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Supplementary methods

SNAI2 quantification in human tumors

The expression of SNAI2 in the human tumor epithelium and stroma was analyzed semi-quantitatively employing a three-point scale. SNAI2 expression in the epithelium was considered intense positive when it was detected in virtually all the tumor nuclei examined (always more than 75%). In contrast, it was considered focal positive when observed in less than 75% of the tumor nuclei (there were no tumors with negative expression of Snai2 in the epithelium). The stroma was considered to express SNAI2 (positive) when nuclear staining was evident at 4x magnification. Focal stromal staining (focal positive) was considered when there was occasional staining of fibroblasts (less than 50% evident at 20x magnification). When no staining was observed, the stroma was considered to be negative for SNAI2 expression. We evaluated HER2-positive (+++) and HER2-negative tumors. ER+ tumors were considered those with more than 10% positive cells. Ki-67 cut-off was considered in 15% of positive cells. PR+ tumors were those with more than 5% positive cells. The slides were all evaluated by two pathologists (MMAH and SFG) who were unaware of the clinical status of the patients.

Immunohistochemistry in mouse tissues

To analyze the protein expression in mouse tumors, tumor sections (3 µm) were deparaffinized and processed to detect cleaved CASPASE-3 after microwaving the tissue in citrate buffer (pH 6) to achieve antigen retrieval. The anti-Ki-67 (MAD020310Q, Master Diagnostica, Granada, Spain), anti-ERBB2 (Abcam, catalog number ab2428), anti-phospho-ERBB2 (Tyr1248) (Abcam, catalog number ab47755), anti-SNAI1/SNAIL (Abcam, ab53519), and cleaved CASPASE-3 (Asp175; Cell Signaling) primary antibodies were used at a 1:50 dilution in the Ventana Discovery automated immunohistochemistry research slide-staining system (Tucson, AZ85755). Ki-67, ERBB2, phospho-ERBB2(Tyr1248) and SNAI1/SNAIL expressing cells in tumors were quantified with the ARIOL-slide scanner software on tissue-array sections of tumors from *Snai2* WT^{ErbB2} and *Snai2* KO^{ErbB2} nulliparous and parous mice (10 tumors from each group), each stained in triplicate.

MEF generation

To generate MEFs, embryos from *Snai2* WT^{ErbB2+} and *Snai2* KO^{ErbB2+} mice were isolated on day E13.5 of pregnancy. The embryo’s head, limbs and most of the internal organs were removed, the tissue was minced and trypsinized for 30 min, and the cells recovered were seeded in culture dishes with 15 mL of complete DMEM. Once confluent, the MEFs were split at a ratio of 1:3, passaged twice and frozen or expanded for the different studies.

Cancer-associated fibroblasts

Human fibroblasts and CAFs were obtained using a co-implantation breast tumor xenograft model, as described previously (29). Briefly, primary mammary hNFs were isolated from reduction mammoplasty tissue and immortalized with hTERT, the catalytic subunit of the telomerase holoenzyme. Retroviral constructs encoding GFP and the puromycin-resistance protein were also introduced into these fibroblasts. Mouse CAFs were obtained from tumors by flow cytometry, as indicated above.

ELISA

The phosphorylated and total AKT2 or AKT3, and the total ERK, were measured using Sandwich ELISA Kits: pAKT2(Ser474) [catalog number 7932]; total AKT2 [catalog number 7930]; pAKT3(Ser472) [catalog number 7942]; total AKT3 [catalog number

7934]; and total ERK1/2 [catalog number 7050]. The levels of phosphorylated and total AKT1, and of phosphorylated ERK were measured using the ELISA Sandwich Antibody Pair, and by coating a 96-well Microtest Plate (BD Falcon, catalog number 353077) with capture antibody according to the manufacturer's instructions (Pathscan Cell Signaling Technology): pAKT (Thr308) [catalog number 7144]; pAKT1 (Ser473) [catalog number 7143]; total AKT1 [catalog number 7142]; pERK (Thr202/Tyr204) [catalog number 7246]. Absorbance was measured at 450 nm on a Synergy-4 Microplate Reader (Biotek). All assays using proteins from tumors were carried out with 5 µg of protein and serial dilutions (1:2) of the protein extracted from each tumor sample were assayed on each plate (3-50 µg) to control for inter-assay variability.

Protein analyses

The proteins in the tumor samples were analyzed in western blots. Extracting proteins from the frozen tumor tissue in RIPA buffer (150 mM NaCl, 1% [v/v] NP40, 50 mM Tris-HCl [pH 8.0], 0.1% [v/v] SDS, 1 mM EDTA, 0.5% [w/v] Deoxycholate) containing protease and phosphatase inhibitor cocktails (Roche, Basel, Switzerland). The proteins were quantified with a BCA Protein Assay Kit (Thermo Fisher Scientific Inc., catalog number 23228, Waltham, MA USA), resolved by SDS-PAGE and transferred to polyvinylidene difluoride membranes (Immobilon-P, Millipore, Darmstadt, Germany) that were then probed with the following primary antibodies: anti-phospho-AKT1(Ser473, D9E, catalog number 3787); anti-AKT1 (2H10, catalog number 2967); anti-TUBULIN (DM1A, catalog number T6199: Sigma, St Louis, MO, USA); anti-CYCLIN D1 (C-20, sc-717: Santa Cruz, Dallas, TX, USA); anti-αSMA (E184, Abcam, catalog number ab32575), anti-SNAI2 (C19G17, Cell Signaling, catalog number 9584); anti-GAPDH (Sigma, catalog number G8795), anti-FAP (Abcam, catalog number ab53066); anti-S100A4 (Abcam, catalog number ab-27957); anti-ACTIN (C4, Santa Cruz Biotechnology, catalog number sc-47778); anti-ERBB2 (Abcam, catalog number ab2428); anti-phospho-ERBB2(Tyr1248) (Abcam, catalog number ab47755); anti-HSP90 (4F10, Santa Cruz Biotechnology, sc-69703) and anti-SDF1 (D32F9, Cell Signaling, catalog number 3530). Antibody binding was detected with horseradish peroxidase-conjugated anti-mouse, anti-rabbit or anti-goat secondary antibodies (1:10,000 dilution: BIO-RAD, Berkeley, CA, USA), which were visualized by enhanced chemiluminescence (ECL, Thermo Scientific). The phosphorylated and total AKT2 or AKT3, and the total ERK, were measured by ELISA, as described in the supplementary methods.

Cytokine and growth factor quantification

The cytokines and growth factors in tumor protein lysates were quantified by Luminex technology using Luminex xMAP kits and the Milliplex MAP Angiogenesis/Growth Factor Magnetic Bead Panel (#MAGPMAG-24K, Millipore), assessing: angiopoietin-2, sFASL, amphiregulin, betacellulin, EGF, endoglin, endothelin, FGF-2, follistatin, G-CSF, HGF, IL-1β, IL-6, IL-17A, KC, leptin, MIP-1α, MCP-1, PLGF-2, prolactin, sALK-1, sCD31/PECAM 1, SDF-1, VEGF-A, VEGF-C, VEGF-D and TNFα. TGFβ1, TGFβ2 and TGFβ3 were measured using the Milliplex MAP TGFβ Magnetic Bead 3 Plex Kit (#TGFMAG64K-03, Millipore). Protein lysates were prepared in lysis buffer (#43-040, Millipore) and passed through a 0.65 μm filter (Ultrafree-MC-DV, #UFC30DV00, Millipore). Each protein was quantified following the manufacturer’s instructions and the amount of protein lysate loaded was optimized for each assay: 20 μg for #MAGPMAG-24K and 13.5 μg for TGFMAG64K-03.

The cytokine levels in the culture supernatant from CAFs were quantified using a membrane panel and analyzed following the manufacturer’s recommendations (Proteome Profiler™ Mouse Cytokine R&D Systems ARY006), incubating the membranes with the supernatant from CAFs isolated from *Snai2* WT^{ErbB2+} and *Snai2*

KO^{ErbB2+} tumors after six days of growth. This arrays screened for the relative levels of 40 different cytokines and chemokines, and their relative expression was quantified with Quantity One software.

Flow Cytometry and cell sorting

For tumors from *Snai2* WT^{ErbB2+} and *Snai2* KO^{ErbB2+} mice, flow cytometry was used to analyze the stromal composition and immune cell infiltration, and to sort epithelial, endothelial cells and fibroblasts. Tumors were dissected out from female mice and after mechanical dissociation with two scalpels (Swann-Morton, catalog number 0511, Sheffield, United Kingdom), the tissue was digested with collagenase (600 units/mL: Sigma, C2674, St Louis, MO, USA) and hyaluronidase (200 units/ml: Sigma, H3506, St Louis, MO, USA) in culture medium (DMEM/F12, 10% FBS, 1% penicillin/streptomycin, 1% Glutamine). The tissue was digested for 2 hours at 37 °C to analyze infiltrating immune cells, or for 6 hours to sort and quantify the endothelial cells and fibroblasts.

Stromal leukocytes were quantified by flow cytometry. To quantify infiltrating immune cell populations, cell suspensions were stained with anti-B220-FITC (Becton Dickinson #553088), CD4-PE (Becton Dickinson #553048), CD8-PE (Becton Dickinson #553033) and CD45-APC (Becton Dickinson #559864), and the different CD45+ populations were analyzed on an AccuriC6 FACS apparatus (Becton Dickinson). Tumor cells were stained with anti-EpCAM to identify epithelial cells (Immunostep #M236PC7), anti-CD31-FITC to identify endothelial cells (Beckton Dickinson #553372), and anti-CD140-PE to identify fibroblasts (eBioscience #12-140-81), and they were then sorted on a FACS Aria III apparatus (Becton Dickinson). The cells were incubated with antibodies for 30 minutes at 4 ºC, washed with 2% FBS in PBS (phosphate-buffered saline, wash buffer), and resuspended in wash buffer with 1 µM SYTOX blue to exclude dead cells from the analysis.

RNA extraction, cDNA synthesis and QPCR

Total RNA was isolated using the TRIZOL Reagent (Invitrogen, Carlsbad, CA) and cDNAs were synthesized from equal amounts of RNA using the Transcriptor First-strand cDNA synthesis kit (Roche) to quantify *Snai2* expression. For the TaqMan assays, the primer and probe mixes were obtained from Applied Biosystems (*Snai2* #Mm00441531_1, *Gapdh* #Mm99999915_g1).

Gelatin zymography

Gelatinase activity was assessed as described previously (68). The cell culture supernatants were collected and centrifuged at 1,500 rpm for 5 minutes and the cell-free supernatant was mixed with 2x sample buffer (non-reducing conditions) and separated for 1 hour on gels at 4 ºC (10% polyacrylamide, 0.1% gelatin). The subsequent enzymatic reaction was performed at 37 ºC overnight, visualizing the gelatinase activity using specific staining solutions and destaining in an acetic acid-methanol-dH_2O solution (1:3:6). The gels were then analyzed semi-quantitatively using ImageJ software.

Cell-migration/invasion assay

Cell migration was assayed in Boyden chambers, using a Falcon cell-culture insert with an 8 µm pore-size polyethylene terephthalate membrane (Millipore). The cells were recovered by trypsinization and counted, and cell suspensions containing $5\text{-}10\times10^4$ cells in 300 µl of serum-free medium were added to the upper chamber, with 500 µl of the appropriate medium added to the lower chamber. The transwells were incubated for 24 hours at 37 °C, after which the cells on the inside of the transwell inserts were removed with a cotton swab, while those on the underside of the insert fixed and stained. Photographs were taken of five random fields, and the cells were counted to calculate the proportion of transmigrated cells. The invasion was assayed using Boyden chambers with Matrigel (Cell Biolabs, #CBA-110).

QPCR reagents and conditions

A reaction mixture (20 μL) containing 9 μL of the cDNA template and 10 μL of the TaqMan Universal PCR master mix was amplified as follows: denaturation at 95 °C for 10 min, and 36 cycles at 95 °C for 15 s and 60 °C for 60 s. Gene expression was quantified in $CD140^+$ sorted cells, synthesizing cDNAs as described above and pre-amplifying for 12 cycles using the SsoAdvanced PreAmp Supermix (Bio-Rad) containing specific primers. The pre-amplification product was then used as a template in the qPCR reactions with PerfeCTa SYBR® Green SuperMix Reagent and amplified using the following program: denaturation at 95°C for 10 min, and 40 cycles at 95 °C for 15 s and 59 °C for 60 s. The primers used were: *Cxcl1* Forward (CCCAAACCGAAGTCATAGCCA) and Reverse (TTCTCCGTTACTTGGGGACAC), *Mmp2* Forward (TCGCCCATCATCAAGTTCCC) and Reverse (CCTTGGGGCAGCCATAGAAA), *Mmp9* Forward (TTCCCCAAAGACCTGAAAACCT) and Reverse (AAAGCCGGCCGTAGAGACT), *Sdf1* Forward (GAGAGCCACATCGCCAGAGC) and Reverse (GGATCCACTTTAATTTCGGGTCAA) and *Gapdh* Forward (TGCACCACCAACTGCTTAG) and Reverse (GGATGCAGGGATGATGTTC), human *SDF1* Forward (CTAGTCAAGTGCGTCCACGA) and Reverse (GGACACACCACAGCACAAAC). QPCR results were analyzed by the ΔΔCT method.

Fig. S1. Expression of SNAI2 in HER2-positive tumors from patients. Different levels of SNAI2 expression in the epithelium and stroma of human ERBB2-positive tumors determined by immunohistochemistry. (**a**) Epithelium with focal SNAI2. (**b**) Epithelium expressing SNAI2. (**c**) Stroma with focal SNAI2. (**d**) Stroma expressing SNAI2. (**e**) SNAI2 negative stroma. See the material and methods for more details.

Supplementary Figure S1

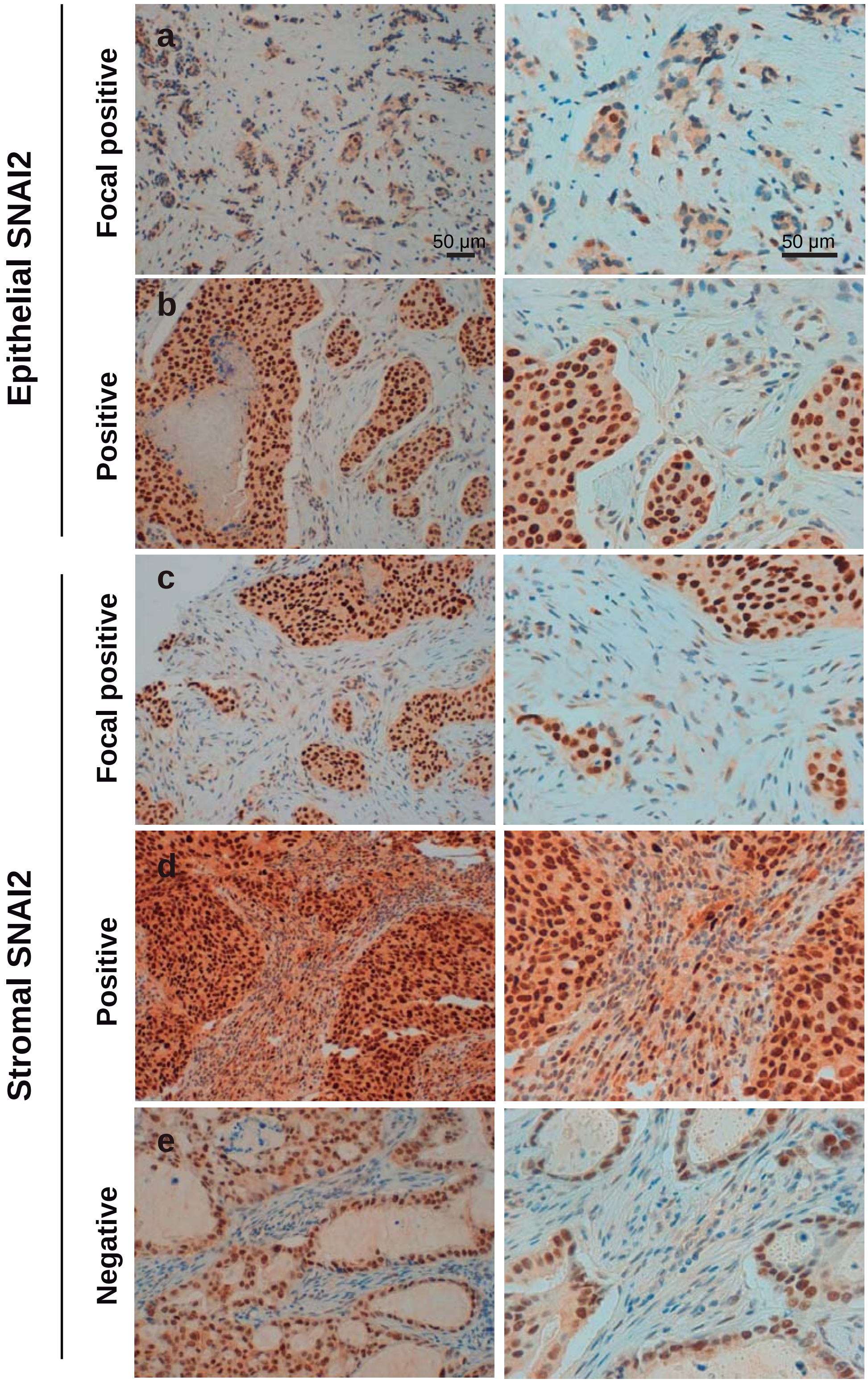


Fig. S2. Metastasis capability and ERBB2 expression in tumors from nulliparous and parous *SNAI2* WT ^{ErbB2} and *SNAI2* KO ^{ErbB2} mice. (**A**) Detection of SNAI2 in mouse embryonic fibroblasts (MEFs) and mammary glands in western blots. (**B**) Comparison of the absolute number of metastasis in nulliparous mice considering all mice with breast cancer. (**C**) The same comparison in the parous female mice. (**D**) Comparison of the absolute number of metastasis in nulliparous mice considering only tumors that metastasized. (**E**) The same comparison in parous mice. A Student's T-test was used for panels B-D. (**F**) Detection of pERBB2 and total ERBB2 in tumors assessed by western blots. (**G**) Quantification of ERBB2 and phospho-ERBB2 expression in tumors from both *Snai2* WT^{Erbb2} and *Snai2* KO^{Erbb2} nulliparous and parous female mice assessed by immunohistochemistry and quantified by the Ariol system. (**H**) SNAI2 expression in hCAF control (scrambled siRNA) and SNAI2-depleted cells with a different pool of two siRNAs (siRNA#2) (a different siRNA to that shown in Figure 2i) analyzed by immunoblotting. (**I**) Migration of MDA-MB-231 cells in the presence of conditioned medium from control or *SNAI2*-depleted hCAFs with the siRNA#2 (N=3).

Supplementary Figure S2

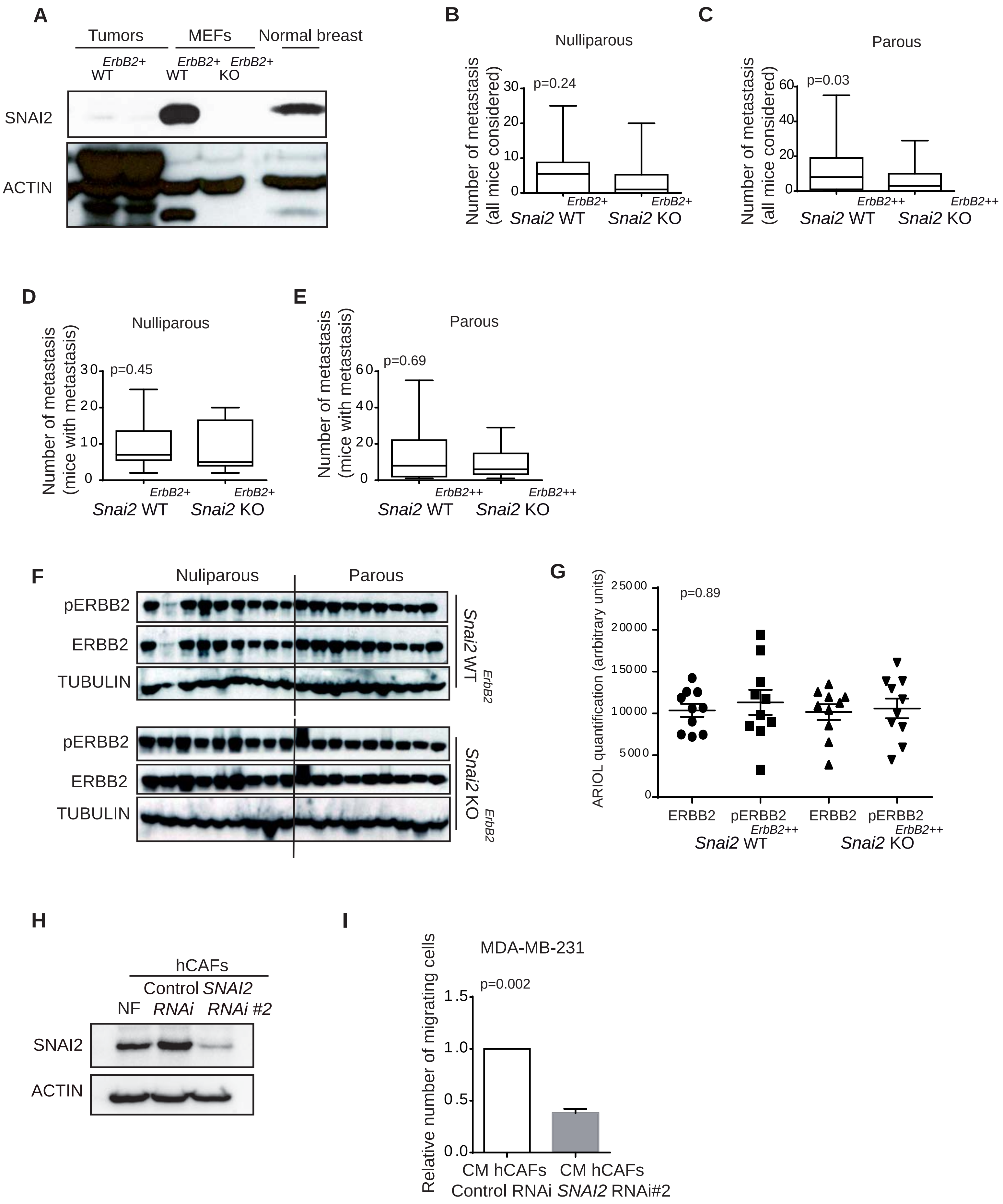


Fig. S3. Tumor growth rate and white blood cell infiltration in breast tumors from Snai2 WT$^{\textit{ErbB2}}$ and Snai2 KO$^{\textit{ErbB2}}$ mice.

(**A**) Comparison of the growth rate of tumors from Snai2 WT$^{\mathrm{ErbB2}}$ and Snai2 KO$^{\mathrm{ErbB2}}$ nulliparous and parous mice. Mann-Whitney *U* test. (**B**) SNAI2 expression in CAF control and SNAI2-depleted cells analyzed by immunoblotting to show that the cells from which the conditioned medium (hCM) were collected, did not express SNAI2. (**C**, **D**) The proportion of intratumoral CD31^{+} cells was quantified by flow cytometry. Mann-Whitney U-test. (**E**) KC expression analyzed by multiplex bead array (Luminex, 10 tumors per group were studied). Unpaired t-test. (**F**) Quantification of different intratumoral leukocyte subpopulations by flow cytometry. Mann-Whitney *U* test. (**G**) Detail of the expression of SNAI1/SNAIL in breast tumors from *Snai2* WT$^{\mathrm{Erbb2}}$ and *Snai2* KO$^{\mathrm{Erbb2}}$ mice by immunohistochemistry. SNAI1/SNAIL was expressed in the epithelial and stromal compartments (See also Table S6).

Supplementary Figure S3

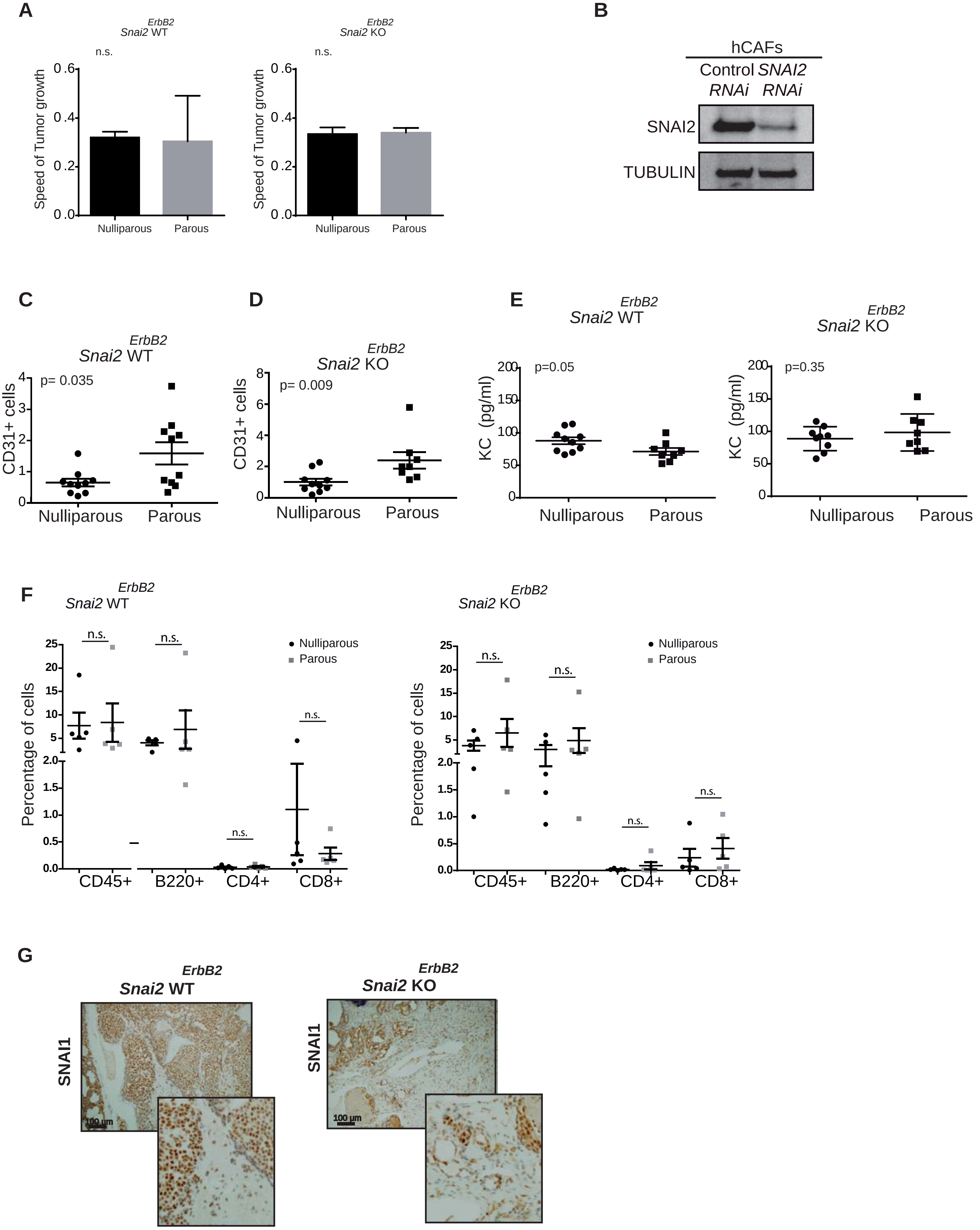


Fig. S4. ERK and ERK1/2(T185/Y187: pERK1/2) levels in tumors derived from *Snai2* WT^{ErbB2+} and *Snai2* KO^{ErbB2+} mice. (**A** and **B**) In nulliparous mice: (**A**) Total ERK1/2; (**B**) pERK1/2. (**C** and **D**) In parous mice: (**C**) total ERK1/2; (**D**) pERK1/2. The assays were carried out by ELISA (N = 20 mice per group were analyzed, Mann-Whitney *U* test). (**E**) Detection of total ERK1/2 and pERK1/2 by western blots of selected tumors (weaker and stronger expression) to confirm the sensitivity of the technique (N = 4 mice per group). (**F**) SNAI2 expression in CAF control and SNAI2-depleted cells analyzed by immunoblotting to show that SNAI2-targeting siRNA efficiently reduced the expression of SNAI2. (**G**) hCAFs cells were treated with control or *SNAI2* siRNA#2 for two days and then co-cultured in transwell inserts with BT474 cells for two days before analyzing the ERK and AKT signaling pathways in BT474 cells by western blots.

Supplementary Figure 4

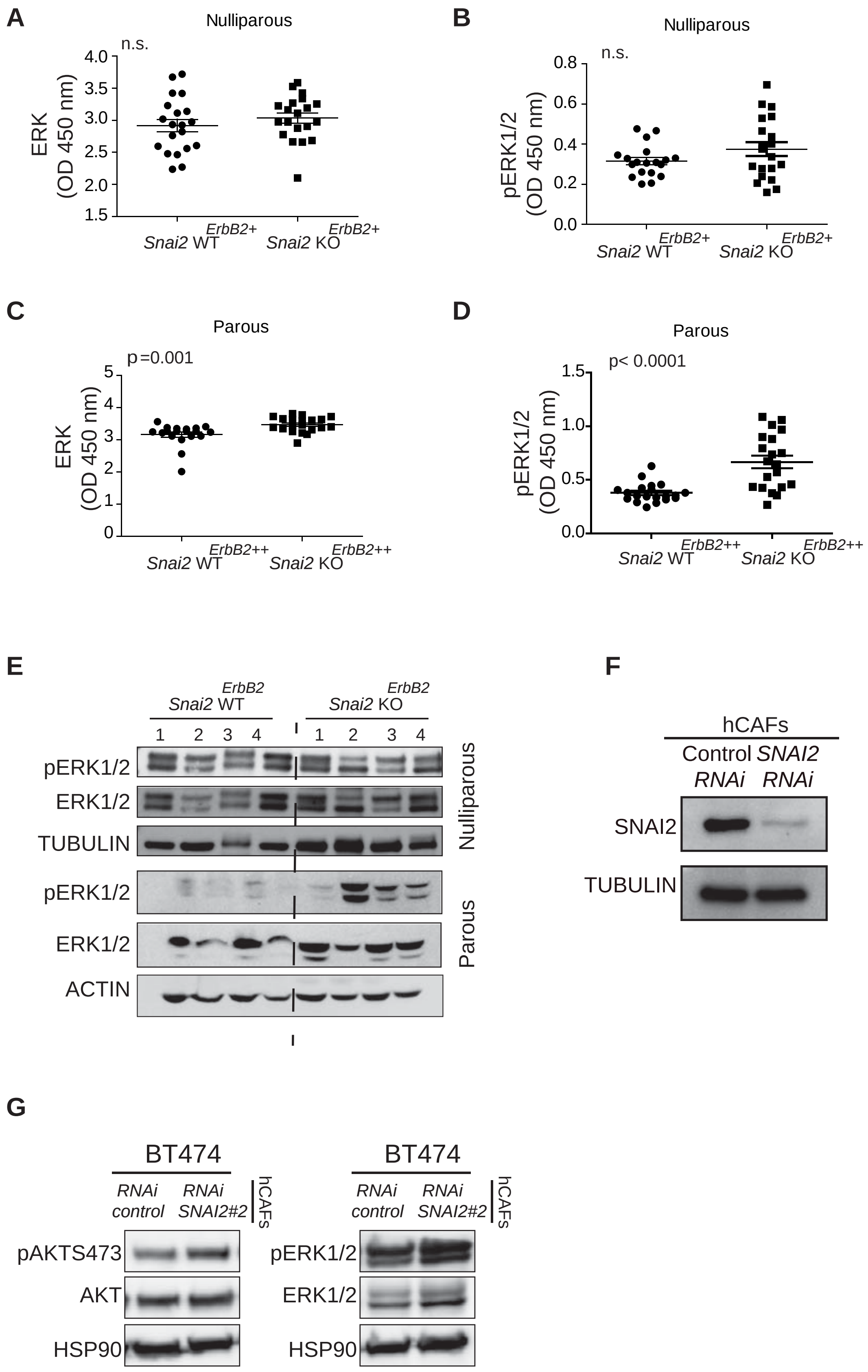
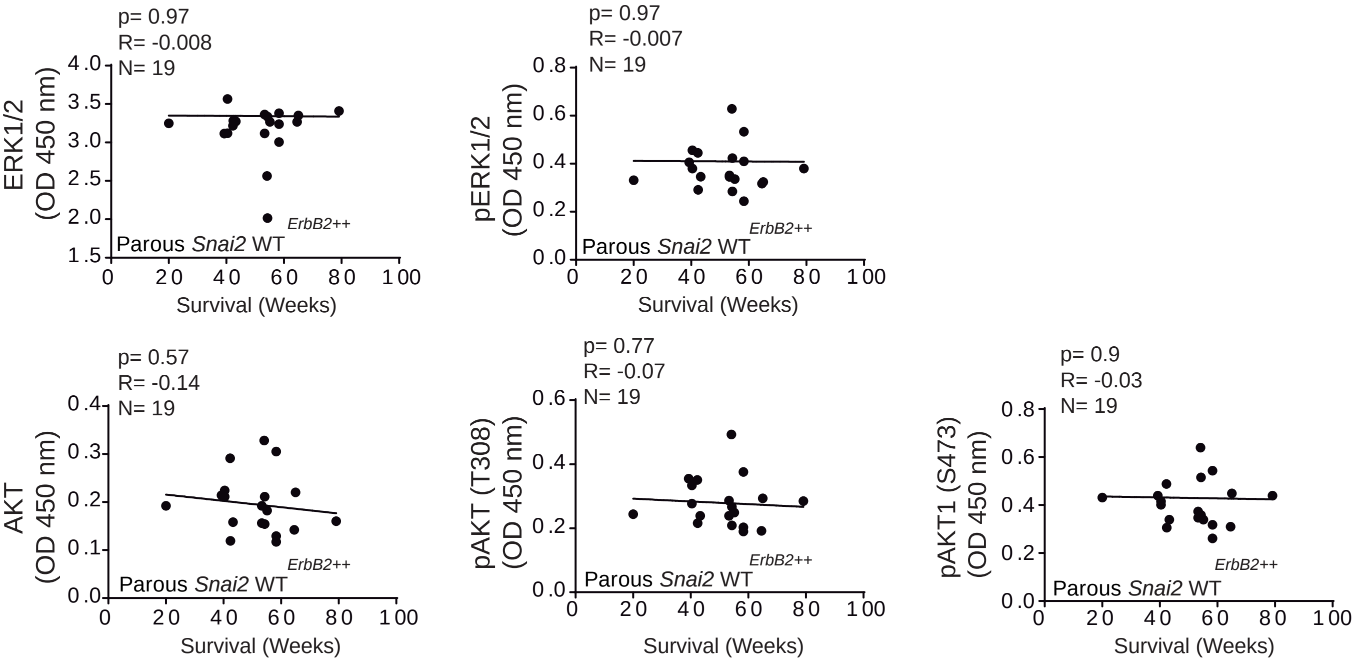


Fig. S5. Correlation between the AKT and ERK tumor levels, and survival in: (**A**) Snai2 WT $^{ErbB2++}$ parous mice and (**B**) Snai2 KO $^{ErbB2++}$ parous mice. The assays were carried out by ELISA (N = 20 mice per group, Spearman's Rank Order Correlation test).

Supplementary Figure S5

A



B

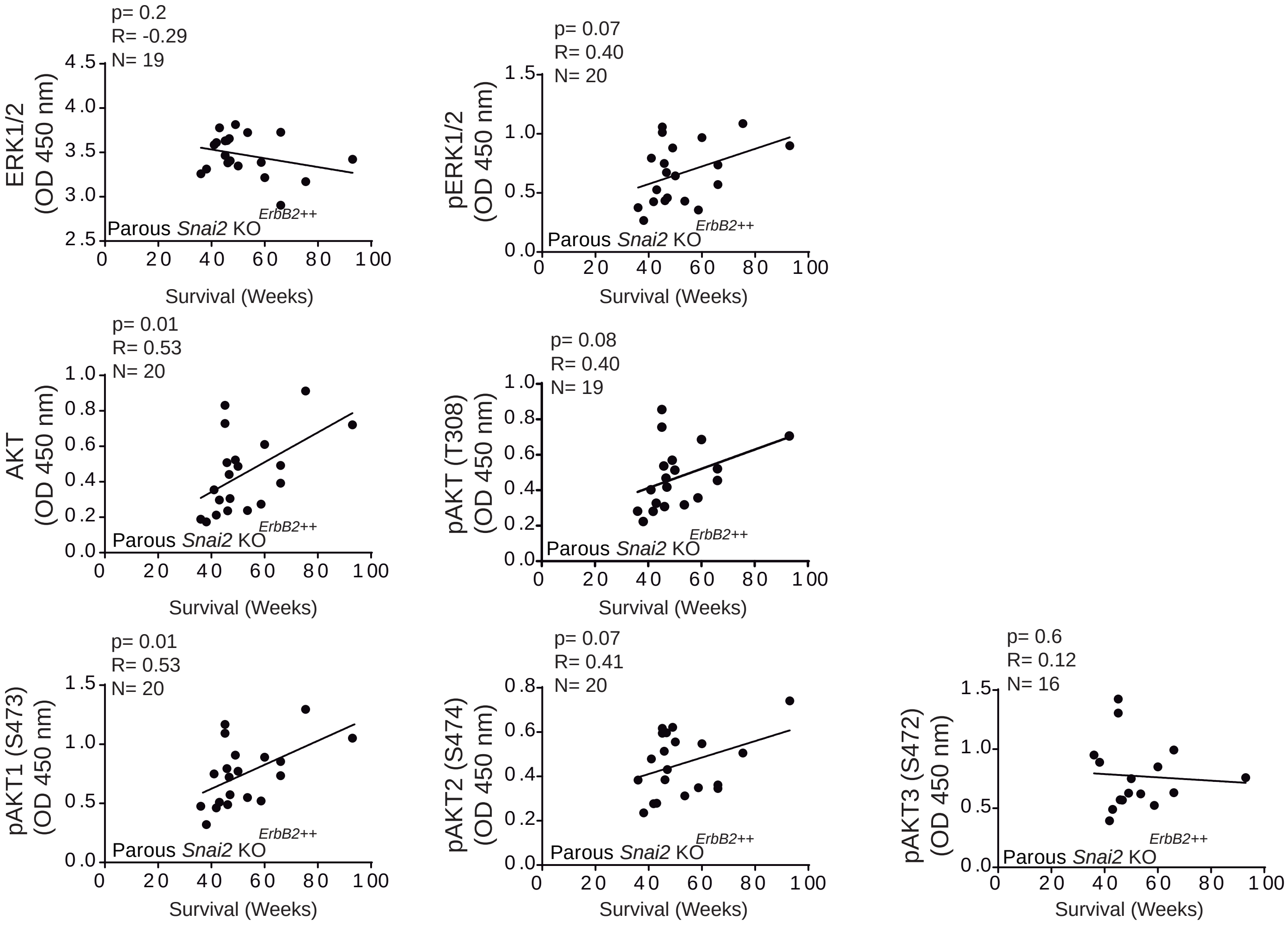
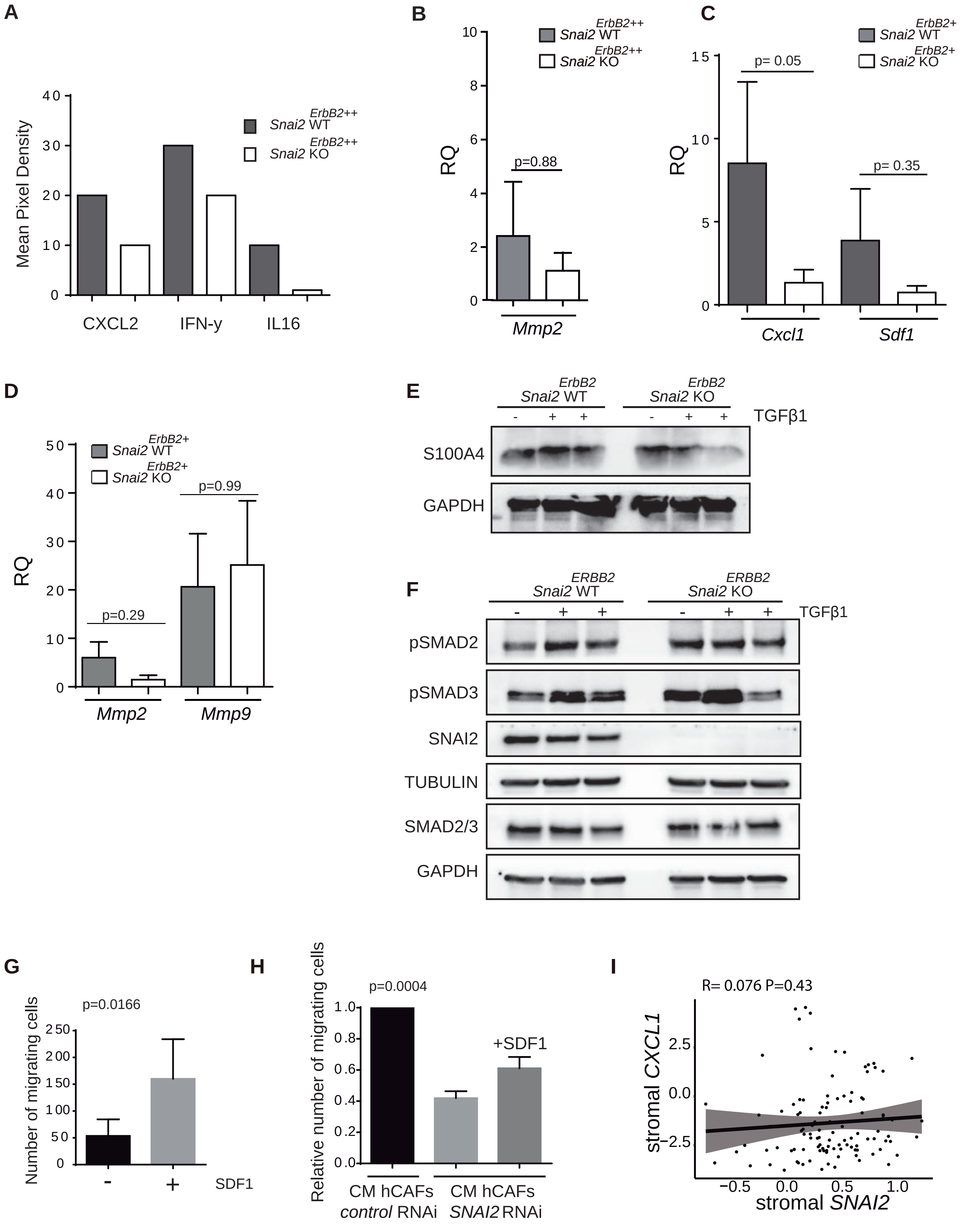


Fig. S6. Supernatant from CAF cells influences tumor cell migration by altering cytokine production. (**A**) Densitometric quantification of cytokine arrays using ImageJ software. (**B**) Relative *Mmp2* mRNA expression in mCAFs isolated from tumors developed by parous mice (WT, N =8; KO, N =9: Mann-Whitney U test). (**C**) Relative *Cxcl1* and *Sdf1* mRNA expression in mCAFs from tumors developed by nulliparous mice (WT, N =8; KO, N =9: Mann-Whitney U test). (**D**) *Mmp2* and *Mmp9* mRNA expression was quantified in the same samples as in panel C. (Mann-Whitney U test). (**E**) pSMAD2, pSMAD3, total SMAD2/3 and SNAI2 expression were analyzed in the same samples as in panel F. (**F**) Effect of SDF1 treatment (10 ng/ml) on MDA-MB-231 cell migration (unpaired t-test). (**G**) Migration of MDA-MB-231 cells in the presence of conditioned medium from control or *SNAI2*-depleted hCAFs in the presence or absence of exogenous SDF1 (N=3, ANOVA). (**H**) Absence of correlation between the mRNA levels of stromal *SNAI2* and stromal *CXCL1* (Pearson´s tests).

Supplementary Figure S6



Supplementary Table S1. Evaluation of the survival of patients with strong and weak tumor *SNAI2* expression in different subtypes of breast cancer. Data were obtained with the Kaplan-Meier plotter (30). Breast cancer subtypes were defined based on the 2013 St Gallen criteria, using the expression of ER1, HER2 and Ki67: Luminal A tumors are defined as ER-positive (ER+), HER2-negative (HER-) and Ki67 low; Luminal B tumors are defined as ER+, HER- and Ki67 high, or ER+, HER+; Basal breast cancer is defined as ER-, HER-; and finally, HER2-enriched tumors as ER-, HER+- (Log Rank test, see also Figure 1A-F).

Tumor subtype		**StGallen difinition**	***SNAI2* expression**		**Patients (n)**	**P- value**
			Low	**High**		
All tumors		n.a.	1976	1975	3951	0.3
Intrinsic subtypes	Luminal A	ER+, HER2-, Ki67 low	966	967	1933	1
	Luminal B	ER+, HER2-, Ki67 high or ER+, HER2+	574	575	1149	0.2
		HER2+, ER+	57	57	114	**0.06**
	Basal	ER-, HER2-	309	309	618	0.09
	HER2-enriched	ER-, HER2+	126	125	251	0.56
Pietenpol subtypes	Basal-like 1	n.a.	86	38	124	0.78
	Basal-like 2	n.a.	38	38	76	0.67
	Immunomoduladory	n.a.	102	101	203	0.82
	Mesenchymal	n.a.	88	89	177	0.69
	Mesenchymal stem-like	n.a.	32	31	63	0.55
	Luminal androgen-receptor	n.a.	49	37	86	0.16

Supplementary Table S2. Clinical and histopathological characteristics of tumors from patients with ERBB2-positive breast cancer evaluated by immunohistochemistry. CPR, Complete Pathological Response (see alsoFigure 1K-N).

Case number	Age at diagnosis	Tumor stage after surgery	KI67 (%)	HER2	PR (%)	ER %	SNAI2		Time of Follo up (weeks)	Relapse / Progression	Type of relapse or progressi n
							Epithelial	Stromal			
1	57	pT1cN0	10	3	<5	40	-	+	269.7	No	
2	49	pT2N1	50	3	-	-	+ focal	+	222.4	Yes	Local and distance relapse
3	28	pT1cN0	10	3	90	90	+	+	263.1	No	
4	59	pT1aN1	20	3	-	-	-	+ focal	261.1	No	
5	39	pT2N0	10	3	1	75	+ focal	+	816.7	Yes	Local relapse
6	52	pT1bN0	12	3	60	50	+	+	259.0	No	
7	37	pT1cN1	20	3	75	90	+ focal	+ focal	255.9	No	
8	56	pT2N3	20	3	-	-	-	+ focal	253.7	No	
9	48	pT3N2	5	3	<5	50	+ focal	-	251.6	No	
10	35	pT2N2	2	3	-	-	+ focal	+	281.9	Yes	Distant metastasis
11	75	pT2N1	30	3	70	90	+	+	250.7	No	
12	81	pT2N3	1	3	50	50	+ focal	+	129.9	No	
13	65	pTisN0	<5	3	-	-	+	+	474.1	Yes	Local relapse
14	50	pT1aN1	25	3	<5	90	-	+	216.0	No	
15	47	ypT1cN1	20	3	80	90	+ focal	+ focal	164.7	No	
16	58	ypT0N0	30	3	-	-	+	+ focal	199.0	No	
17	86	pT3N3M1	70	3	-	<10	+ focal	+	185.7	Yes	Metastasis at diagnosis
18	48	pT3N3M0	30	3	-	70	+ focal	+ focal	169.3	Yes	Distant metastasis
19	84	pT1cN0M0	1	3	-	70	+	-	190.0	No	
20	44	pT2N0	10	3	-	-	+ focal	+	416.3	Yes	Local relapse
21	91	pT2N0	20	3	-	90	+	-	167.7	Yes	Local and ganglionar relapse
22	47	pT2N0	5	3	-	90	+	+	178.0	No	
23	76	pT4N2a	40	3	-	-	+	+	90.4	Yes	Distant metastasis
24	91	ypT0N0	5	3	50	100	+ focal	+	n.a.	n.a.	Exitus letalis
25	72	pTisN0	5	3	70	100	-	+ focal	195.7	No	
26	72	pT1bN0	10	3	-	-	+ focal	+ focal	216.6	No	
27	42	pT3N2a	20	3	75	90	+	+ focal	198.0	No	
28	58	pT1cN0	20	3	75	90	+	-	846.4	No	
29	49	pT2pNmic	70	3	-	100	+ focal	+	191.7	No	
30	60	pTisN0M0	40	3	-	<10	+ focal	+	847.0	Yes	Local relapse
31	63	pT1bN0	10	3	-	-	+ focal	+	716.1	Yes	Local relapse
32	38	ypT0N0	20	3	<1	80	+ focal	+	114.1	No	
33	30	ypT1cN1	25	3	-	50	+ focal	+	140.1	No	
34	42	cT2N2M1	30	3	<1	90	+ focal	+ focal	150.0	No	
35	91	pT2N0	50	3	-	20	+	-	169.0	Yes	Local relapse
36	57	pT1aN0	30	3	-	5	+ focal	+ focal	83.7	No	
37	68	pT1cN0	15	3	-	50	+	+	58.7	No	
38	50	ypT1bypNmic	60	3	-	-	+	+	37.7	No	
39	54	cT4N3M1	40	3	-	5	+	+ focal	67.0	Yes	Metastasis at diagnosis
40	48	ypT2N0	5	3	-	90	+ focal	-	82.7	No	
41	53	CPR	50	3	-	70	+	+	66.0	No	
42	79	pT1cN2	30	3	-	90	+	+	85.1	No	
43	47	ypT2N0	35	3	-	90	+	+ focal	6.1	No	
44	61	yPTx,pN2a	40	3	-	-	+ focal	+ focal	28.1	No	
45	67	ypT1cN0	5	3	-	5	+ focal	-	53.0	No	
46	83	pT2N0M0	30	3	-	90	+ focal	+ focal	49.0	No	
47	93	pT2Nmic	70	3	-	-	+	+ focal	3.4	No	
48	35	pT2N1M0	30	3	-	-	+ focal	+ focal	574.0	Yes	Local and axilar relapse
49	35	pT2N1M0	10	3	-	-	+ focal	+	50.0	No	
50	60	mpT2 pN3a	5	3	-	50	+	-	38.7	Yes	Distant metastasis

Supplementary Table S3. Linear models for SNAI2 and Ki67. The "glm" function of the R "stats" package was used to fit generalized linear models (logistic regression) (see also Figure 1O). A.) Stromal SNAI2. B.) Epithelial SNAI2.

A.		**Stromal SNAI2**										
		Estimate	**Std. Error**	**z value**	**Pr(>|z|)**	**Min**	**1Q**	**Median**	**3Q**	**Max**	**AIC**	**N**
All tumors	Intercept	10 296	0.521	1 976	0.0481							
	Ki-67	1 204	0.8002	1 505	0.1325	-21 612	0.4512	0.4512	0.7815	0.7815	45 613	50
ER-	Intercept	1 792	1.08	1 659	0.0971							
	Ki-67	18 774	5 345 908	0.004	0.9972	-197 277	0.00005	0.00005	0.55525	0.55525	97 416	18
ER+	Intercept	0.6931	0.6124	1 132	0.258							
	Ki-67	10 415	0.8759	1 189	0.234	-19 479	0.5701	0.5701	0.6527	0.9005	36 185	32
ER+PR+	Intercept	20.57	7929.26	0.003	0.996							
	Ki-67	-19.18	7929.26	-0.002	0.996	-179 412	0.00005	0.00005	0.66805	0.66805	9 004	10
ER+PR-	Intercept	-0.2877	0.7638	-0.377	0.706							
	Ki-67	21 595	10 772	2 005	0.045	-20 074	-0.6597	0.535	0.535	13 018	25 341	22

B.		**Epithelial SNAI2**										
		Estimate	**Std. Error**	**z value**	**Pr(>|z|)**	**Min**	**1Q**	**Median**	**3Q**	**Max**	**AIC**	**N**
All tumors	Intercept	214 007	0.74751	2 863	0.0042							
	Ki-67	0.09353	0.96319	0.097	0.9226	-21 612	0.4512	0.4512	0.4717	0.4717	36 499	50
ER-	Intercept	19.57	4064.63	0.005	0.996							
	Ki-67	-18.06	4064.63	-0.004	0.996	-184 648	0.00008	0.3168	0.63352	0.63352	14 431	18
ER+	Intercept	16 094	0.7746	2 078	0.0377							
	Ki-67	1 335	12 855	1 039	0.299	-24 478	0.3203	0.3203	0.6039	0.6039	22 754	32
ER+PR+	Intercept	1 386	1 118	1.24	0.215							
	Ki-67	19.18	7 929 263	0.002	0.998	-179 412	0.00005	0.00005	0.66805	0.66805	9 004	10
ER+PR-	Intercept	17 918	10 801	1 659	0.0971							
	Ki-67	0.8473	1 496	0.566	0.5711	-23 272	0.3715	0.3715	0.5093	0.5553	17.09	22

Supplementary Table S4. Differential expression analysis between nulliparous and parous *Snai2* WT ^{ErbB2} mice. The 602 gene probe set was obtained from a SAM test with a cut-off of FDR = 0.05 (≈5% false positives). Overexpressed genes are shown in red and inhibited genes are shown in green.

	Probeset ID	d-value	p-value	q-value	R fold	Genename	Description
1	10459241	13.1721062	2.0089E-05	0.0321007	1.8114672	Afap1l1	actin filament associated protein 1-like 1
2	10507885	11.9890864	3.05353E-05	0.0321007	1.6596438	Mycbp	c-myc binding protein
3	10446596	-17.579075	6.42849E-06	0.0321007	0.0940015	Dlgap1	discs, large (Drosophila) homolog-associated protein 1
4	10420837	10.9937752	4.74101E-05	0.0321007	1.409892	Extl3	exostoses (multiple)-like 3
5	10513268	12.5177867	2.49104E-05	0.0321007	1.4905297	AI314180	expressed sequence AI314180
6	10471360	11.2524334	4.25888E-05	0.0321007	1.2579993	Golga2	golgi autoantigen, golgin subfamily a, 2
7	10595371	-11.651576	3.69638E-05	0.0321007	0.6919971	Hmgn3	high mobility group nucleosomal binding domain 3
8	10514668	15.6396282	9.64274E-06	0.0321007	1.7721342	Jak1	Janus kinase 1
9	10518372	11.7598168	3.45531E-05	0.0321007	1.6312772	Miip	migration and invasion inhibitory protein
10	10510957	11.8686858	3.2946E-05	0.0321007	1.5161356	Pank4	pantothenate kinase 4
11	10514558	-13.489281	1.76784E-05	0.0321007	0.6919462	Gm12696	predicted gene 12696
12	10421021	-17.669108	5.62493E-06	0.0321007	0.7086152	Gm6878	predicted gene 6878
13	10485429	14.9975159	1.2857E-05	0.0321007	1.3806702	Pdhx	pyruvate dehydrogenase complex, component X
14	10481155	10.9405242	4.90172E-05	0.0321007	1.4859686	Rexo4	REX4, RNA exonuclease 4 homolog (S. cerevisiae)
15	10554129	-14.866541	1.36605E-05	0.0321007	0.4167378	B130024G19Rik	RIKEN cDNA B130024G19 gene
16	10504926	15.3322532	1.12499E-05	0.0321007	1.5528957	Rnf20	ring finger protein 20
17	10515700	17.9630504	4.01781E-06	0.0321007	1.50994	Szt2	seizure threshold 2
18	10515729	12.8695286	2.24997E-05	0.0321007	1.5026044	Szt2	seizure threshold 2
19	10515716	10.7865745	4.98208E-05	0.0321007	1.5495063	Szt2	seizure threshold 2
20	10506968	11.0538585	4.41959E-05	0.0321007	2.0530492	Ttc39a	tetratricopeptide repeat domain 39A
21	10532839	-14.829202	1.44641E-05	0.0321007	0.4657279	Trpv4	transient receptor potential cation channel, subfamily V, member 4
22	10507804	12.0821412	2.81246E-05	0.0321007	1.7510043	Trit1	tRNA isopentenyltransferase 1
23	10516229	11.7383499	3.53567E-05	0.0321007	1.3466567	Utp11l	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)
24	10399407	15.3333429	1.04463E-05	0.0321007	17.91217	Vsnl1	visinin-like 1
25	10544089	12.1764955	2.65175E-05	0.0321007	1.4083537	Zc3hav1	zinc finger CCCH type, antiviral 1
26	10516007	13.4591002	1.84819E-05	0.0321007	1.4626186	Zmpste24	zinc metallopeptidase, STE24
27	10514985	17.8971494	4.82137E-06	0.0321007	1.6666366	Zyg11b	zyg-ll family member B, cell cycle regulator
28	10510814	10.775626	5.14279E-05	0.0322157	1.4646645	Cep104	centrosomal protein 104
29	10478776	8.63435062	0.000168748	0.0331183	1.6045149	Arfgef2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)
30	10592023	-10.094837	7.8749E-05	0.0331183	0.7185447	Aplp2	amyloid beta (A4) precursor-like protein 2
31	10510552	9.75697976	9.1606E-05	0.0331183	1.4036022	Rere	arginine glutamic acid dipeptide (RE) repeats
32	10498710	-8.8181013	0.00015348	0.0331183	0.1690807	Bche	butyrylcholinesterase
33	10513583	10.3611971	7.07134E-05	0.0331183	1.5019706	Cdc26	cell division cycle 26
34	10606513	-8.7790401	0.000158302	0.0331183	0.8540778	Chm	choroidermia (RAB escort protein 1)
35	10420225	10.7079696	5.78564E-05	0.0331183	1.2027628	Cma1	chymase 1, mast cell
36	10539822	9.17169359	0.000125356	0.0331183	1.0947324	Copg1	coatomer protein complex, subunit gamma 1
37	10507309	10.4653717	6.74992E-05	0.0331183	1.4648839	Ccdc17	coiled-coil domain containing 17
38	10518957	10.5873611	6.18742E-05	0.0331183	1.316945	Dffb	DNA fragmentation factor, beta subunit
39	10509542	10.582236	6.26778E-05	0.0331183	1.4448265	Ddost	dolichyl-di-phosphooligosaccharide-protein glycotransferase
40	10588495	8.67675428	0.000165534	0.0331183	1.5889151	Dusp7	dual specificity phosphatase 7
41	10509965	10.4599349	6.83027E-05	0.0331183	5.3454183	Epha2	Eph receptor A2
42	10452980	8.91649578	0.000143837	0.0331183	1.9098375	Eif2ak2	eukaryotic translation initiation factor 2-alpha kinase 2
43	10510365	10.6976254	5.866E-05	0.0331183	1.5187966	Exosc10	exosome component 10
44	10508737	9.43220912	0.000108481	0.0331183	1.5561727	Eya3	eyes absent 3 homolog (Drosophila)
45	10506989	9.0895173	0.000132588	0.0331183	1.6569404	Faf1	Fas-associated factor 1
46	10405464	8.7118426	0.000162319	0.0331183	1.3863103	Grk6	G protein-coupled receptor kinase 6
47	10386951	-8.8189459	0.000152677	0.0331183	0.461421	Hs3st3b1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1
48	10466932	9.21211305	0.000120534	0.0331183	1.7389714	Insl6	insulin-like 6
49	10508883	9.13494677	0.000130177	0.0331183	1.5752423	Kdf1	keratinocyte differentiation factor 1
50	10506880	8.78520695	0.000156694	0.0331183	1.6997678	Kti12	KTI12 homolog, chromatin associated (S. cerevisiae)
51	10507238	9.27220986	0.000115713	0.0331183	1.6261797	Lrrc41	leucine rich repeat containing 41
52	10553537	-8.7833331	0.000157498	0.0331183	0.2127956	Luzp2	leucine zipper protein 2
53	10517465	9.57368626	9.88381E-05	0.0331183	1.7631417	Kdm1a	lysine (K)-specific demethylase 1A
54	10517425	8.90649404	0.000144641	0.0331183	1.654858	Lypla2	lysophospholipase 2
55	10510305	10.0695615	8.03561E-05	0.0331183	1.7073642	Mtor	mechanistic target of rapamycin (serine/threonine kinase)
56	10507529	9.18840412	0.000122945	0.0331183	1.684721	Med8	mediator complex subunit 8
57	10512901	8.61553681	0.000170355	0.0331183	1.4650093	Mrpl50	mitochondrial ribosomal protein L50
58	10508829	9.06883137	0.000133391	0.0331183	1.5469267	Map3k6	mitogen-activated protein kinase kinase kinase 6
59	10596925	9.35262124	0.000111695	0.0331183	1.2584842	Ndufaf3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 3
60	10356312	-8.9764722	0.000140623	0.0331183	0.7963927	Ncl	nucleolin
61	10479411	8.65216602	0.000167944	0.0331183	1.776885	Ogfr	opioid growth factor receptor
62	10515051	8.82898587	0.000151873	0.0331183	1.6397359	Osbpl9	oxysterol binding protein-like 9
63	10550509	-10.044151	8.19633E-05	0.0331183	0.0961	Pglyrp1	peptidoglycan recognition protein 1
64	10585186	9.17002832	0.000126159	0.0331183	1.1579773	Plet1	placenta expressed transcript 1
65	10565910	-8.6730316	0.000166337	0.0331183	0.617499	Plekhb1	pleckstrin homology domain containing, family B (evectins) member 1
66	10429843	9.93030488	8.35704E-05	0.0331183	1.4995393	Parp10	poly (ADP-ribose) polymerase family, member 10
67	10488594	9.92041754	8.51775E-05	0.0331183	1.3857773	Rbck1	RanBP-type and C3HC4-type zinc finger containing 1
68	10517744	9.06630695	0.000134195	0.0331183	1.5503899	Arhgef10l	Rho guanine nucleotide exchange factor (GEF) 10-like
69	10552252	8.97368072	0.000141427	0.0331183	1.3528307	1600014C10Rik	RIKEN cDNA 1600014C10 gene
70	10437171	8.83844333	0.00015107	0.0331183	1.2032625	1700093J21Rik	RIKEN cDNA 1700093J21 gene
71	10567735	-9.4639533	0.000107677	0.0331183	0.9245197	3110040M04Rik	RIKEN cDNA 3110040M04 gene
72	10383196	8.86319138	0.000148659	0.0331183	2.637517	Rnf213	ring finger protein 213
73	10515731	10.3587295	7.1517E-05	0.0331183	1.5075272	Szt2	seizure threshold 2
74	10515649	10.1158507	7.79455E-05	0.0331183	1.4707188	Szt2	seizure threshold 2
75	10515737	9.55264538	0.000101249	0.0331183	1.3341152	Szt2	seizure threshold 2
76	10515735	9.28543774	0.000114106	0.0331183	1.5102695	Szt2	seizure threshold 2
77	10376007	8.62815563	0.000169551	0.0331183	1.9071001	Shroom1	shroom family member 1
78	10404675	-9.5672151	9.96416E-05	0.0331183	0.7103743	Snrnp48	small nuclear ribonucleoprotein 48 (U11/U12)
79	10505630	8.71865701	0.000161516	0.0331183	1.7367443	Snapc3	small nuclear RNA activating complex, polypeptide 3
80	10507914	9.51209546	0.000104463	0.0331183	1.6113245	Sf3a3	splicing factor 3a, subunit 3
81	10481147	8.97673274	0.00013982	0.0331183	1.562889	Surf4	surfeit gene 4
82	10554863	-8.6705961	0.000167141	0.0331183	0.4629362	Sytl2	synaptotagmin-like 2
83	10516982	9.29026738	0.000113302	0.0331183	1.5800723	Stx12	syntaxin 12
84	10448593	9.54816059	0.000103659	0.0331183	1.2945878	Traf7	TNF receptor-associated factor 7
85	10550316	9.54873792	0.000102856	0.0331183	1.2928507	Tmem160	transmembrane protein 160
86	10461012	9.41583091	0.000109284	0.0331183	1.364831	Trmt112	tRNA methyltransferase 11-2
87	10518642	9.4145545	0.000110088	0.0331183	1.5362541	Ube4b	ubiquitination factor E4B
88	10518228	9.25719268	0.00011732	0.0331183	1.3976341	Vps13d	vacuolar protein sorting 13 D (yeast)
89	10399421	-9.8638117	8.59811E-05	0.0331183	0.705222	Mycn	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)
90	10506668	10.7289079	5.46422E-05	0.0331183	1.618357	Yipf1	Yip1 domain family, member 1
91	10509998	10.4428993	6.91063E-05	0.0331183	1.4862889	Zbtb17	zinc finger and BTB domain containing 17

92	10570963	-9.190257	0.000122141	0.0331183	0.9064918	Zmat4	zinc finger, matrin type 4
93	10371603	-8.5535218	0.000175176	0.0331971	0.8890669	Gm6653	predicted gene 6653
94	10515012	8.58893818	0.000172766	0.0331971	1.3657554	Prpf38a	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A
95	10489127	8.56009805	0.000174373	0.0331971	1.2539191	Rbl1	retinoblastoma-like 1 (p107)
96	10411287	8.5215632	0.000177587	0.0333735	1.4311153	Btf3l4	basic transcription factor 3-like 4
97	10431229	-8.4854246	0.000184016	0.0342958	0.601381	Celsr1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)
98	10572378	-8.3727501	0.000200087	0.0350164	0.3143347	Comp	cartilage oligomeric matrix protein
99	10414661	-8.3366018	0.000203301	0.0350164	0.8502977	Hk1	hexokinase 1
100	10513020	8.31983539	0.000205712	0.0350164	1.6633143	Ikbkap	inhibitor of kappa light polypeptide enhancer in B cells, kinase complex-associated protein
101	10514830	8.3426047	0.000202497	0.0350164	1.6934189	Ttc4	tetratricopeptide repeat domain 4
102	10508468	8.42417063	0.000192855	0.0350164	1.4441017	Tmem234	transmembrane protein 234
103	10517312	8.41387802	0.000196069	0.0350164	1.4422663	Tmem57	transmembrane protein 57
104	10509379	8.32288497	0.000204908	0.0350164	1.4821152	Usp48	ubiquitin specific peptidase 48
105	10366038	8.31652956	0.000206515	0.0350164	1.3792807	Galnt4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4
106	10478774	8.1794936	0.00022339	0.0361322	1.5713664	Arfgef2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)
107	10510452	8.11618399	0.000229819	0.0361322	1.5133688	Dffa	DNA fragmentation factor, alpha subunit
108	10510604	8.04157485	0.000245086	0.0361322	1.6268481	Dnajc11	DnaJ (Hsp40) homolog, subfamily C, member 11
109	10515528	8.16126777	0.000226604	0.0361322	1.3478193	Dph2	DPH2 homolog (S. cerevisiae)
110	10481909	7.94267567	0.00025955	0.0361322	1.3468512	Fbxw2	F-box and WD-40 domain protein 2
111	10508019	8.0598769	0.000242676	0.0361322	1.5351475	Gnl2	guanine nucleotide binding protein-like 2 (nucleolar)
112	10533720	7.93637441	0.000261157	0.0361322	1.7242791	Hcar2	hydroxycarboxylic acid receptor 2
113	10513397	8.22204446	0.000217765	0.0361322	1.6610459	Inip	INTS3 and NABP interacting protein
114	10507218	7.92241069	0.000262765	0.0361322	1.8614835	Mknk1	MAP kinase-interacting serine/threonine kinase 1
115	10597648	8.07616558	0.000239461	0.0361322	1.3562011	Myd88	myeloid differentiation primary response gene 88
116	10394392	8.04079745	0.000246693	0.0361322	1.5675456	Nfyc	nuclear transcription factor-Y gamma
117	10518546	8.08223463	0.00023464	0.0361322	1.4625788	Pex14	peroxisomal biogenesis factor 14
118	10474028	8.18041583	0.000222587	0.0361322	1.3965483	Pex16	peroxisomal biogenesis factor 16
119	10497399	-8.0010356	0.000253925	0.0361322	0.6239982	Pde7a	phosphodiesterase 7A
120	10405866	-8.0704692	0.000241068	0.0361322	0.6711832	Gm10139	predicted gene 10139
121	10519096	8.01736251	0.000251515	0.0361322	1.637015	Rer1	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)
122	10383194	7.94460511	0.000258747	0.0361322	2.2139404	Rnf213	ring finger protein 213
123	10515733	8.15060698	0.000227408	0.0361322	1.5551542	Szt2	seizure threshold 2
124	10481457	8.08624293	0.000232229	0.0361322	1.4113076	Sh3glb2	SH3-domain GRB2-like endophilin B2
125	10513952	7.93620574	0.000261961	0.0361322	1.4329411	Tmem261	transmembrane protein 261
126	10535231	8.0766318	0.000238658	0.0361322	1.6237844	Ttyh3	tweety homolog 3 (Drosophila)
127	10383200	7.91061816	0.000265979	0.0362427	2.3715297	Rnf213	ring finger protein 213
128	10444068	7.90975163	0.000266782	0.0362427	1.7045197	Tapbp	TAP binding protein
129	10537463	-7.8752621	0.000271604	0.0366742	0.8287651	Agk	acylglycerol kinase
130	10508805	7.86721165	0.000273211	0.0366742	1.594074	Wasf2	WAS protein family, member 2
131	10516393	7.77381781	0.000290889	0.0370526	1.5269343	38200	argonaute RISC catalytic subunit 4
132	10508454	7.77761403	0.000289282	0.0370526	1.5302709	Bsdc1	BSD domain containing 1
133	10517250	7.74682014	0.000294103	0.0370526	3.5753377	Extl1	exostoses (multiple)-like 1
134	10394971	7.76767301	0.000291693	0.0370526	1.2411067	Klf11	Kruppel-like factor 11
135	10507213	7.83387231	0.00028205	0.0370526	1.4404692	Mob3c	MOB kinase activator 3C
136	10383198	7.83773191	0.000279639	0.0370526	2.3641792	Rnf213	ring finger protein 213
137	10516666	7.82626999	0.000283657	0.0370526	1.7493571	Txlna	taxilin alpha
138	10517443	7.81504928	0.000286068	0.0370526	1.4530487	Tceb3	transcription elongation factor B (SIII), polypeptide 3
139	10512766	7.81716856	0.000285264	0.0370526	2.6814182	Trim14	tripartite motif-containing 14
140	10446986	-7.6996746	0.000303746	0.0373202	0.5778747	Crim1	cysteine rich transmembrane BMP regulator 1 (chordin like)
141	10508182	7.71073216	0.000301336	0.0373202	1.6215104	Psmb2	proteasome (prosome, macropain) subunit, beta type 2
142	10515072	7.70837996	0.000302139	0.0373202	1.5342323	Rnf11	ring finger protein 11
143	10383202	7.69854877	0.00030455	0.0373202	2.2980061	Rnf213	ring finger protein 213
144	10471201	7.66507785	0.000309371	0.0374958	1.3310932	Abl1	c-abl oncogene 1, non-receptor tyrosine kinase
145	10588836	7.65219946	0.000312585	0.0374958	1.5880168	Gmppb	GDP-mannose pyrophosphorylase B
146	10546661	-7.6399143	0.000316603	0.037571	0.5817561	Foxp1	forkhead box P1
147	10471571	7.63758578	0.000317407	0.037571	1.5060814	Mapkap1	mitogen-activated protein kinase associated protein 1
148	10516427	7.63637476	0.00031821	0.037571	1.6547352	Ncdn	neurochondrin
149	10385081	-7.6065274	0.000320621	0.0376584	0.7331383	Anp32-ps	acidic (leucine-rich) nuclear phosphoprotein 32 family, pseudogene
150	10524631	7.58271902	0.000331871	0.0379816	2.8740429	Oasl1	2'-5' oligoadenylate synthetase-like 1
151	10508686	7.58806939	0.000328657	0.0379816	1.4666625	Mecr	mitochondrial trans-2-enoyl-CoA reductase
152	10584827	-7.591761	0.000327853	0.0379816	0.5190104	Mpzl2	myelin protein zero-like 2
153	10515337	7.57676547	0.000333478	0.0379816	1.5446351	Nasp	nuclear autoantigenic sperm protein (histone-binding)
154	10584870	7.58437463	0.000331067	0.0379816	1.7715366	Tmprss13	transmembrane protease, serine 13
155	10517028	7.58690638	0.00032946	0.0379816	1.4886189	Tmem222	transmembrane protein 222
156	10383365	7.52745585	0.000349549	0.038266	1.0710922	Hgs	HGF-regulated tyrosine kinase substrate
157	10518585	7.53624593	0.000343924	0.038266	1.8452698	Kif1b	kinesin family member 1B
158	10506893	7.53536973	0.000345531	0.038266	1.6466549	Nrd1	nardilysin, N-arginine dibasic convertase, NRD convertase 1
159	10497372	7.53618705	0.000344728	0.038266	1.3853371	Gm5150	predicted gene 5150
160	10508697	7.53150827	0.000347139	0.038266	1.5164494	Srsf4	serine/arginine-rich splicing factor 4
161	10508860	7.53387694	0.000346335	0.038266	1.6360198	Slc9a1	solute carrier family 9 (sodium/hydrogen exchanger), member 1
162	10517328	7.55644818	0.000339103	0.038266	1.4721908	Tmem50a	transmembrane protein 50A
163	10403842	7.51510851	0.000353567	0.0383137	1.2602456	Elmo1	engulfment and cell motility 1
164	10515590	7.49803381	0.000356781	0.0383137	1.5139241	Kdm4a	lysine (K)-specific demethylase 4A
165	10383212	7.50047092	0.000355174	0.0383137	2.6366992	Rnf213	ring finger protein 213
166	10514896	7.49863172	0.000355978	0.0383137	1.2675096	Tceanc2	transcription elongation factor A (SII) N-terminal and central domain containing 2
167	10507203	7.48187683	0.000360799	0.0384651	1.6234067	Atpaf1	ATP synthase mitochondrial F1 complex assembly factor 1
168	10509868	7.48162794	0.000361603	0.0384651	1.4151643	Atp13a2	ATPase type 13A2
169	10363392	7.39450591	0.000376067	0.0388078	1.1224096	Dnajb12	DnaJ (Hsp40) homolog, subfamily B, member 12
170	10450069	7.39417956	0.00037687	0.0388078	1.6982329	H2-K2	histocompatibility 2, K region locus 2
171	10507961	7.39484023	0.000375263	0.0388078	1.4955282	Mtf1	metal response element binding transcription factor 1
172	10484888	7.42213926	0.000370442	0.0388078	1.304951	Ptprj	protein tyrosine phosphatase, receptor type, J
173	10463911	-7.3171237	0.000408209	0.0388946	0.5903582	Add3	adducin 3 (gamma)
174	10515352	7.33850449	0.000400174	0.0388946	1.4046893	Akr1a1	aldo-keto reductase family 1, member A1 (aldehyde reductase)
175	10509178	7.27408167	0.000422673	0.0388946	1.9373643	Asap3	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3
176	10516348	7.29300601	0.000418655	0.0388946	1.5654384	37834	argonaute RISC catalytic subunit 3
177	10476817	7.32247682	0.000406602	0.0388946	1.7082485	Atpaf1	ATP synthase mitochondrial F1 complex assembly factor 1
178	10470381	7.3646092	0.000388924	0.0388946	1.5300661	Cacfd1	calcium channel flower domain containing 1
179	10478799	7.29464509	0.000417048	0.0388946	1.2515279	Cse1l	chromosome segregation 1-like (S. cerevisiae)
180	10542310	-7.3537624	0.000394549	0.0388946	0.7075075	Cdkn1b	cyclin-dependent kinase inhibitor 1B
181	10546685	7.31703091	0.000409013	0.0388946	1.8700558	Eif4e3	eukaryotic translation initiation factor 4E member 3
182	10346303	-7.3772054	0.000385709	0.0388946	0.7542481	Hspe1	heat shock protein 1 (chaperonin 10)
183	10487359	7.33107109	0.000400977	0.0388946	1.6221629	Itpripl1	inositol 1,4,5-triphosphate receptor interacting protein-like 1
184	10506397	7.29454684	0.000417852	0.0388946	1.655257	Mier1	mesoderm induction early response 1 homolog (Xenopus laevis
185	10437224	7.3233751	0.000405798	0.0388946	4.4187165	Mx2	MX dynamin-like GTPase 2
186	10531370	7.34736992	0.000396959	0.0388946	1.5956261	Naaa	N-acylethanolamine acid amidase
187	10515242	7.32223803	0.000407406	0.0388946	1.4171254	Nsun4	NOL1/NOP2/Sun domain family, member 4
188	10489043	7.27908987	0.000421066	0.0388946	1.4228422	2900097C17Rik	RIKEN cDNA 2900097C17 gene
189	10511321	7.37795096	0.000384906	0.0388946	1.05746	9430025C20Rik	RIKEN cDNA 9430025C20 gene

190	10383206	7.30158214	0.000413834	0.0388946	2.4082888	Rnf213	ring finger protein 213
191	10456717	-7.3253465	0.000404995	0.0388946	0.6627768	Snord58b	small nucleolar RNA, C/D box 58B
192	10544732	-7.3390977	0.00039937	0.0388946	0.5655842	Skap2	src family associated phosphoprotein 2
193	10545720	-7.266206	0.00042428	0.0388946	0.8710797	Stambp	STAM binding protein
194	10509023	7.32919117	0.000401781	0.0388946	1.5343537	Syf2	SYF2 homolog, RNA splicing factor (S. cerevisiae)
195	10506870	7.27551949	0.00042187	0.0388946	1.8639093	Txndc12	thioredoxin domain containing 12 (endoplasmic reticulum)
196	10507677	7.26093249	0.000430709	0.0392993	1.5836706	Hivep3	human immunodeficiency virus type I enhancer binding protein 3
197	10482229	7.25411031	0.000433923	0.0392993	1.2804225	Psmb7	proteasome (prosome, macropain) subunit, beta type 7
198	10516296	7.26002159	0.000432316	0.0392993	1.3926063	Thrap3	thyroid hormone receptor associated protein 3
199	10391207	7.23632871	0.000439548	0.0393226	2.6938332	Dhx58	DEXH (Asp-Glu-X-His) box polypeptide 58
200	10482486	7.24178363	0.000437941	0.0393226	1.3938467	Mmadhc	methylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria
201	10510982	7.23989351	0.000438745	0.0393226	1.5844681	Pex10	peroxisomal biogenesis factor 10
202	10514398	7.20702469	0.000444369	0.0394532	1.5560658	Caap1	caspase activity and apoptosis inhibitor 1
203	10383214	7.20005445	0.00044678	0.0395117	2.2883236	Rnf213	ring finger protein 213
204	10480121	7.18177982	0.000452405	0.039811	1.6681647	Fam188a	family with sequence similarity 188, member A
205	10507299	7.14887531	0.000457226	0.039811	1.3698646	Gpbp1l1	GC-rich promoter binding protein 1-like 1
206	10566144	7.16075271	0.000455619	0.039811	1.9715863	Trim21	tripartite motif-containing 21
207	10540622	7.14385468	0.000461244	0.0399919	1.2391526	Brpf1	bromodomain and PHD finger containing, 1
208	10420316	-7.1388189	0.000462851	0.0399919	0.8448114	Gm10873	predicted gene 10873
209	10383233	7.13586911	0.000466066	0.040116	2.1978507	Rnf213	ring finger protein 213
210	10446136	-7.0630067	0.000487762	0.040656	0.7015725	Catsperd	catsper channel auxiliary subunit delta
211	10455472	7.06762933	0.000485351	0.040656	1.2839216	Dcp2	DCP2 decapping enzyme homolog (S. cerevisiae)
212	10508190	7.07828681	0.000483744	0.040656	1.6093811	AU040320	expressed sequence AU040320
213	10506298	7.06915538	0.000484548	0.040656	1.5336105	Leprot	leptin receptor overlapping transcript
214	10383168	7.06606849	0.000486155	0.040656	2.1537995	Rnf213	ring finger protein 213
215	10517243	7.04681387	0.000493387	0.0408228	1.462245	Pdik1l	PDLIM1 interacting kinase 1 like
216	10508619	7.04534527	0.00049419	0.0408228	1.4738906	Pum1	pumilio RNA-binding family member 1
217	10384940	-7.0407375	0.000498208	0.0410045	0.7224565	Erlec1	endoplasmic reticulum lectin 1
218	10385926	6.9910209	0.000512672	0.0413193	1.2345732	Cdc42se2	CDC42 small effector 2
219	10454564	6.97950011	0.00051669	0.0413193	1.2009843	Ercc3	excision repair cross-complementing rodent repair deficiency, complementation group 3
220	10561498	-6.9913392	0.000511065	0.0413193	0.6494816	Papl	iron/zinc purple acid phospatase-like
221	10534324	7.02125369	0.00050544	0.0413193	1.5003519	Limk1	LIM-domain containing, protein kinase
222	10374793	6.99860925	0.000509458	0.0413193	1.3664808	Pnpt1	polyribonucleotide nucleotidyltransferase 1
223	10383152	6.98494453	0.000515083	0.0413193	2.3091518	Rnf213	ring finger protein 213
224	10521667	-6.9051059	0.000548832	0.0413448	0.4948866	Bst1	bone marrow stromal cell antigen 1
225	10507557	6.87726672	0.000561689	0.0413448	1.5138069	Ebna1bp2	EBNA1 binding protein 2
226	10421394	6.86935843	0.0005641	0.0413448	1.2259839	Fam160b2	family with sequence similarity 160, member B2
227	10603151	-6.9553233	0.000526333	0.0413448	0.544998	Gpm6b	glycoprotein m6b
228	10483110	6.92973475	0.000537583	0.0413448	2.8771594	Ifih1	interferon induced with helicase C domain 1
229	10469289	6.89647322	0.000551243	0.0413448	1.8419616	Il15ra	interleukin 15 receptor, alpha chain
230	10492355	-6.9265867	0.000539993	0.0413448	0.1110699	Mme	membrane metallo endopeptidase
231	10406614	-6.9253646	0.0005416	0.0413448	0.6961461	Mtx3	metaxin 3
232	10501909	-6.8678717	0.000564904	0.0413448	0.7805685	Mettl14	methyltransferase like 14
233	10515295	6.94139275	0.000533565	0.0413448	1.9280461	Mast2	microtubule associated serine/threonine kinase 2
234	10354054	6.90968601	0.000548029	0.0413448	1.5353056	Mitd1	MIT, microtubule interacting and transport, domain containing 1
235	10415408	-6.9487368	0.000528743	0.0413448	0.3167655	Nynrin	NYN domain and retroviral integrase containing
236	10516576	6.93968096	0.000535172	0.0413448	1.4246277	Rbbp4	retinoblastoma binding protein 4
237	10508392	6.88760033	0.000555261	0.0413448	1.9594409	Rnf19b	ring finger protein 19B
238	10505008	6.88298937	0.000556868	0.0413448	1.4942676	Slc44a1	solute carrier family 44, member 1
239	10443110	-6.9495872	0.00052794	0.0413448	0.7558806	Syngap1	synaptic Ras GTPase activating protein 1 homolog (rat)
240	10508135	6.93181337	0.000535975	0.0413448	1.587252	Trappc3	trafficking protein particle complex 3
241	10466374	6.9268121	0.00053919	0.0413448	1.6062538	Tle4	transducin-like enhancer of split 4, homolog of Drosophila E(spl)
242	10516859	6.95412129	0.000527136	0.0413448	1.4307658	Ythdf2	YTH domain family 2
243	10516435	6.89106505	0.000553654	0.0413448	1.490989	Zmym4	zinc finger, MYM-type 4
244	10401564	6.85977339	0.000569725	0.0413627	1.5040197	Arel1	apoptosis resistant E3 ubiquitin protein ligase 1
245	10516640	6.83723858	0.000576957	0.0413627	1.7914203	Eif3i	eukaryotic translation initiation factor 3, subunit I
246	10514466	6.83573131	0.000577761	0.0413627	1.5161916	Jun	jun proto-oncogene
247	10415413	-6.843228	0.000573743	0.0413627	0.2871578	Nynrin	NYN domain and retroviral integrase containing
248	10598279	-6.7415883	0.000617135	0.0419022	0.9070725	Akap4	A kinase (PRKA) anchor protein 4
249	10494322	-6.7405321	0.000617939	0.0419022	0.7096312	Anp32e	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
250	10435676	-6.7681682	0.000605885	0.0419022	0.8541321	Gsk3b	glycogen synthase kinase 3 beta
251	10434719	-6.7428496	0.000616332	0.0419022	0.889362	Kng1	kininogen 1
252	10502778	-6.7382896	0.000618742	0.0419022	0.6622789	Lphn2	latrophilin 2
253	10541410	-6.744857	0.000615528	0.0419022	0.869534	Mug1	murinoglobulin 1
254	10409240	6.79285744	0.000596243	0.0419022	1.4381887	Sema4d	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM)
255	10367224	6.77882373	0.00060026	0.0419022	3.1443313	Stat2	signal transducer and activator of transcription 2
256	10470768	6.77043398	0.000603475	0.0419022	1.3774313	Urm1	ubiquitin related modifier 1 homolog (S. cerevisiae)
257	10397912	-6.7752024	0.000601064	0.0419022	0.2047604	Unc79	unc-79 homolog (C. elegans)
258	10478754	6.71361677	0.000631599	0.042248	1.577323	Arfgef2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)
259	10410207	-6.6959572	0.000638831	0.042248	0.7775571	Cbx3	chromobox 3
260	10405874	-6.6959572	0.000638831	0.042248	0.7775571	Cbx3	chromobox 3
261	10405868	-6.6944739	0.000639635	0.042248	0.7788154	Cbx3	chromobox 3
262	10545528	-6.6969792	0.000637224	0.042248	0.7319566	Pigp	phosphatidylinositol glycan anchor biosynthesis, class P
263	10518145	6.68824761	0.000644456	0.042248	1.3247996	Prdm2	PR domain containing 2, with ZNF domain
264	10515714	6.72135067	0.000626778	0.042248	1.2262996	Szt2	seizure threshold 2
265	10414659	-6.6944144	0.000640438	0.042248	0.6810549	Snord58b	small nucleolar RNA, C/D box 58B
266	10514133	6.7157619	0.000630796	0.042248	2.8480866	Ttc39b	tetratricopeptide repeat domain 39B
267	10383204	6.6824554	0.000649278	0.0424407	2.2580497	Rnf213	ring finger protein 213
268	10544133	6.66774922	0.000654099	0.0426323	2.8794752	Parp12	poly (ADP-ribose) polymerase family, member 12
269	10507606	6.65403425	0.000662938	0.0427293	1.4044289	Ccdc23	coiled-coil domain containing 23
270	10603567	-6.6461801	0.000666956	0.0427293	0.7985207	Dynlt3	dynein light chain Tctex-type 3
271	10506736	6.64633675	0.000666152	0.0427293	1.5479161	Magoh	mago-nashi homolog, proliferation-associated (Drosophila)
272	10561335	6.64683441	0.000665349	0.0427293	1.7204415	Prkcz	protein kinase C, zeta
273	10490544	6.65018752	0.000663742	0.0427293	1.2353558	Ythdf1	YTH domain family 1
274	10393668	-6.6170959	0.000674188	0.0429486	0.7289744	Aatk	apoptosis-associated tyrosine kinase
275	10582719	6.62696201	0.000673384	0.0429486	1.4276828	Sipa1l2	signal-induced proliferation-associated 1 like 2
276	10362186	6.60873725	0.000679009	0.0429562	5.0231237	Moxd1	monooxygenase, DBH-like 1
277	10416709	-6.6086708	0.000679813	0.0429562	0.8320566	Tdrd3	tudor domain containing 3
278	10482517	6.59345797	0.000687849	0.0429692	2.0602285	Nmi	N-myc (and STAT) interactor
279	10517666	6.59407199	0.000687045	0.0429692	1.4353099	Otud3	OTU domain containing 3
280	10509500	6.59157395	0.000691063	0.043032	1.4428832	Hp1bp3	heterochromatin protein 1, binding protein 3
281	10565341	-6.5871307	0.00069267	0.043032	0.6682399	Gm6155	predicted pseudogene 6155
282	10425923	-6.5739957	0.000698295	0.0431061	0.6448408	Fam118a	family with sequence similarity 118, member A
283	10506201	6.57497355	0.000696688	0.0431061	1.2984083	Ror1	receptor tyrosine kinase-like orphan receptor 1
284	10508217	6.56844174	0.000700706	0.0431061	1.210078	Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)
285	10595171	6.55897992	0.00070392	0.0431367	1.2120167	Mb21d1	Mab-21 domain containing 1
286	10346678	-6.5218921	0.000720795	0.043231	0.632919	Carf	calcium response factor
287	10509053	6.54884409	0.000709545	0.043231	1.6946716	Ifnlr1	interferon lambda receptor 1

288	10517060	6.5313824	0.000716777	0.043231	1.3341442	Nudc	nuclear distribution gene C homolog (Aspergillus)
289	10383012	6.52852106	0.00071758	0.043231	1.3949713	Pgs1	phosphatidylglycerophosphate synthase 1
290	10514070	6.52822409	0.000718384	0.043231	1.6752651	2310067E19Rik	RIKEN cDNA 2310067E19 gene
291	10502395	-6.5459273	0.000711955	0.043231	0.9146519	4930579F01Rik	RIKEN cDNA 4930579F01 gene
292	10505064	6.52234142	0.000719991	0.043231	1.5700788	Tmem38b	transmembrane protein 38B
293	10442396	-6.4946214	0.000732044	0.0432925	0.612824	Abca3	ATP-binding cassette, sub-family A (ABC1), member 3
294	10505044	6.49923689	0.000729634	0.0432925	1.5331561	Fktn	fukutin
295	10600504	-6.5006265	0.00072883	0.0432925	0.6534496	Fundc2	FUN14 domain containing 2
296	10505282	6.49225819	0.000733652	0.0432925	1.6431826	Prpf4	PRP4 pre-mRNA processing factor 4 homolog (yeast)
297	10513195	6.49718835	0.000731241	0.0432925	1.1399376	Txn1	thioredoxin 1
298	10509218	6.49077776	0.000735259	0.0432925	1.5231434	Zfp46	zinc finger protein 46
299	10423134	-6.5017562	0.000727223	0.0432925	0.7375132	Zfr	zinc finger RNA binding protein
300	10476287	6.47076955	0.000746509	0.0433885	1.3269442	Pank2	pantothenate kinase 2
301	10508608	6.47095125	0.000745705	0.0433885	1.5424859	Pef1	penta-EF hand domain containing 1
302	10374934	6.47475887	0.000742491	0.0433885	1.346326	Psme4	proteasome (prosome, macropain) activator subunit 4
303	10515698	6.47313404	0.000744098	0.0433885	1.3804444	Szt2	seizure threshold 2
304	10501608	6.47365502	0.000743294	0.0433885	1.8144491	Vcam1	vascular cell adhesion molecule 1
305	10442625	6.46555572	0.000752937	0.0436306	1.4982142	Igfals	insulin-like growth factor binding protein, acid labile subunit
306	10441601	6.46381967	0.000754544	0.0436306	1.7252397	Tagap	T cell activation Rho GTPase activating protein
307	10605571	-6.4469756	0.00076258	0.0437587	0.5665126	Gyk	glycerol kinase
308	10428192	-6.4514024	0.000760169	0.0437587	0.7470607	Pabpc1	poly(A) binding protein, cytoplasmic 1
309	10490632	6.43536843	0.000765794	0.0437631	2.3433827	Helz2	helicase with zinc finger 2, transcriptional coactivator
310	10518113	6.42859443	0.000770615	0.0437631	1.6729889	Kazn	kazrin, periplakin interacting protein
311	10469936	-6.421173	0.000775437	0.0437631	0.7550302	Nrarp	Notch-regulated ankyrin repeat protein
312	10484577	6.43272826	0.000768205	0.0437631	1.0857848	Olfr1049	olfactory receptor 1049
313	10404187	-6.4229504	0.000774633	0.0437631	0.8316163	Tdp2	tyrosyl-DNA phosphodiesterase 2
314	10589596	6.40614346	0.000782669	0.043842	1.1845861	Ccdc12	coiled-coil domain containing 12
315	10597564	-6.4044267	0.000783472	0.043842	0.7707576	Cmc1	COX assembly mitochondrial protein 1
316	10518857	6.3934133	0.000785883	0.043868	1.2542564	Zbtb48	zinc finger and BTB domain containing 48
317	10471953	6.38161852	0.000793115	0.0439465	1.3236552	Acvr2a	activin receptor IIA
318	10487871	6.36215257	0.000805169	0.0439465	1.383565	Cenpb	centromere protein B
319	10442870	-6.3732311	0.000799544	0.0439465	0.9207504	Ccdc78	coiled-coil domain containing 78
320	10355152	-6.3742177	0.000797936	0.0439465	0.6453239	Fzd5	frizzled homolog 5 (Drosophila)
321	10488879	6.36079827	0.000806776	0.0439465	1.5048914	Gss	glutathione synthetase
322	10506004	6.37804457	0.000796329	0.0439465	1.4769059	Hook1	hook homolog 1 (Drosophila)
323	10376033	-6.3857124	0.000792312	0.0439465	0.8269589	Kif3a	kinesin family member 3A
324	10480921	6.370276	0.000801151	0.0439465	1.4340046	Qsox2	quiescin Q6 sulfhydryl oxidase 2
325	10586064	-6.3574494	0.000810793	0.043953	0.7879897	Anp32a	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A
326	10516678	6.35754666	0.000809186	0.043953	1.5789803	Kpna6	karyopherin (importin) alpha 6
327	10498345	6.35070375	0.000814008	0.0439595	1.154839	Gpr171	G protein-coupled receptor 171
328	10495854	-6.3489198	0.000814811	0.0439595	0.2955719	Prss12	protease, serine 12 neurotrypsin (motopsin)
329	10478778	6.32527887	0.000831686	0.0442161	1.6382598	Arfgef2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)
330	10454369	-6.3247996	0.00083249	0.0442161	0.5082382	Fhod3	formin homology 2 domain containing 3
331	10373313	-6.3276709	0.000829275	0.0442161	0.5027652	Nab2	Ngfi-A binding protein 2
332	10383210	6.32691577	0.000830079	0.0442161	2.4807145	Rnf213	ring finger protein 213
333	10516551	6.3230684	0.000833293	0.0442161	1.3391554	S100pbp	S100P binding protein
334	10394082	6.30773788	0.000843739	0.0443244	1.4877081	Ogfod3	2-oxoglutarate and iron-dependent oxygenase domain containing 3
335	10507190	6.28709828	0.000854186	0.0443244	1.6198813	Efcab14	EF-hand calcium binding domain 14
336	10587284	-6.296517	0.000850972	0.0443244	0.4961895	Elovl5	ELOVL family member 5, elongation of long chain fatty acids (yeast)
337	10495685	-6.3009038	0.000848561	0.0443244	0.6847547	Arhgap29	Rho GTPase activating protein 29
338	10490225	6.28671352	0.000854989	0.0443244	1.5063731	Slmo2	slowmo homolog 2 (Drosophila)
339	10443080	-6.28985	0.000853382	0.0443244	0.7975485	Syngap1	synaptic Ras GTPase activating protein 1 homolog (rat)
340	10519007	6.30193121	0.000846954	0.0443244	1.7072276	Tprgl	transformation related protein 63 regulated like
341	10457489	-6.316974	0.000837311	0.0443244	0.8651114	Tmem241	transmembrane protein 241
342	10348889	-6.277925	0.000862221	0.0443932	0.7371807	D2hgdh	D-2-hydroxyglutarate dehydrogenase
343	10516994	6.28016431	0.000861418	0.0443932	1.3651775	Fam76a	family with sequence similarity 76, member A
344	10514884	6.28251606	0.000860614	0.0443932	1.527638	Mrpl37	mitochondrial ribosomal protein L37
345	10524588	6.27061059	0.000867043	0.0444014	1.3439753	Ankrd13a	ankyrin repeat domain 13a
346	10508711	6.26128016	0.000872668	0.0444239	1.4616923	Taf12	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor
347	10460485	6.25009436	0.0008799	0.0446912	1.1622471	Zdhhc24	zinc finger, DHHC domain containing 24
348	10514054	6.24137806	0.000885525	0.0448758	1.184074	Nfib	nuclear factor I/B
349	10488697	6.22646684	0.000899989	0.0452025	1.1698725	Plagl2	pleiomorphic adenoma gene-like 2
350	10515739	6.22893858	0.000898382	0.0452025	1.3381465	Szt2	seizure threshold 2
351	10509246	6.22492771	0.000902399	0.0452228	1.5077833	Luzp1	leucine zipper protein 1
352	10372488	6.21965366	0.000907221	0.0453637	1.1967262	Tmem19	transmembrane protein 19
353	10543551	6.20761498	0.000916864	0.0456434	1.1236161	Rbm28	RNA binding motif protein 28
354	10450145	6.20183546	0.000919274	0.0456626	3.4009238	Psmb9	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2)
355	10518473	6.19545223	0.000923292	0.0457614	1.456567	Fbxo6	F-box protein 6
356	10542317	-6.1799948	0.000934542	0.0459127	0.593599	Cdkn1b	cyclin-dependent kinase inhibitor 1B
357	10471770	-6.1793264	0.000936953	0.0459127	0.9562617	Olfr357	olfactory receptor 357
358	10574872	-6.1818048	0.000930524	0.0459127	0.8969244	4933405L10Rik	RIKEN cDNA 4933405L10 gene
359	10531199	-6.1748807	0.000941774	0.0459702	0.5790358	D130050E23Rik	RIKEN cDNA D130050E23 gene
360	10543306	-6.1716344	0.000944185	0.0459883	0.529348	Tspan12	tetraspanin 12
361	10573128	6.16235219	0.000948202	0.0460845	1.9519451	Tbc1d9	TBC1 domain family, member 9
362	10578904	-6.1551994	0.000953827	0.0461552	0.1094794	Cpe	carboxypeptidase E
363	10480652	6.14513589	0.000957845	0.0461552	1.4060127	Ndor1	NADPH dependent diflavin oxidoreductase 1
364	10507894	6.15086711	0.000955434	0.0461552	1.6360037	Rragc	Ras-related GTP binding C
365	10509858	6.15000591	0.000956238	0.0461552	1.7201131	Sdhb	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)
366	10415411	-6.1429868	0.000961059	0.0462114	0.3193604	Nynrin	NYN domain and retroviral integrase containing
367	10505326	6.1306699	0.000971506	0.0463101	1.2415719	Rgs3	regulator of G-protein signaling 3
368	10517116	6.12571014	0.000977934	0.0463101	1.96199	Rps6ka1	ribosomal protein S6 kinase polypeptide 1
369	10410078	6.13041409	0.000972309	0.0463101	1.2597174	Slc35d2	solute carrier family 35, member D2
370	10510391	6.13478113	0.000967488	0.0463101	1.7102531	Srm	spermidine synthase
371	10444244	6.12267305	0.000978738	0.0463101	3.573465	Tap1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)
372	10607346	-6.1345311	0.000968291	0.0463101	0.7040215	Tspyl2	TSPY-like 2
373	10493565	6.09883174	0.000996416	0.0464266	1.6832344	Adar	adenosine deaminase, RNA-specific
374	10505749	6.10862152	0.000988381	0.0464266	1.5055685	Dennd4c	DENN/MADD domain containing 4C
375	10514255	6.10052879	0.000994005	0.0464266	1.7535813	Mllt3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)
376	10441902	6.1019919	0.000992398	0.0464266	2.1850513	Smoc2	SPARC related modular calcium binding 2
377	10425335	-6.1145977	0.000985166	0.0464266	0.5818045	Syngr1	synaptogyrin 1
378	10383436	6.08680422	0.001004452	0.0466289	1.1934763	Aspscr1	alveolar soft part sarcoma chromosome region, candidate 1 (human)
379	10376959	6.06128469	0.001024541	0.0466289	1.2215317	Elac2	elaC homolog 2 (E. coli)
380	10509463	6.080519	0.001010077	0.0466289	1.7890632	Eif4g3	eukaryotic translation initiation factor 4 gamma, 3
381	10510708	6.06012635	0.001026148	0.0466289	1.4460316	Icmt	isoprenylcysteine carboxyl methyltransferase
382	10517263	6.06664741	0.00102213	0.0466289	1.5641282	Mtfr1l	mitochondrial fission regulator 1-like
383	10567851	6.05787685	0.001030969	0.0466289	1.2815409	Nfatc2ip	nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 2 interacting protein
384	10515974	6.0743409	0.001015702	0.0466289	1.5401294	Nfyc	nuclear transcription factor-Y gamma
385	10476702	6.08395448	0.001007666	0.0466289	1.3745998	Sec23b	SEC23B (S. cerevisiae)

386	10519105	6.06000524	0.001026951	0.0466289	1.5030805	Ski	ski sarcoma viral oncogene homolog (avian)
387	10537428	6.0553809	0.001034184	0.0466444	1.3799677	Rab19	RAB19, member RAS oncogene family
388	10416566	6.04812321	0.001040612	0.0468195	2.2998566	Epsti1	epithelial stromal interaction 1 (breast)
389	10505172	6.01061969	0.00106954	0.0472932	1.5916766	Dnajc25	DnaJ (Hsp40) homolog, subfamily C, member 25
390	10506170	6.01937985	0.001062308	0.0472932	1.472593	Efcab7	EF-hand calcium binding domain 7
391	10507784	6.01320349	0.001068737	0.0472932	1.3837923	Ppt1	palmitoyl-protein thioesterase 1
392	10514405	6.01891334	0.001063915	0.0472932	1.7995666	Plaa	phospholipase A2, activating protein
393	10452639	6.00366553	0.001076772	0.0473618	1.1987415	Myl12b	myosin, light chain 12B, regulatory
394	10505000	6.00058455	0.001081594	0.0473618	1.612446	Nipsnap3b	nipsnap homolog 3B (C. elegans)
395	10515688	6.00540222	0.001075165	0.0473618	1.3680778	Szt2	seizure threshold 2
396	10404380	5.99178633	0.001091236	0.0474904	1.2519093	Dusp22	dual specificity phosphatase 22
397	10477966	5.98833051	0.001097665	0.0474904	1.2009092	Manbal	mannosidase, beta A, lysosomal-like
398	10511007	5.99173464	0.00109204	0.0474904	1.3885787	2610002J02Rik	RIKEN cDNA 2610002J02 gene
399	10541089	5.98601433	0.001099272	0.0474904	1.4062414	2900097C17Rik	RIKEN cDNA 2900097C17 gene
400	10368101	5.97459633	0.001109718	0.0475558	1.4275995	Arfgef3	ARFGEF family member 3
401	10518069	5.96239485	0.0011282	0.0475558	1.6402824	Efhd2	EF hand domain containing 2
402	10383409	5.9729575	0.001110522	0.0475558	1.1730418	Gcgr	glucagon receptor
403	10506058	5.9646664	0.001123379	0.0475558	1.4422431	Inadl	InaD-like (Drosophila)
404	10507933	5.97035264	0.001115343	0.0475558	1.5747587	Inpp5b	inositol polyphosphate-5-phosphatase B
405	10508036	5.96357105	0.001125789	0.0475558	1.3146205	Snip1	Smad nuclear interacting protein 1
406	10518774	5.9530116	0.001133825	0.0476149	1.3869134	Park7	Parkinson disease (autosomal recessive, early onset) 7
407	10383208	5.95828267	0.001132218	0.0476149	2.4464676	Rnf213	ring finger protein 213
408	10513082	5.9488473	0.00113945	0.0477622	1.266881	Tmem245	transmembrane protein 245
409	10516371	5.93122469	0.001157932	0.0479702	1.5568556	37104	argonaute RISC catalytic subunit 1
410	10515712	5.92480874	0.001161146	0.0479702	1.6311245	Szt2	seizure threshold 2
411	10346191	5.92273693	0.001162753	0.0479702	2.6232112	Stat1	signal transducer and activator of transcription 1
412	10515994	5.93270396	0.001157128	0.0479702	1.4199182	Smap2	small ArfGAP 2
413	10515385	5.92945374	0.001159539	0.0479702	1.5940317	Urod	uroporphyrinogen decarboxylase
414	10514319	5.91102846	0.0011732	0.0480167	1.2212035	Klhl9	kelch-like 9
415	10373628	5.91430714	0.001169985	0.0480167	1.0703475	Olfr798	olfactory receptor 798
416	10371230	5.91010328	0.00117561	0.0480281	1.3090912	Gna11	guanine nucleotide binding protein, alpha 11
417	10358637	5.89951542	0.001181235	0.0481707	1.1971166	Hmcn1	hemicentin 1
418	10409294	5.89775953	0.001183646	0.0481819	1.1872077	Sptlc1	serine palmitoyltransferase, long chain base subunit 1
419	10481772	5.87963195	0.001204539	0.0483236	2.0915407	Garnl3	GTPase activating RANGAP domain-like 3
420	10557211	5.88426275	0.001202128	0.0483236	1.4777988	Rbbp6	retinoblastoma binding protein 6
421	10537353	5.87252662	0.001208556	0.0483236	1.354359	Ttc26	tetratricopeptide repeat domain 26
422	10514128	5.89206031	0.001190878	0.0483236	2.7456033	Ttc39b	tetratricopeptide repeat domain 39B
423	10526145	5.8830199	0.001202931	0.0483236	1.3469321	Tmem248	transmembrane protein 248
424	10510844	5.86656268	0.001212574	0.048377	1.520791	Wrap73	WD repeat containing, antisense to Trp73
425	10480999	5.85253344	0.001225431	0.0484611	1.3708282	Sdccag3	serologically defined colon cancer antigen 3
426	10480672	5.85232717	0.001226235	0.0484611	1.3719298	Ssna1	Sjogren's syndrome nuclear autoantigen 1
427	10478590	5.85071102	0.001227038	0.0484611	1.6150578	Zswim1	zinc finger SWIM-type containing 1
428	10505791	5.8426529	0.001238288	0.0485967	1.6043358	Focad	focadhesin
429	10383245	5.84600198	0.001235074	0.0485967	1.1386606	Rptor	regulatory associated protein of MTOR, complex 1
430	10515326	5.84234358	0.001239092	0.0485967	1.3867849	Tmem69	transmembrane protein 69
431	10472589	5.83873694	0.001243913	0.0486167	1.3387224	Phospho2	phosphatase, orphan 2
432	10478772	5.82855404	0.001255966	0.0488218	1.5570774	Arfgef2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)
433	10393955	5.79626774	0.001284895	0.0490432	1.2661866	Dus1l	dihydrouridine synthase 1-like (S. cerevisiae)
434	10558274	5.80339523	0.001282484	0.0490432	1.1115731	Fam175b	family with sequence similarity 175, member B
435	10564960	5.80464744	0.00128168	0.0490432	1.4468807	Furin	furin (paired basic amino acid cleaving enzyme)
436	10438445	5.79046434	0.001289716	0.0490432	1.5131492	Klhl6	kelch-like 6
437	10515702	5.80194894	0.001283288	0.0490432	1.5431545	Szt2	seizure threshold 2
438	10586242	5.77993247	0.001300162	0.049061	1.2454296	Dennd4a	DENN/MADD domain containing 4A
439	10568988	5.72180526	0.00136284	0.0495163	1.223585	Bet1l	blocked early in transport 1 homolog (S. cerevisiae)-like
440	10510034	5.71428829	0.001369269	0.0495163	1.2838341	Casp9	caspase 9
441	10506843	5.75941423	0.001323466	0.0495163	1.7158711	Cc2d1b	coiled-coil and C2 domain containing 1B
442	10439268	5.72549067	0.001355608	0.0495163	1.8475301	Dtx3l	deltex 3-like (Drosophila)
443	10509147	5.74657539	0.001334715	0.0495163	1.7854643	Gale	galactose-4-epimerase, UDP
444	10369774	5.70603657	0.001378911	0.0495163	1.305451	Nrbf2	nuclear receptor binding factor 2
445	10521337	5.74264928	0.00133793	0.0495163	1.4410252	Rgs12	regulator of G-protein signaling 12
446	10515690	5.73225486	0.001349983	0.0495163	1.4282895	Szt2	seizure threshold 2
447	10515710	5.72783411	0.001354804	0.0495163	1.3406504	Szt2	seizure threshold 2
448	10476033	5.73792316	0.001343555	0.0495163	1.3623079	Stk35	serine/threonine kinase 35
449	10600301	5.73112749	0.00135159	0.0495163	1.1834382	Ssr4	signal sequence receptor, delta
450	10508269	5.74820091	0.001333108	0.0495163	1.3099763	Smim12	small integral membrane protein 12
451	10584034	5.74329499	0.001337126	0.0495163	1.2787461	Snx19	sorting nexin 19
452	10357917	5.72254124	0.001361233	0.0495163	1.1714838	Tmem183a	transmembrane protein 183A
453	10395039	5.69768869	0.001390161	0.0496691	4.138261	Cmpk2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial
454	10458355	5.68529853	0.00140784	0.0498267	1.2376704	Apbb3	amyloid beta (A4) precursor protein-binding, family B, member 3
455	10518031	5.66797534	0.001426321	0.0498267	1.6140621	Dnajc16	DnaJ (Hsp40) homolog, subfamily C, member 16
456	10381408	5.66739083	0.001427929	0.0498267	1.7740171	Ifi35	interferon-induced protein 35
457	10419731	5.66949163	0.001423911	0.0498267	1.3441224	Nrbf2	nuclear receptor binding factor 2
458	10419729	5.66949163	0.001423911	0.0498267	1.3441224	Nrbf2	nuclear receptor binding factor 2
459	10482139	5.68414181	0.00141025	0.0498267	1.3409772	Pdcl	phosducin-like
460	10550131	5.68591085	0.001404625	0.0498267	1.5579329	Pla2g4c	phospholipase A2, group IVC (cytosolic, calcium-independent)
461	10482509	5.67454814	0.001419893	0.0498267	1.6885293	Rbm43	RNA binding motif protein 43
462	10489850	5.68724126	0.001402215	0.0498267	2.5308649	Znfx1	zinc finger, NFX1-type containing 1
463	10365005	5.65785007	0.001439982	0.0499592	1.1019858	Dapk3	death-associated protein kinase 3
464	10490370	5.65898513	0.001438375	0.0499592	1.3147786	Psma7	proteasome (prosome, macropain) subunit, alpha type 7
465	10515708	5.65406938	0.001445607	0.0500561	1.2891417	Szt2	seizure threshold 2
466	10348194	5.64520452	0.001452839	0.0501247	6.3515983	Efhd1	EF hand domain containing 1
467	10506118	5.63928674	0.001456857	0.0501588	1.4710122	Usp1	ubiquitin specific peptidase 1
468	10481056	5.63683859	0.001461678	0.0501992	1.9440074	Notch1	notch 1
469	10560122	5.61634463	0.001490606	0.0507781	1.1011598	Sult2a6	sulfotransferase family 2A, dehydroepiandrosterone (DHEA)-preferring, member 6
470	10477637	5.61310858	0.001493821	0.0507889	2.2696384	Map1lc3a	microtubule-associated protein 1 light chain 3 alpha
471	10463557	5.60482768	0.001500249	0.0508593	1.2673692	Gbf1	golgi-specific brefeldin A-resistance factor 1
472	10514779	5.60022089	0.001504267	0.0508593	1.5451578	Prkaa2	protein kinase, AMP-activated, alpha 2 catalytic subunit
473	10457780	5.59784767	0.001506678	0.0508646	2.1694978	Garem	GRB2 associated, regulator of MAPK1
474	10442629	5.59561019	0.001509892	0.0508969	1.2525219	Spsb3	splA/ryanodine receptor domain and SOCS box containing 3
475	10379636	5.59220681	0.001512303	0.0509021	1.5632322	Slfn4	schlafen 4
476	10451993	5.58920289	0.001521142	0.0510472	1.2336185	Mydgf	myeloid derived growth factor
477	10579532	5.58778636	0.001525963	0.0511329	2.9551101	Bst2	bone marrow stromal cell antigen 2
478	10392056	5.58256477	0.001536409	0.0512545	1.4003265	Cyb561	cytochrome b-561
479	10544273	5.57331552	0.001549266	0.0513881	1.4270955	Clec5a	C-type lectin domain family 5, member a
480	10365286	5.57447656	0.001546052	0.0513881	1.3988889	Eid3	EP300 interacting inhibitor of differentiation 3
481	10517036	5.57134522	0.001550873	0.0513881	1.7694843	Wdtc1	WD and tetratricopeptide repeats 1
482	10468949	5.54402496	0.001585427	0.0517678	1.3027191	Dclre1c	DNA cross-link repair 1C, PSO2 homolog (S. cerevisiae)
483	10476952	5.54796913	0.001581409	0.0517678	1.2703208	Entpd6	ectonucleoside triphosphate diphosphohydrolase 6

484	10506939	5.54760413	0.001582212	0.0517678	1.6293374	Eps15	epidermal growth factor receptor pathway substrate 15
485	10572622	5.54918152	0.001578195	0.0517678	1.3035393	Gtpbp3	GTP binding protein 3
486	10515277	5.55577401	0.001571766	0.0517678	1.6496421	Lurap1	leucine rich adaptor protein 1
487	10478401	5.54384829	0.00158623	0.0517678	1.3095355	Ttpal	tocopherol (alpha) transfer protein-like
488	10481320	5.5408767	0.001592659	0.0519025	1.4672895	Gtf3c4	general transcription factor IIIC, polypeptide 4
489	10501164	5.52917609	0.001606319	0.0520308	1.434469	Csf1	colony stimulating factor 1 (macrophage)
490	10506415	5.53526818	0.001601498	0.0520308	1.7634984	Oma1	OMA1 homolog, zinc metallopeptidase (S. cerevisiae)
491	10383192	5.53268093	0.001603909	0.0520308	2.2612419	Rnf213	ring finger protein 213
492	10359181	5.52803494	0.00160873	0.0520308	1.9342182	Tor3a	torsin family 3, member A
493	10516778	5.52419973	0.001611944	0.0520308	1.4561535	Zcchc17	zinc finger, CCHC domain containing 17
494	10505623	5.51598518	0.001629622	0.052054	1.9048283	Lurap1l	leucine rich adaptor protein 1-like
495	10379262	5.51674585	0.001628819	0.052054	1.4752164	Nf1	neurofibromatosis 1
496	10489368	5.51240592	0.001639265	0.0522141	1.7976796	Fitm2	fat storage-inducing transmembrane protein 2
497	10516051	5.4874684	0.001680247	0.052774	1.4715536	Cap1	CAP, adenylate cyclase-associated protein 1 (yeast)
498	10509930	5.4875325	0.001679443	0.052774	1.5853739	Fbxo42	F-box protein 42
499	10479335	5.48956546	0.001675425	0.052774	1.3506545	Osbpl2	oxysterol binding protein-like 2
500	10485342	5.48958681	0.001674622	0.052774	1.2104517	Ttc17	tetratricopeptide repeat domain 17
501	10515368	5.48426551	0.001686675	0.0529023	1.3904422	Toe1	target of EGR1, member 1 (nuclear)
502	10514590	5.47794434	0.001701943	0.0531359	1.3291383	Dock7	dedicator of cytokinesis 7
503	10434778	5.471824	0.001713193	0.0533157	2.243513	Rtp4	receptor transporter protein 4
504	10489904	5.47093673	0.0017148	0.0533157	1.3627393	Spata2	spermatogenesis associated 2
505	10496580	5.46615804	0.001722032	0.0533435	3.0231481	Gbp3	guanylate binding protein 3
506	10382470	5.46417248	0.00172605	0.0533463	1.1652357	Tmem104	transmembrane protein 104
507	10478077	5.45842168	0.001731675	0.0533491	1.3641267	Ralgapb	Ral GTPase activating protein, beta subunit (non-catalytic)
508	10467149	5.45443785	0.001736496	0.0533779	1.5721743	2010002M12Rik	RIKEN cDNA 2010002M12 gene
509	10378068	5.45189674	0.00173971	0.0533779	2.4215605	Xaf1	XIAP associated factor 1
510	10462621	5.44188711	0.001747746	0.0535516	5.3900886	I830012O16Rik	RIKEN cDNA I830012O16 gene
511	10486166	5.42976612	0.001772656	0.053611	1.4042136	Ccdc32	coiled-coil domain containing 32
512	10537426	5.43163075	0.001767031	0.053611	1.4065218	4930599N23Rik	RIKEN cDNA 4930599N23 gene
513	10360589	5.42654549	0.001775871	0.053612	1.1384724	Ahctf1	AT hook containing transcription factor 1
514	10507931	5.42424849	0.001778281	0.053613	1.1636318	Mir697	microRNA 697
515	10379530	5.40543443	0.001806406	0.0536506	1.5547047	Ccl12	chemokine (C-C motif) ligand 12
516	10577838	5.40327427	0.00180962	0.0536506	2.1007332	Ddhd2	DDHD domain containing 2
517	10468992	5.40305833	0.001810424	0.0536506	1.5677801	Frmd4a	FERM domain containing 4A
518	10516706	5.40234167	0.001812031	0.0536506	1.3156838	Khdrbs1	KH domain containing, RNA binding, signal transduction associated 1
519	10510286	5.41466598	0.001792745	0.0536506	1.5849387	Mad2l2	MAD2 mitotic arrest deficient-like 2
520	10518385	5.41184135	0.00179837	0.0536506	1.6001748	Mfn2	mitofusin 2
521	10500911	5.40918638	0.001802388	0.0536506	1.5862113	Mov10	Moloney leukemia virus 10
522	10550237	5.41404851	0.001793549	0.0536506	1.1451498	Napa	N-ethylmaleimide sensitive fusion protein attachment protein alpha
523	10394627	5.4007717	0.001812834	0.0536506	1.3618954	Nbas	neuroblastoma amplified sequence
524	10513381	5.41348585	0.001795156	0.0536506	1.3876838	Ptbp3	polypyrimidine tract binding protein 3
525	10464924	5.40554459	0.001805602	0.0536506	1.1641486	Rab1b	RAB1B, member RAS oncogene family
526	10566067	5.41491367	0.001791942	0.0536506	1.1450048	Rnf121	ring finger protein 121
527	10502791	5.39375278	0.001820067	0.0537236	3.3360021	Ifi44	interferon-induced protein 44
528	10540860	5.37821936	0.00184578	0.0540816	1.1464509	Atg7	autophagy related 7
529	10508151	5.38376239	0.001840156	0.0540816	1.3263543	Clspn	claspin
530	10462623	5.38441467	0.001837745	0.0540816	4.4430261	Ifit1	interferon-induced protein with tetratricopeptide repeats 1
531	10515613	5.38056055	0.00184337	0.0540816	1.6118892	Ptprf	protein tyrosine phosphatase, receptor type, F
532	10515046	5.36348654	0.00186587	0.0542239	1.3530138	Btf3l4	basic transcription factor 3-like 4
533	10403273	5.35725956	0.001878727	0.0544572	1.4509987	Asb13	ankyrin repeat and SOCS box-containing 13
534	10508042	5.33640593	0.001925333	0.0551689	1.3258168	Meaf6	MYST/Esa1-associated factor 6
535	10518679	5.34023511	0.001916494	0.0551689	1.5874401	Nmnat1	nicotinamide nucleotide adenylyltransferase 1
536	10349724	5.3352884	0.001927744	0.0551689	1.9515165	Rab29	RAB29, member RAS oncogene family
537	10515844	5.33693213	0.001923726	0.0551689	1.4547014	Zfp691	zinc finger protein 691
538	10410173	5.32718826	0.001940601	0.0552564	1.2269215	Hiatl1	hippocampus abundant transcript-like 1
539	10444991	5.32578904	0.001945422	0.0553238	1.3520879	Gm6034	predicted gene 6034
540	10481870	5.32221857	0.001953458	0.0554824	1.3558359	Gapvd1	GTPase activating protein and VPS9 domains 1
541	10481654	5.31749557	0.0019631	0.0555464	1.4549995	Fpgs	folylpolyglutamyl synthetase
542	10510422	5.31221263	0.001971136	0.0556341	1.7810604	Casz1	castor zinc finger 1
543	10500406	5.30975434	0.00197435	0.0556552	1.1425616	Cd160	CD160 antigen
544	10348424	5.29947435	0.001983189	0.055765	1.176968	Sh3bp4	SH3-domain binding protein 4
545	10505747	5.29372952	0.00199685	0.055891	1.6724243	Rraga	Ras-related GTP binding A
546	10379633	5.29394774	0.001996046	0.055891	1.8289296	Slfn1	schlafen 1
547	10454580	5.28655273	0.002008903	0.0559262	1.2785407	Bin1	bridging integrator 1
548	10498367	5.28845104	0.002004886	0.0559262	1.7369804	P2ry13	purinergic receptor P2Y, G-protein coupled 13
549	10448676	5.2850585	0.002011314	0.0559262	1.3783356	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2
550	10460085	5.27837729	0.002028189	0.0561651	1.3420549	Cndp2	CNDP dipeptidase 2 (metallopeptidase M20 family)
551	10393926	5.27060193	0.002038635	0.0561938	1.2163763	Dcxr	dicarbonyl L-xylulose reductase
552	10505587	5.26508903	0.002048278	0.0561938	1.3620205	Kdm4c	lysine (K)-specific demethylase 4C
553	10363379	5.26920697	0.002041849	0.0561938	1.2446471	Micu1	mitochondrial calcium uptake 1
554	10517436	5.26573911	0.002045867	0.0561938	1.4825182	Pithd1	PITH (C-terminal proteasome-interacting domain of thioredoxin-like) domain containing 1
555	10515481	5.25465872	0.002065956	0.0562221	1.2948746	Dmap1	DNA methyltransferase 1-associated protein 1
556	10574098	5.25592015	0.002061939	0.0562221	5.2910015	Nlrc5	NLR family, CARD domain containing 5
557	10435457	5.25568202	0.002062742	0.0562221	1.7084558	Parp9	poly (ADP-ribose) polymerase family, member 9
558	10471519	5.25996307	0.002056314	0.0562221	1.5835265	Tor2a	torsin family 2, member A
559	10533304	5.2418769	0.002087652	0.0565177	1.8322372	Trafd1	TRAF type zinc finger domain containing 1
560	10388861	5.23085993	0.002104527	0.0567456	1.3630948	Tmem199	transmembrane protein 199
561	10450325	5.22071823	0.00212542	0.0569498	3.852683	Cfb	complement factor B
562	10475630	5.21134723	0.002140688	0.0569498	1.240071	Galk2	galactokinase 2
563	10574151	5.21415091	0.002133455	0.0569498	3.5663089	Nlrc5	NLR family, CARD domain containing 5
564	10353524	5.21100863	0.002141491	0.0569498	1.8990569	Ogfrl1	opioid growth factor receptor-like 1
565	10516974	5.21182401	0.002139884	0.0569498	1.5708193	Ppp1r8	protein phosphatase 1, regulatory (inhibitor) subunit 8
566	10509127	5.20322787	0.002159169	0.0570495	1.4148013	Fuca1	fucosidase, alpha-L- 1, tissue
567	10476189	5.19882584	0.002168009	0.0570495	1.373142	Mrps26	mitochondrial ribosomal protein S26
568	10508649	5.20131199	0.002163991	0.0570495	1.3309919	Gm23711	predicted gene, 23711
569	10508647	5.20131199	0.002163991	0.0570495	1.3309919	Gm23711	predicted gene, 23711
570	10508112	5.19913904	0.002166401	0.0570495	1.4157609	Lsm10	U7 snRNP-specific Sm-like protein LSM10
571	10359405	5.19579394	0.002176044	0.0571276	1.1636365	Klhl20	kelch-like 20
572	10477090	5.18380511	0.002198544	0.0573843	1.4546735	Tbc1d20	TBC1 domain family, member 20
573	10513551	5.18267422	0.002204169	0.0574646	1.5285438	Fkbp15	FK506 binding protein 15
574	10517090	5.17212537	0.002217829	0.0574706	1.3081678	Arid1a	AT rich interactive domain 1A (SWI-like)
575	10517147	5.16594666	0.002229883	0.0574706	1.474239	Dhdds	dehydrodolichyl diphosphate synthase
576	10439249	5.16894961	0.002224258	0.0574706	2.8031911	Parp14	poly (ADP-ribose) polymerase family, member 14
577	10515461	5.16759927	0.002226669	0.0574706	1.4708668	Rnf220	ring finger protein 220
578	10445758	5.16910815	0.002223454	0.0574706	1.1999262	Treml4	triggering receptor expressed on myeloid cells-like 4
579	10517600	5.15828315	0.002245151	0.0576626	1.836026	Pink1	PTEN induced putative kinase 1
580	10354233	5.15773233	0.002247561	0.0576626	1.283994	Tgfbrap1	transforming growth factor, beta receptor associated protein 1
581	10388065	5.15307007	0.002255597	0.057713	1.0975996	Nlrp1b	NLR family, pyrin domain containing 1B

582	10453276	5.15196952	0.002257204	0.057713	1.1340274	Thada	thyroid adenoma associated
583	10481164	5.14605432	0.002272472	0.0579719	1.9162677	Slc2a6	solute carrier family 2 (facilitated glucose transporter), member 6
584	10444821	5.14357012	0.002278097	0.0579802	2.3874011	H2-Q5	histocompatibility 2, Q region locus 5
585	10494335	5.13659796	0.002293364	0.0580167	1.1153593	Otud7b	OTU domain containing 7B
586	10542414	5.13713513	0.00229015	0.0580167	1.2213453	Ptpro	protein tyrosine phosphatase, receptor type, O
587	10510629	5.13153894	0.002304614	0.0580207	1.5628865	Nol9	nucleolar protein 9
588	10490150	5.13106397	0.002305418	0.0580207	4.4862421	Zbp1	Z-DNA binding protein 1
589	10510270	5.12489598	0.002316667	0.058178	1.696075	Mthfr	5,10-methylenetetrahydrofolate reductase
590	10464128	5.1203741	0.0023239	0.0582572	1.4420932	Casp7	caspase 7
591	10566846	5.11628344	0.002329524	0.0582572	1.3357373	Dennd5a	DENN/MADD domain containing 5A
592	10516823	5.11742414	0.002327917	0.0582572	1.4545914	Epb4.1	erythrocyte protein band 4.1
593	10352097	5.11544693	0.002330328	0.0582572	1.1206592	1700016C15Rik	RIKEN cDNA 1700016C15 gene
594	10517559	5.11178887	0.002339167	0.0582887	1.3226459	Cdc42	cell division cycle 42
595	10533256	5.10470899	0.002355238	0.0585597	2.5163261	Oas1a	2'-5' oligoadenylate synthetase 1A
596	10351163	5.09662979	0.002375327	0.0587999	1.1942522	Scyl3	SCY1-like 3 (S. cerevisiae)
597	10517883	5.09398176	0.002380952	0.0588745	1.7236847	Necap2	NECAP endocytosis associated 2
598	10517996	5.08698063	0.002393809	0.0590475	1.4802193	Plekhm2	pleckstrin homology domain containing, family M (with RUN domain) member 2
599	10405125	5.08361134	0.002405863	0.0591017	1.7627607	Fbxw17	F-box and WD-40 domain protein 17
600	10535780	5.07303438	0.002421934	0.0592527	1.1526578	Flt3	FMS-like tyrosine kinase 3
601	10429128	5.07195272	0.002423541	0.0592527	1.88872	Sla	src-like adaptor
602	10444056	5.06424246	0.002440416	0.0593416	1.2732644	Daxx	Fas death domain-associated protein

Supplementary Table S5. Quantification of angiogenic factors in mammary tumors of nulliparous and parous mice in the presence or absence of SNAI2. Angiogenic factors were quantified in the protein lysate of tumors developed by *Snai2* WT^{erbb2} and *Snai2* KO^{erbb2} mice by a multiplex bead array (Luminex assay): nulliparous mice, N=10 mice per group; parous mice, No=8 mice per group (n.d., non-detectable).

	Nulliparous *vs.* Parous	
	WT (p-value)	**KO (p-value)**
Angiopoietin-2	0.0531	0.7558
G-CSF	0.9645	0.5052
sALK-1	0.7896	0.5043
Leptin	0.1196	0.1682
IL-1B	0.8933	0.3026
EGF	0.4501	0.2667
Endoglin	1	0.6251
FGF-2	0.894	0.5634
Follistatin	0.2667	0.8242
HGF	0.3496	0.8589
sCD31/PECAM-1	0.3986	0.6893
PLGF-2	0.6893	0.8242
KC	0.0561	0.3508
Prolactin	0.8565	0.5036
MIP-1a	0.8239	0.3501
SDF-1	0.1824	0.3281
VEGF-A	0.3508	0.7558
TGFb1	0.5636	0.5634
TGFb2	0.0832	0.5636
TGFb3	0.4501	0.0832
sFasL	n.d.	n.d.
Amphiregulin	n.d.	n.d.
Betacellulin	n.d.	n.d.
IL-6	n.d.	n.d.
Endothelin-1	n.d.	n.d.
IL-17A	n.d.	n.d.
MCP-1	n.d.	n.d.
VEGF-C	n.d.	n.d.
VEGF-D	n.d.	n.d.
TNFα	n.d.	n.d.

Supplementary Table S6. SNAI1 expression and breast cancer in Snai2-deficient mice. A) Comparison between the proportion of SNAI1-positive cells in the stroma and epithelium of tumors quantified by immunohistochemistry (IHC) in different groups of mice (Mann-Whitney U test). **B**) Correlation between the proportion of SNAI1-positive stroma or epithelium cells in the tumors quantified by IHC with survival, tumor latency and the number of metastasis (Spearman's test). **C**) Comparison between the proportions of SNAI1-positive tumor stroma or epithelium cells quantified by IHC with the presence/absence of metastasis (Mann-Whitney *U* test).

A.	**Tissue zone**	**Nulliparous/Parous**	***Snai2* WT^{Erbb2} (N=19)**	***Snai2* KO^{Erbb2} (N=20)**	**p-value**
Percentage of SNAI1+ cells	**Stroma**	Nulliparous	11.15	23.84	**0.05**
		Parous	37.395	24.26	**0.4963**
		p-value	**0.03738**	**0.8798**	
	Epithelium	Nulliparous	76.59	85.865	**0.8065**
		Parous	93.24	86.69	**0.7624**
		p-value	**0.3272**	**0.2568**	

B.		**Survival**		**Latency**		**Number of metastasis**	
		***Snai2* WT^{Erbb2}**	***Snai2* KO^{Erbb2}**	***Snai2* WT^{Erbb2}**	***Snai2* KO^{Erbb2}**	***Snai2* WT^{Erbb2}**	***Snai2* KO^{Erbb2}**
% of SNAI1+ cells in the stroma							
Nulliparous	N	8	10	8	10	8	10
	p-value	**0.4927**	**0.1869**	**0.5479**	**0.6272**	**0.4226**	**0.836**
	r	-0.2857	0.4545	-0.2515	0.1758	-0.3314	-0.0754
Parous	N	8	10	8	10	8	10
	p-value	**0.5653**	**0.4325**	**0.4346**	**0.26**	**0.5091**	**0.8792**
	r	0.241	-0.2805	0.3234	-0.3939	0.2755	-0.0554
% of SNAI1+ cells in the epithelium							
Nulliparous	N	8	10	8	10	8	10
	p-value	**0.5309**	**0.1276**	**0.6287**	**0.1497**	**0.8852**	**0.582**
	r	0.2619	0.5152	0.2036	0.4909	0.0614	-0.1988
Parous	N	8	10	8	10	8	10
	p-value	**0.2829**	**0.226**	**0.3652**	**0.9602**	**0.9775**	**0.3771**
	r	-0.4338	-0.4207	-0.3713	0.0182	-0.012	-0.3139

C.		**Metastasis (yes/no)**			
		***Snai2* WT^{Erbb2}**		***Snai2* KO^{Erbb2}**	
		No	**Yes**	**No**	**Yes**
% of SNAI1+ cells in the stroma					
Nulliparous	N	3	5	6	4
	median	18.182	10.952	23.84	26.768
	p-value	**0.4561**		**0.8312**	
Parous	N	1	7	2	8
	median	5.405	41.463	45.703	24.26
	p-value	**0.2752**		**0.4334**	
% of SNAI1+ cells in the epithelium					
Nulliparous	N	3	5	6	4
	median	76.59	76.193	86.196	70.362
	p-value	**0.6547**		**0.6698**	
Parous	N	1	7	2	8
	median	16.223	94.391	87.836	86.693
	p-value	**0.2752**		**0.4334**	

Supplementary Table S7. Total and phosphorylated levels of ERK1/2 and AKT in breast cancer from *Snai2* WT^{ErbB2} and *Snai2* KO^{ErbB2}, nulliparous and parous mice.

Quantifications were assessed by ELISA. Mean (me) and standard deviation (sd) are shown. Twenty mice per group were analyzed. Red, significant P-values. T-test.

	***Snai2* WT^{ERBB2}** (me ± sd)	***Snai2* KO^{ERBB2}** (me ± sd)	*P*- value
Total ERK 1/2			
Nulliparous	2.9290 ±0.4326	3.0420 ±0.3527	0.3076
Parous	3.2670 ±0.3454	3.4440 ±0.2344	< 0.0001
P- value	0.0294	< 0.0001	
pERK 1/2(pT202/Y204)			
Nulliparous	0.309 ±0.07854	0.356 ±0.154	0.1071
Parous	0.3525 ±0.08864	0.658 ±0.2565	0.0002
P- value	0.0145	0.0006	
Total AKT			
Nulliparous	0.171 ±0.1468	0.177 ±0.1613	0.528
Parous	0.187 ±0.05973	0.392 ±0.197	0.0001
P- value	0.5248	0.002	
pAKT (T308)			
Nulliparous	0.219 ±0.04706	0.241 ±0.1269	0.2846
Parous	0.258 ±0.0759	0.462 ±0.2002	0.0001
P- value	0.044	0.0005	
pAKT1 (S473)			
Nulliparous	0.366 ±0.218	0.397 ±0.2466	0.4142
Parous	0.387 ±0.09257	0.741 ±0.2649	< 0.0001
P- value	0.6263	0.002	

Supplementary Table S8. Correlation of total and phosphorylated ERK1/2 and AKT levels with survival and tumor latency. Protein levels were quantified by ELISA (Spearman´s correlation: red: statistically significant values; blue, values with a trend towards significance).

		Survival		Latency	
		Snai2 WT^{ErbB2}	*Snai2 KO*^{ErbB2}	*Snai2 WT*^{ErbB2}	*Snai2 KO*^{ErbB2}
Total ERK1/2					
Nulliparous	*P*- value	0.933	0.979	0.758	0.870
	r	-0.020	0.006	-0.073	-0.039
Parous	*P*- value	0.974	0.205	0.761	0.279
	r	-0.008	-0.296	0.075	-0.254
ERK1/2 (pT202/Y204)					
Nulliparous	*P*- value	0.214	0.411	0.446	0.373
	r	0.291	0.195	0.181	0.211
Parous	*P*- value	0.976	**0.075**	0.512	**0.009**
	r	-0.007	0.406	-0.156	0.566
Total AKT					
Nulliparous	*P*- value	0.224	0.139	0.485	0.102
	r	0.285	0.343	0.166	0.376
Parous	*P*- value	0.573	**0.016**	0.332	**0.011**
	r	-0.138	0.532	-0.229	0.601
AKT (pT308)					
Nulliparous	*P*- value	0.191	0.242	0.436	0.177
	r	0.305	0.274	0.185	0.314
Parous	*P*- value	0.771	**0.087**	0.566	**0.014**
	r	-0.071	0.403	-0.137	0.552
AKT1 (pS473)					
Nulliparous	*P*- value	0.206	0.103	0.427	0.742
	r	0.295	0.375	0.194	0.081
Parous	*P*- value	0.913	**0.015**	0.611	**0.002**
	r	-0.027	0.536	-0.121	0.657

Supplementary Table S9. Age of mice used in all experiments involving animals and showed in the figures across the manuscript. (*) Tissue microarray (TMA) experiments, including the assessment of Ki-67, Caspase-3, ERBB2, pERBB2 and SNAI1 by immunohistochemistry.

	Genotype	Nulliparous / Parous	Age (weeks)	ELISA	Expression Array	Tissue array studies (TMA) (*)
1	WT	Nulliparous	68.14	ELISA		TMA
2	WT	Nulliparous	39.43	ELISA		
3	WT	Nulliparous	45.57	ELISA		
4	WT	Nulliparous	44.57	ELISA		
5	WT	Nulliparous	77.57	ELISA		
6	WT	Nulliparous	62.57	ELISA		
7	WT	Nulliparous	40.57	ELISA		
8	WT	Nulliparous	57.57	ELISA		
9	WT	Nulliparous	58.43	ELISA		
10	WT	Nulliparous	40.43	ELISA		
11	WT	Nulliparous	56.43	ELISA		TMA
12	WT	Nulliparous	61.29	ELISA		TMA
13	WT	Nulliparous	51.00	ELISA		TMA
14	WT	Nulliparous	50.29	ELISA		TMA
15	WT	Nulliparous	55.71	ELISA		TMA
16	WT	Nulliparous	67.14	ELISA	ARRAY	
17	WT	Nulliparous	75.14	ELISA	ARRAY	
18	WT	Nulliparous	72.14	ELISA	ARRAY	
19	WT	Nulliparous	71.71	ELISA	ARRAY	TMA
20	WT	Nulliparous	59.14	ELISA		
21	WT	Nulliparous	66.57			TMA
22	WT	Nulliparous	62.43			TMA
23	KO	Nulliparous	59.71	ELISA		
24	KO	Nulliparous	44.29	ELISA		
25	KO	Nulliparous	50.43	ELISA		
26	KO	Nulliparous	49.71	ELISA		
27	KO	Nulliparous	45.00	ELISA		
28	KO	Nulliparous	51.29	ELISA		
29	KO	Nulliparous	55.00	ELISA		TMA
30	KO	Nulliparous	42.29	ELISA		TMA
31	KO	Nulliparous	38.86	ELISA		TMA
32	KO	Nulliparous	38.29	ELISA		TMA
33	KO	Nulliparous	42.71	ELISA		TMA
34	KO	Nulliparous	40.00	ELISA		TMA
35	KO	Nulliparous	77.00	ELISA		
36	KO	Nulliparous	62.71	ELISA	ARRAY	
37	KO	Nulliparous	105.57	ELISA	ARRAY	TMA
38	KO	Nulliparous	93.71	ELISA	ARRAY	TMA
39	KO	Nulliparous	73.14	ELISA		TMA
40	KO	Nulliparous	51.57	ELISA	ARRAY	TMA
41	KO	Nulliparous	44.00	ELISA		
42	KO	Nulliparous	46.00	ELISA		
43	WT	Parous	79.14	ELISA	ARRAY	

44	WT	Parous	42.43	ELISA		
45	WT	Parous	40.43	ELISA		
46	WT	Parous	54.14	ELISA		
47	WT	Parous	43.29	ELISA		
48	WT	Parous	40.43	ELISA		
49	WT	Parous	39.29	ELISA		
50	WT	Parous	58.29	ELISA		
51	WT	Parous	58.29	ELISA		
52	WT	Parous	42.29	ELISA		
53	WT	Parous	44.71	ELISA		TMA
54	WT	Parous	20.00	ELISA		TMA
55	WT	Parous	53.29	ELISA		TMA
56	WT	Parous	53.29	ELISA		TMA
57	WT	Parous	55.14	ELISA		TMA
58	WT	Parous	54.29	ELISA		TMA
59	WT	Parous	64.57	ELISA	ARRAY	
60	WT	Parous	58.29	ELISA	ARRAY	
61	WT	Parous	65.00	ELISA	ARRAY	
62	WT	Parous	54.29	ELISA		
63	KO	Parous	45.14	ELISA		
64	KO	Parous	45.14	ELISA		
65	KO	Parous	50.00	ELISA		
66	KO	Parous	46.14	ELISA		
67	KO	Parous	49.00	ELISA		
68	KO	Parous	46.71	ELISA		TMA
69	KO	Parous	53.57	ELISA		TMA
70	KO	Parous	58.71	ELISA		TMA
71	KO	Parous	47.00	ELISA		TMA
72	KO	Parous	45.86	ELISA		TMA
73	KO	Parous	41.86	ELISA		TMA
74	KO	Parous	38.14	ELISA		TMA
75	KO	Parous	43.00	ELISA		TMA
76	KO	Parous	41.86	ELISA		TMA
77	KO	Parous	36.00	ELISA		TMA
78	KO	Parous	93.00	ELISA	ARRAY	
79	KO	Parous	75.43	ELISA	ARRAY	
80	KO	Parous	60.00	ELISA	ARRAY	
81	KO	Parous	66.00	ELISA	ARRAY	
82	KO	Parous	66.00	ELISA	ARRAY	
83	KO	Parous	57.86			TMA