554P06 gene	75249	0.31872605	0.00231873
Fbxl16	F-box and leucine-rich repeat protein 16	214931	0.31685690	0.00000204
Igll1	immunoglobulin lambda-like polypeptide 1	16136	0.31632730	0.00329989
LOC545191	similar to zinc finger protein 616	545191	0.30913769	0.00423694
Kazald1	Kazal-type serine peptidase inhibitor domain 1	107250	0.30898711	0.00064343
A130040M12Rik	RIKEN cDNA A130040M12 gene	319269	0.30877926	0.00002560
5430405G05Rik	RIKEN cDNA 5430405G05 gene	108832	0.30783202	0.00686966
LOC666806	similar to X-linked eukaryotic translation initiation factor 1A	666806	0.30730566	0.00015482
Clec4b1	C-type lectin domain family 4, member b1	69810	0.30493211	0.00698201
Pgcp	plasma glutamate carboxypeptidase	54381	0.30344399	0.00013048
Kctd15	potassium channel tetramerisation domain containing 15	233107	0.30301913	0.00001482
Hip1	huntingtin interacting protein 1	215114	0.30195880	0.00619644
Krt28	keratin 28	70843	0.29922522	0.00477924
Scrn1	secernin 1	69938	0.29512222	0.00033980
Mkx	mohawk	210719	0.29455279	0.00002964
Trim2	tripartite motif protein 2	80890	0.29414866	0.00097864
Gzme	granzyme E	14942	0.29096228	0.00004622
Nell1	RIKEN cDNA B230343H07 gene	338352	0.29074974	0.00585774
Bscl2	Bernardinelli-Seip congenital lipodystrophy 2 homolog (human)	14705	0.29005888	0.00038581
Klf12	Kruppel-like factor 12	16597	0.28939246	0.00087625
Tubb3	tubulin, beta 3	22152	0.28937198	0.00289493
Sntg1	syntrophin, gamma 1	71096	0.28923203	0.00974082
Wnt9a	wingless-type MMTV integration site 9A	216795	0.28816004	0.00101468
BC042720	cDNA sequence BC042720	329178	0.28789004	0.00061057
E530011L22Rik	RIKEN cDNA E530011L22 gene	320301	0.28683843	0.00198387
4930486G11Rik	RIKEN cDNA 4930486G11 gene	75033	0.27649602	0.00002783
B230112C05Rik	RIKEN cDNA B230112C05 gene	320557	0.27459255	0.00265819
Dand5	DAN domain family, member 5	23863	0.26429348	0.00004338
7530403E16Rik	RIKEN cDNA 7530403E16 gene	100224	0.26356025	0.00052468
Flt1	FMS-like tyrosine kinase 1	14254	0.26308910	0.00201479
4933404G15Rik	RIKEN cDNA 4933404G15 gene	74066	0.25950773	0.00019837
Ppargc1b	peroxisome proliferative activated receptor, gamma, coactivator 1 beta	170826	0.25945835	0.00132373
Hmgn3	high mobility group nucleosomal binding domain 3	94353	0.25715782	0.00003639
A830082K12Rik	RIKEN cDNA A830082K12 gene	320174	0.25375726	0.00187642
D10Ertd494e	DNA segment, Chr 10, ERATO Doi 494, expressed	52638	0.25355243	0.00538344
Sfmbt2	Scm-like with four mbt domains 2	353282	0.25342913	0.00054650
Lrch2	Leucine-rich repeats and calponin homology (CH) domain containing 2	210297	0.25283664	0.00535245
Pdcl2	phosducin-like 2	79455	0.25174107	0.00658841
1500016O10Rik	RIKEN cDNA 1500016O10 gene	68952	0.25069422	0.00654072
Cpeb1	cytoplasmic polyadenylation element binding protein 1	12877	0.24542925	0.00001472
Tph2	tryptophan hydroxylase 2	216343	0.24532961	0.00044745
Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2	18606	0.24324435	0.00134099
Rwdd1	RWD domain containing 1	66521	0.24147081	0.00065008

6430701C03Rik	RIKEN cDNA 6430701C03 gene	76229	0.24059729	0.00324307
Foxd1	forkhead box D1	15229	0.23804115	0.00007654
2210010N04Rik	RIKEN cDNA 2210010N04 gene	70381	0.23764737	0.00887850
Serpinb3b	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3B	383548	0.22314761	0.00852083
AA407787	expressed sequence AA407787	106842	0.22083317	0.00400348
Lrrc39	leucine rich repeat containing 39	109245	0.21742982	0.00001734
Hmgn3	high mobility group nucleosomal binding domain 3	94353	0.21036054	0.00009262
Pcdh19	protocadherin 19	279653	0.19874612	0.00011809
Rnf157	ring finger protein 157	217340	0.19777255	0.00046739
4933401D09Rik	RIKEN cDNA 4933401D09 gene	71008	0.19740230	0.00428329
Ubash3a	ubiquitin associated and SH3 domain containing, A	328795	0.19250009	0.00599699
AI848149	expressed sequence AI848149	102944	0.19108640	0.00293068
KIAA0415	KIAA0415 protein	231855	0.19104934	0.00094136
C630007C17Rik	RIKEN cDNA C630007C17 gene	241514	0.18618931	0.00597507
Srgap3	SLIT-ROBO Rho GTPase activating protein 3	259302	0.18548022	0.00788862
Prkcm	protein kinase C, mu	18760	0.18380766	0.00066114
4932431H17Rik	RIKEN cDNA 4932431H17 gene	545527	0.18309685	0.00718160
Cd300lb	CD300 antigen like family member B	217304	0.18169261	0.00007820
Actr3b	ARP3 actin-related protein 3 homolog B (yeast)	242894	0.18076368	0.00050402
Rps6ka6	ribosomal protein S6 kinase polypeptide 6	67071	0.17614935	0.00004343
Sigirr	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	24058	0.17540167	0.00009039
Aqp5	aquaporin 5	11830	0.17132585	0.00000971
4921539E11Rik	RIKEN cDNA 4921539E11 gene	70941	0.16873731	0.00017905
Frmd3	FERM domain containing 3	242506	0.16312229	0.00119307
Foxf1a	forkhead box F1a	15227	0.16039436	0.00036117
Pde4b	phosphodiesterase 4B, cAMP specific	18578	0.15769662	0.00266251
6530418L21Rik	RIKEN cDNA 6530418L21 gene	109050	0.15453806	0.00447424
Col4a4	procollagen, type IV, alpha 4	12829	0.15084713	0.00473171
Etv1	ets variant gene 1	14009	0.14937973	0.00000231
S100a4	S100 calcium binding protein A4	20198	0.14888722	0.00002360
Gata3	GATA binding protein 3	14462	0.14412779	0.00259783
Dnm2	dynamin 2	13430	0.14084309	0.00651548
Edaradd	EDAR (ectodysplasin-A receptor)-associated death domain	171211	0.14020978	0.00096788
Tchh	trichohyalin	99681	0.12184640	0.00016765
D730039F16Rik	RIKEN cDNA D730039F16 gene	77996	0.11969589	0.00032191
C130009A20Rik	RIKEN cDNA C130009A20 gene	399614	0.11274827	0.00000999
Etv1	ets variant gene 1	14009	0.10351602	0.00004491
9330118A15Rik	RIKEN cDNA 9330118A15 gene	319756	0.10100289	0.00699562
Serpinb1a	serine (or cysteine) peptidase inhibitor, clade B, member 1a	66222	0.09910204	0.00101410
Dmc1h	disrupted meiotic cDNA 1 homolog	13404	0.09542884	0.00042844
LOC230628	similar to C05G5.5	230628	0.08861725	0.00001625
D10Bwg1379e	DNA segment, Chr 10, Brigham & Women's Genetics 1379 expressed	215821	0.07773491	0.00663328
D10Bwg1379e	DNA segment, Chr 10, Brigham & Women's Genetics 1379 expressed	215821	0.03506715	0.00262716
Rps6ka6	ribosomal protein S6 kinase polypeptide 6	67071	0.01518947	0.00009573

Supplemental Table 2. qPCR primers used in this study

gene	**forward (5'→3')**	**reverse (5'→3')**
Akt1	CTAGGCATCCCTTCCTTACGG	GGTCGTGGGTCTGGAATGAG
Akt2	CGGGAACGAGCTCAGCGTGG	CCTCTCCGGCCGGGCTCTAC
Areg	GCAGATACATCGAGAACCTGGAG	CCTTGTCATCCTCGCTGTGAGT
Bdh1	GAAGCAGACACATCAAGCCC	TCCCCGCAGGGTGTAATAAG
Bicc	CGAGGACGATCTGGTGGC	CGCTCCTCGCTCCACTC
Btc	TTCGTGGTGGACGAGCAAACTC	CCATGACCACTATCAAGCAGACC
Cdh1	TACGGCGGTGGTGAGGACGA	GCCACACGGGGGAGACTTGC
Cdh10	TCCTACCGCCCCAGATAACA	TGCTCTTTGAGTCGCTCGTT
Cdh2	CCTCCAGAGTTTACTGCCATGAC	CCACCACTGATTCTGTATGCCG
Cldn3	CACCTGACTACCGGGCCTAG	GGTTTCTTTGTCCATTCGGCT
Crb3	CGGACCCTTTCACAAATAGCA	CGTTGGACTCATCACCTGGG
Cxcl5	AAAAGGGGTGCAGTGGGTTT	GTGTGGAGATTGGGGCTCTAC
Dnm2	GCTGAACAAGAAGAGGGCCA	GCGGATCACCAAGATCTCCC
Edaradd	GTGAGGTGTGCACGTGAGTA	TCTGGGGGAATCTGACACCT
Egf	ACTGGTGTGACACCAAGAGGTC	CCACAGGTGATCCTCAAACACG
Eif4e	TCGATCTAAGATGGCGACTGTGGA	GCAGGTGGGGGATTAGTGGTAGGG
Eif4ebp1	CCAGCCAGAGCCAACTGCCC	GACTCTTCACCGCCTGCCCG
Epgn	GAGCGAAGAAGCAGAGGTGATC	GGTCTTCCAGACAAGGATGAGAG
Ereg	CAGGCAGTTATCAGCACAACCG	CATGCAAGCAGTAGCCGTCCAT
Etv1	TCTGTCAGAGGCGCTTTCGG	TAATTATTGCCCAGCACTTCCCCT
Flt1	CACGGGGAGTTAAGTGGTCC	GCCCATCAGTAGGCAACCTT
FLT1	GCACGTCAGCGAAGGCAAGC	CCAGCTCAGCGTGGTCGTAGG
Fn1	GGGCTGGCGCTGTGACAACT	CGGGACTGGGTTCAGCAGCC
Fog2	GACACCGCAGGAACCCCAGC	TTCGCCGGGACATTTCGGCC
Gata3	GTTCCTCCGACCCCTTCTAC	TTCATGATACTGCTCCTGCG
Gata6	CTACACAAGCGACCACCTCA	TCTCCCACTGCAGACATCAC
H3bp	CTGTGCCGGATATGACCCTC	CCTCGTTACGGCGTCCATAG
Hbegf	GAGTTCCGTACTCCCTCTTGCA	CAGCCAAGACTGTAGTGTGGTC
Inadl	GGAAGATTTGCCTCTGTACCGAC	GCTGAAGTTCGGTGTCTCCTCT
L32	GGAGAAGGTTCAAGGGCCAG	TGCTCCCATAACCGATGTTTG
Lgals4	AGGTACCCGCCCTTTACTCT	AGGCCACAGGAATGTCTGAAC
Maob	CTGGAACCTAGCAAGCAGCA	CCACCACGATCACATCGCTT
Mlst8	GGCCACCCCTGACACCTCCA	CGGGCAGAACGTGAGTGGGC
mTOR	GTGTGGGACCCCAAGCAGGC	CAGACAGGCACGAAGGGCCG
Myh10	GGGCGTGGAGATGGCCCAATG	CGCCGGGCTCCTTTAGCACTG
Nrg1	GCTCATCACTCCACGACTGTCA	TGCCTGCTGTTCTCTACCGATG
Nrg2	CCGGAGTCGTGATATTCGCA	TTCCCAAGGATGTTCTCGGC
Nrg3	CGAGACAAGGACCTGGCGTATT	TCACAACGGACTCCTTGGTAGC
Nrg4	TCCTCCTCACTCTTACCATCGC	GTCTCTACCAGGCTGATCTCAC
Pard3	GTCGGCACTCGGTGTCCGTG	GCTGGGCCTGCTGGAAGCTC
Pard6b	TTTCCACCGCCAATCCACTGCT	GCTGATGACGATGTGAGGCTTC
Pdpk1	GCTGTGCAGTGACGTGGCCT	GGGGCAGGTATCCTGGCAGC
Pik3ca	GCTCCCGGCTTCTCCACTGC	CATGCCACTGCCTGCCTGCT
Pik3cb	TGCCCACCCTGTGTTCCCGA	GGGCCTCCATGCTGCTGCTC
Pik3cg	AGTTCCGTCCAGCAAGGGCT	TCCGCACAAACAAAAACAGAAAGAAC
Pik3r1	GAAATGGATCCACCAGCACTGCCC	TGGCTACAGTAGTGGGCTTGGGT
Pten	CCATTACCCGGCTGCGGTCC	TCGCTGATGCCCCTCGCTCT
Raptor	TGCCCACCTACCCACCCACC	CTGGCCACGGCCAAGTCAGG
Rheb	TGTGGTTGGGTCGGGGCTGA	TCCGGGACTTGGACTGAGGCA
Rictor	TTCTGGCTGCAGCGATGGCG	GGTGCTGCTGGCTGAGCCTT

Rps6ka6	TTTCCAACGGCCCCAATGAT	TGCCTATGCGCAGCAGTATT
S6K1	GGGGAAGCATCAGCGCCACT	TGTACGGCCCGGAGTTGGGT
S6K2	CACCCCCATCAGCCCCCTCA	GACTGGGCCGGAACCCCTCA
Scrib	CCCAGGAAGGCCGTGGCAAG	GCCTCAGCCAGCCGTTCCAA
Serpinb1a	AGCTGTAAGTGGAGCCAGAC	CTGCTCCATGGTGAAGTCTCT
Six4	GGCAGATTGCAAGTGCGG	GCGCTTTCCATCCCATTCTC
Slc43a	CGATGGGGCTTGCCATTTTC	CTCACGGTACACCAGGAAGG
Snai1	CCCAAGGCCGTAGAGCTGA	GCTTTTGCCACTGTCCTCATC
Snai2	ATCCTCACCTCGGGAGCATA	TGCCGACGATGTCCATACAG
Stk11	CGAGGCCCTGCACCCTTTCG	CCTGGCTTGTCCGGCAGGTG
Tceal1	AGACCGTATTCCCATGGAGC	CTAGCTTGTGTTTGCCCACC
Tchh	AGAGCCCTGCCCAATGAAAA	TCTTGCCTGCGATCTTGTGA
Tgfa	CAGGCTCTGGAGAACAGCACAT	GACACATGCTGGCTTCTCTTCC
Tns1	GTCCCAGGTCGGATGACAAG	ACCCACAAGCTACACTTCCG
Trf	TTGACAATACCCGCAAGCCA	CGAGCCAGGTAGCAATCCTC
Tsc1	AGGTTCAGCAGCCGGTGGGA	GATGCTGCTGGAGGGCTCGC
Tsc2	TGTGGTCCGCAGCAGAATACAGA	TCATCCGCAGACCCCAGGCT
Twist1	TCGACTTCCTGTACCAGGTCCT	CCATCTTGGAGTCCAGCTCG
Vim	GCGTGCGGCTGCTTCAAGAC	ATGGCGTCGGCCAGCGAGAA
Zeb1	GCTCAGCCAGGAACCCGCAG	TGGGCACCCTCTGCCACACA
Zeb2	AGGCGCGAGAGAAAGGGCAC	CCCGGTTCATCAGCAGCTCGG

Supplemental Table 3. PCR primers for ChIP assays

promoter	**forward (5'→3')**	**reverse (5'→3')**
Pol-II ChIP		
Areg	CGGTGGAACCAATGAGAACT	CTCACCCTCCTAGCATGAGC
Btc	TATCCTGGAGCCTTCTGCAC	ACCTTGTTTTGTCCCACAGG
Hbegf	CCTCTGGGTGAGATCCTGTC	CTTCCCCGGAGCCTTATTC
Pik3ca	GGCTATCGGAGTGGGTTACA	GCGGACGTGTCAAACCTATT
Rheb	AAAGTCACGACCGAAACTCG	ACCCTTCCAATCCCCAATAG
GATA6 ChIP		
Btc	GCTCCAGTGTCACCCAGAAC	ATGAACCGTCAGGTGAGACC
Areg	CGGTGGAACCAATGAGAACT	CTCACCCTCCTAGCATGAGC
GATA3 ChIP		
PIK3CA #1	TGAGGCAGAAGAATCGCTTGAAC	CTGAATTGCTAGTCAAAGT
PIK3CA #2	TGGACGGACGTGCGGTGTTC	AGACGTGGGGGATTTTTCGCGT
PIK3CA #3	AGCCACCGCACCTCCTCTCA	GCGTCTTGCTTTTCCGCCCG
RHEB #1	TCGGGGATCTACAGATGGAA	CCCTTACTATGCATAACGCAGT
RHEB #2	GTGGCGTAATTCTCGGTCAT	GGGCAACATAGAAACCTCCA