



Supplementary Information for

Cell Lineage Tracing Links ER α Loss in Erbb2-Positive Breast Cancers to the Arising of a Highly Aggressive Breast Cancer Subtype

Yunfeng Ding, Yonghong Liu, Dong-Kee Lee, Zhangwei Tong, Xiaobin Yu, Yi Li, Yong Xu, Rainer B. Lanz, Bert W. O'Malley, Jianming Xu

Corresponding authors: Jianming Xu, E-mail: jxu@bcm.edu; and Bert W. O'Malley, E-mail: berto@bcm.edu

This PDF file includes:

Supplementary Methods
Figures S1 to S11
Table S1
Supplementary References

Supplementary Methods

Tissue collection, hematoxylin and eosin (H&E) staining, immunohistochemistry (IHC) and immunofluorescence (IF)

Mouse mammary glands and tumor tissues were collected, tissue sections were prepared, and H&E staining, IHC and IF were performed as described previously (1, 2). Briefly, mice were euthanized following complete anesthesia with isoflurane. Euthanized mice were transcardially perfused with phosphate buffered saline (PBS) until the liver became pale. Collected mammary glands or breast tumor tissue or lung were fixed with 4% (w/v) paraformaldehyde (PFA) at 4 °C for overnight. Samples were rinsed and washed three times with PBS for 2 hours each round, and then washed with PBS overnight at room temperature. Samples were dehydrated with 30%, 70%, and 100% ethanol, paraffin-embedded, and sectioned. For H&E staining, sections were de-paraffinized in xylene, rehydrated in 100%, 95%, 70% and 30% ethanol and water, and stained in hematoxalin for 3 min and eosin for 30 seconds. Stained sections were dehydrated with 70%, 95% and 100% ethanol, treated in xylene, and sealed for microscopy.

For IHC and IF staining, rehydrated tissue sections were boiled for antigen retrieve in a citrate buffer (pH 6.0) for 2 minutes, treated with 3% hydrogen peroxide for inactivating endogenous peroxidase, washed in PBS containing 0.05% Tween-20 (PBST), and blocked with 5% normal donkey serum for 2 hours. Prepared sections were incubated with primary antibody solutions overnight at 4 °C. Primary antibodies used in this study include: HA tag (3724, Cell Signaling), ER α (sc-542, Santa Cruz), RFP (600-401-379, Rockland), Ki67 (ab15580, Abcam), BrdU (sc-56258, Santa Cruz), E-cadherin (610182, BD Biosciences), Vimentin (5741S, Cell Signaling), cytokeratin 8 (K8) (MABT 329, Millipore), cytokeratin 14 (K14) (906004, Biolegend), progesterone receptor (PR) (A0098, Dako), GATA3 (5852S, Cell Signaling), FoxA1 (ab23738, Abcam), and p-ERK1/2 (4370S, Cell Signaling). Since HA-tagged Erbb2 was expressed as a transgene, HA antibody was used in IHC and IF to assay the transgenic expression of HA-tagged Erbb2 protein. For IHC staining, secondary antibodies conjugated with horseradish peroxidase were used and visualized using a DAB-staining Kit (SK-4103, Vector Laboratories). IHC-stained sections were counter-stained with Harris-Modified Hematoxylin. For IF staining, biotinylated secondary antibodies were used to incubate with sections for 1 hour at room temperature. Signals were amplified with the Tyramide Signal Amplification Kit (MP20911, Life Technologies). For double or triple IF staining, after finishing the first run of IF staining, sections were boiled for 2 minutes in the citrate buffer for antigen retrieve and the same IF staining steps were repeated one or two more times. Alexa Fluor 488 (green), Alexa Fluor 594 (red) and Alexa Fluor 680 (white) were used for visualizing IF staining signals.

Flow cytometry

Advanced primary tumors were minced into small pieces and digested with 1.5 mM collagenase I (17018-029, Gibco) at 37°C for 2 hours with rotation. After further digestion with 0.25% trypsin and 1 μ g/ml DNase I (DN25, Sigma-Aldrich) at 37°C for 10 minutes, cells were washed with PBS containing 2% fetal bovine serum (FBS), and subsequently incubated for one hour at 4°C with biotin-conjugated antibodies against CD45 (103103, Biolegend), TER119 (30-5921-U500, Tonbo), CD140a (13-1401-82, Invitrogen), and CD31 (553371, Becton Dickinson) for excluding immune, red blood, fibroblast and endothelial cells, respectively. Cells were washed with PBS containing 2% FBS, then incubated for 10 minutes at 4°C with fluor 488-labeled streptavidin, and then washed again with PBS containing 2% FBS. Cells were sorted for RFP-positive/Fluor488-negative (RFP^+ /F488 $^-$) and RFP-negative/Fluor488-negative (RFP^- /F488 $^-$) cells, which mainly consisted of ER α $^+$ RFP $^+$ Erbb2 $^+$ and ER α $^-$ RFP $^-$ Erbb2 $^+$ tumor cells, respectively. To obtain ER α $^+$ and ER α $^-$ luminal epithelial cells, collected mammary glands were cut into small pieces and digested with 1.5 mM collagenase I at 37°C for 1 hours with rotation. To separate branches and fat cells, the digested tissues were centrifuged at 1000 rpm for 5 minutes. The bottom fraction was resuspended, and further digested with collagenase I for 30 minutes and then 0.25% Trypsin for 10 minutes. Cells were washed with PBS containing 2% FBS, and then incubated for one hour at 4°C with FITC-labeled CD24 antibody (101805, BioLegend). Flow cytometry was performed to collect high FITC/RFP $^+$ cells, which were ER α $^+$ mammary gland luminal epithelial cells, and high FITC/RFP $^-$ cells, which were ER α $^-$ mammary gland luminal epithelial cells.

DNA methylation

Genomic DNA samples were prepared from ER α $^+$ RFP $^+$ Erbb2 $^+$ and ER α $^-$ RFP $^-$ Erbb2 $^+$ cell-derived tumors by using the Quick DNA Miniprep Plus Kit (D4068, Zymo Research). DNA samples were treated with bisulfite solution to convert unmethylated cytosines to uracils by following the instructions of the EZ DNA methylation Kit (D5001, Zymo Research). The CpG islands near ER α promoters A, B and C were predicted using the web-based program MethPrimer as described previously (3). The primers used for PCR amplification of each CpG island DNA region were also designed by using MethPrimer program (3). Primers 5'-GGGTTGTTAAGTGTTTGTATTG and 5'-CCAAAATATCCATAAATTATAAAAATC were used to amplify the region with CpG island 1. Primers 5'-TAGAGGTAGGGTTAGGGTTAGTATT, and 5'-CCTCTCCATAAACATCTTAAACTAC were used to amplify the region with CpG island 2. Primers 5'-AAGATGTTATGGAGAGGGTTTG and 5'-AAACCCCCAAACTATTAACACTAAAA were used to amplify the region with CpG island 3 (Fig. S5). PCR was performed with the ZymoTaq PreMix reagent (E2003, Zymo Research). PCR products were cloned using T-vector pGEM-T Easy Vector Systems (A1360, Promega). Individual colonies were picked for plasmid mini-prep. The DNA inserts in these bacteria-amplified

plasmids were sequenced to map the DNA methylation patterns in each CpG island.

RNA-Seq assay

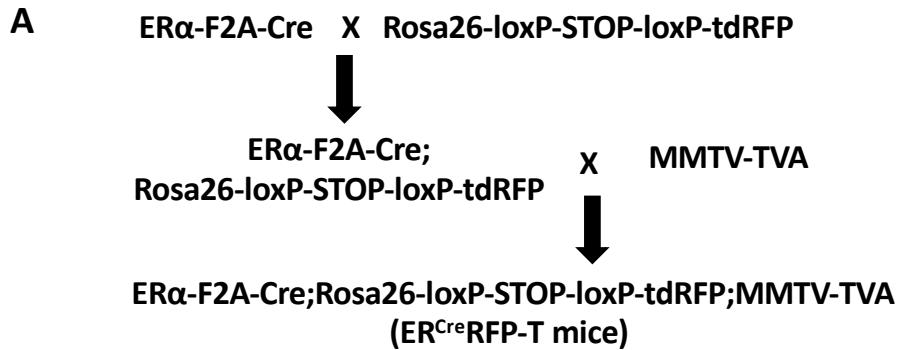
Total RNA samples were prepared from flow cytometry-purified ER α^- RFP $^+$ Erbb2 $^+$ and ER α^- RFP $^-$ Erbb2 $^+$ primary tumor cells using RNeasy Plus Mini Kit (74134, QIAGEN). RNA samples were submitted to Cancer Genomics Center at The University of Texas Health Science Center at Houston (CPRIT RP180734). Three ng of each total RNA sample was quality-checked using Agilent RNA 6000 Pico kit (#5067-1513) by Agilent Bioanalyzer 2100 (Agilent Technologies, Santa Clara, USA). All samples passed quality control standard (RIN > 7) with RNA integrity numbers (RIN) between 8.8 and 9.3. 400 ng of each total RNA sample was used for library construction using KAPA mRNA HyperPrep (KK8581, Roche) and KAPA UDI Adapter Kit (KK8727, Roche). The quality of the final libraries was examined using Agilent High Sensitive DNA Kit (#5067-4626) by Agilent Bioanalyzer 2100 (Agilent Technologies, Santa Clara, USA), and the library concentrations were determined by qPCR using Collibri Library Quantification kit (#A38524500, Thermo Fisher Scientific). The libraries were pooled evenly and went for the paired-end 75-cycle sequencing on an Illumina NextSeq 550 System (Illumina, Inc., USA) using High Output Kit v2.5 (#20024907, Illumina, Inc., USA). Forty-million reads per RNA sample were generated. RNA-Seq data were analyzed using Basepair online program (4). Raw data were preprocessed to remove low-quality reads and adapter sequences. Following the QC step, sequence reads were aligned to the reference sequence of the UCSC Genome Browser assembly mm10. Read counts for each gene transcript were measured using featureCounts (4). Differentially expressed genes between ER α^- RFP $^+$ Erbb2 $^+$ and ER α^- RFP $^-$ Erbb2 $^+$ tumor cell groups were determined using the DESeq2 software with cutoff parameters of p < 0.05 and p-adjusted < 0.1 (5). Differentially expressed genes were subjected to heatmap plotting and pathway analysis. For heatmap, transcripts per million RNA molecules (TPM) for differentially expressed genes generated by RNA-Seq analysis were transformed into Z-Scores. Heatmaps were plotted by using the software package of “ComplexHeatmap” in RStudio. KEGG pathway enrichment analysis of the differentially expressed genes was performed by using the DAVID Bioinformatics Resources (6).

RT-qPCR assay

RNAs were reversely transcribed into cDNAs using the Reverse Transcriptase Core Kit (4368813, Thermo Fisher). Quantitative PCR (qPCR) was performed to measure cDNA concentration by using the matched fluorescence-labeled universal TaqMan probes (4683633001, Sigma-Aldrich), gene specific primers, and qPCR MasterMix Plus Kit (05-QP2X-03-075+, Eurogetek). Primers for Rasgrf1 were 5'-AAACCTGGACGACGAAGC and 5'-CACCCCGATCTTAAACTCCA, and the probe was #93 (GGACCAGA). Primers for Fgf13 were 5'-AGGCAGATGGAACCATTGAT and 5'-CCCACAGGGATGAGGTAAA, and the probe was #56 (TGCTGTCC). Primers for Prlr were 5'-GCAGTGGCTTGAGGGTTA and 5'-GTTCTTCAGACTGCCCTCTC, and the probe was #31 (TTCCACCA). Primers for Lamc3 were 5'-TCACCCCTGAAGCAATGAA and 5'-GCTCCTTCTGCTCCAGCTT, and the probe was #1 (GCTCCAGG). Primers for Itga7 were 5'-CCCTGACAGTCACTACCTCGT and 5'-GGTCAGGGTCTGAGCTATCAA, and the probe was #1. The relative expression levels of these transcripts were normalized to the expression level of endogenous 18S rRNA.

Statistical analysis

The number of samples assayed in each group is indicated in relevant figures. Data are presented as the mean ± S.D. Statistical differences were determined by two-tail Student's t test for comparing two groups of data and One-Way ANOVA for comparing multiple groups of data. If p < 0.05, the difference between or among groups is considered significant.



B

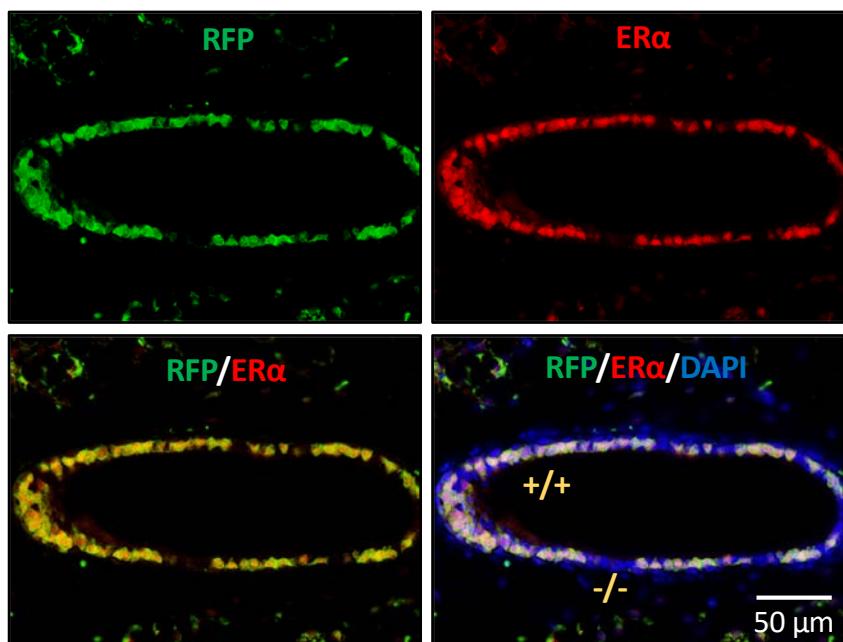


Figure S1. Generation of the tri-genic ER Cre RFP-T mouse model for ER α -positive cell lineage tracing. A. Mouse line breeding strategy. All ER Cre RFP-T mice used in this study were female, and heterozygous for the ER α -F2A-Cre, Rosa26-loxP-STOP-loxP-tdRFP, and MMTV-TVA transgenes. **B.** In female ER Cre RFP-T mice, the Cre expressed in the ER α^+ mammary gland epithelial cells excised the transcriptional STOP sequence, resulting in RFP expression. Double IF staining confirmed that ER α and RFP were co-expressed (indicated by +/+), and RFP (or Cre) was not expressed in ER α^- cells (indicated by -/-). Mammary glands from 3 mice were examined and showed same results.

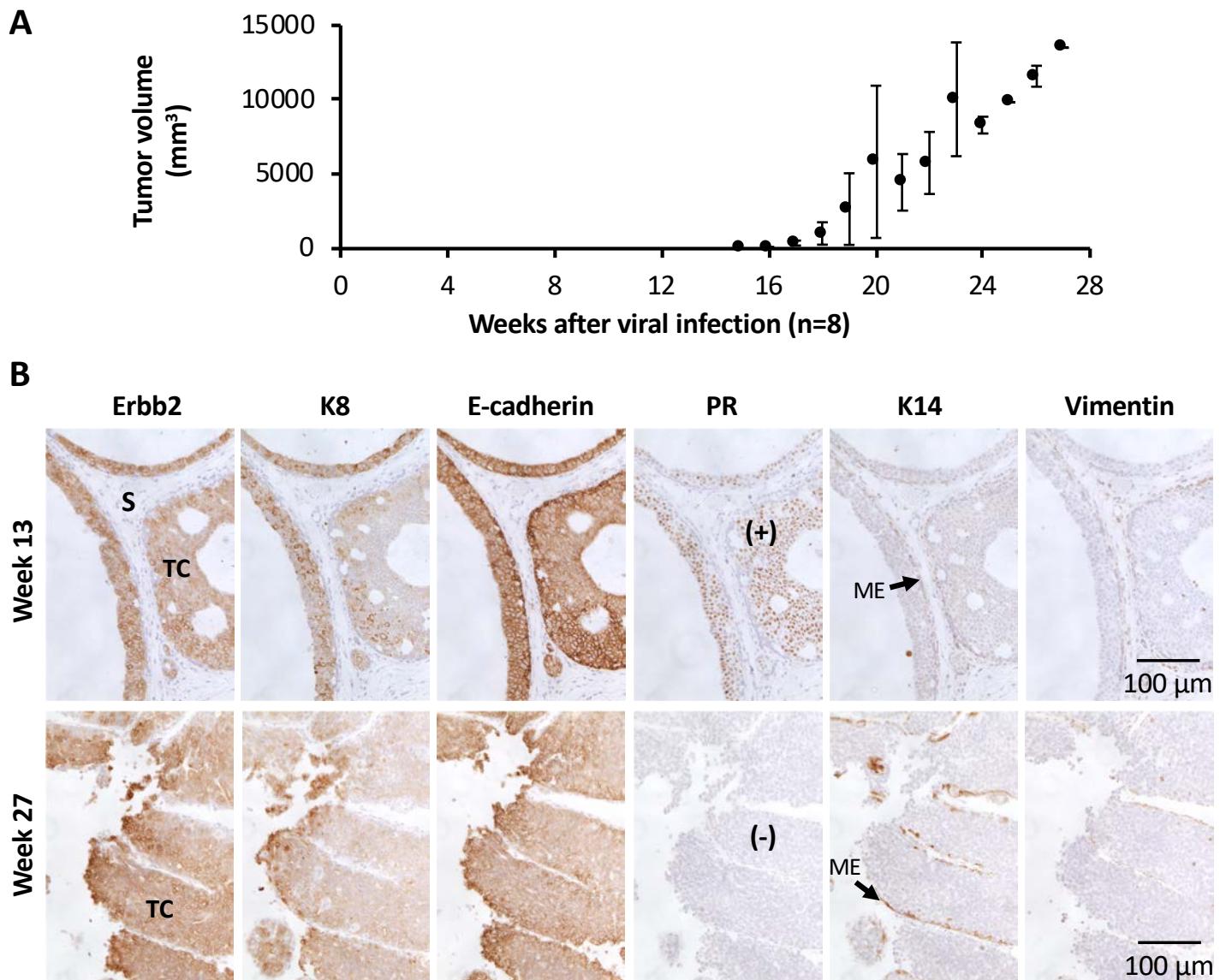


Figure S2. Erbb2-induced tumorigenesis in female ER^{Cre}RFP-T mice. **A.** Mammary gland tumor growth after RCAS-Erbb2HA virus was injected. Tumor formation was detected by palpation. Tumor length (L) and width (W) were measured weekly to calculate tumor volume using the formula $0.5 \times L \times W^2$. Data are presented as average tumor volume \pm SD (standard division). **B.** Adjacent serial sections were prepared from DCIS lesions at week 13 or advanced tumors at week 27 after viral injection as indicated. IHC staining was performed with antibodies against Erbb2, cytokeratin 8 (K8), E-cadherin, progesterone receptor (PR), cytokeratin 14 (K14) and vimentin. TC, tumor cells; ME, myoepithelial cells; S, stroma; (+) and (-), positive and negative staining for PR.

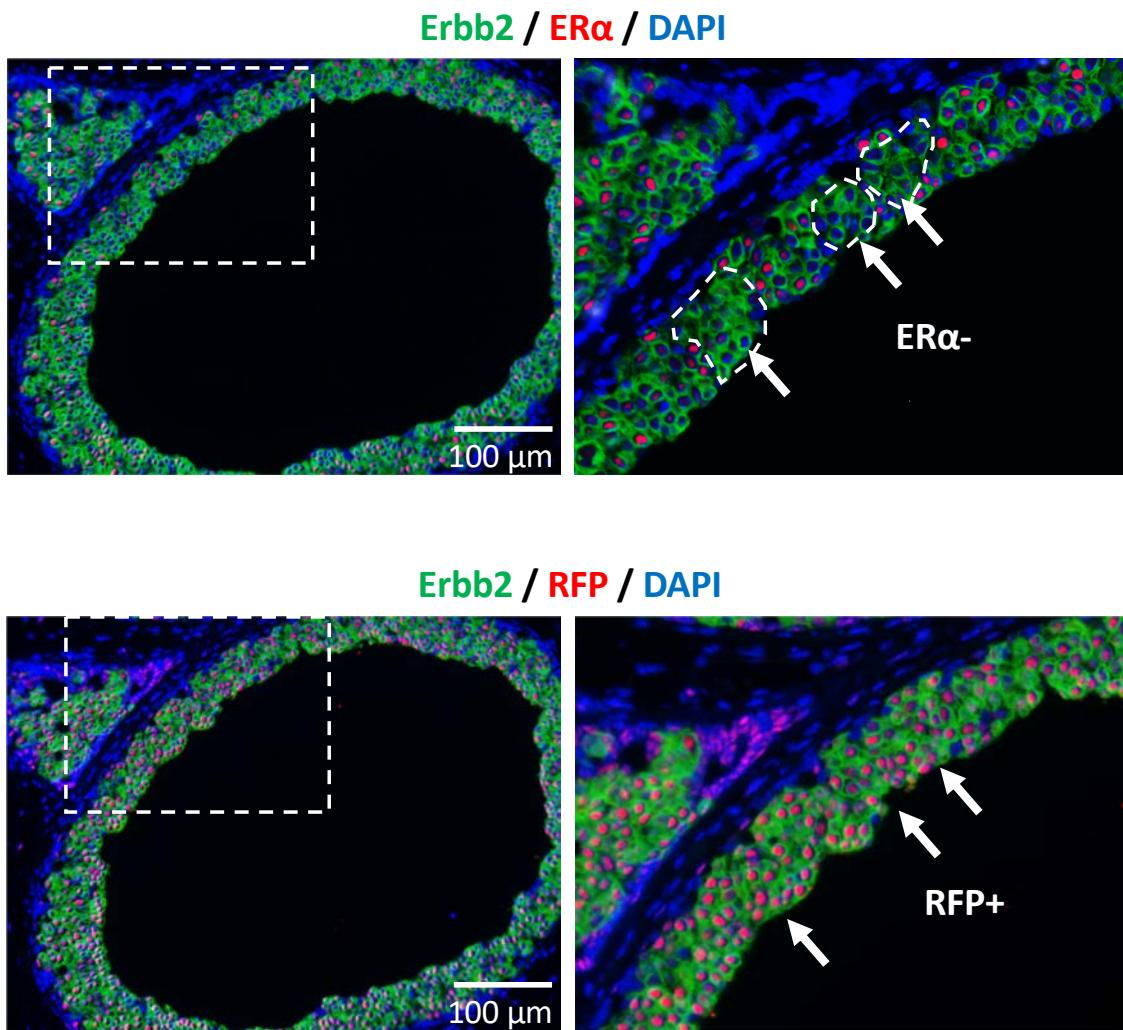


Figure S3. Loss of ER α expression in a subset of RFP $^+$ Erbb2 $^+$ cells in DCIS lesions. Double IF staining for Erbb2/ER α and for Erbb2/RFP on adjacent sections prepared from DCIS lesions at week 13 after viral infection. Boxed regions in the left images are shown amplified in the right images. The arrows indicate areas containing ER α $^-$ RFP $^+$ Erbb2 $^+$ tumor cells derived from ER α $^+$ RFP $^+$ Erbb2 $^+$ tumor cells.

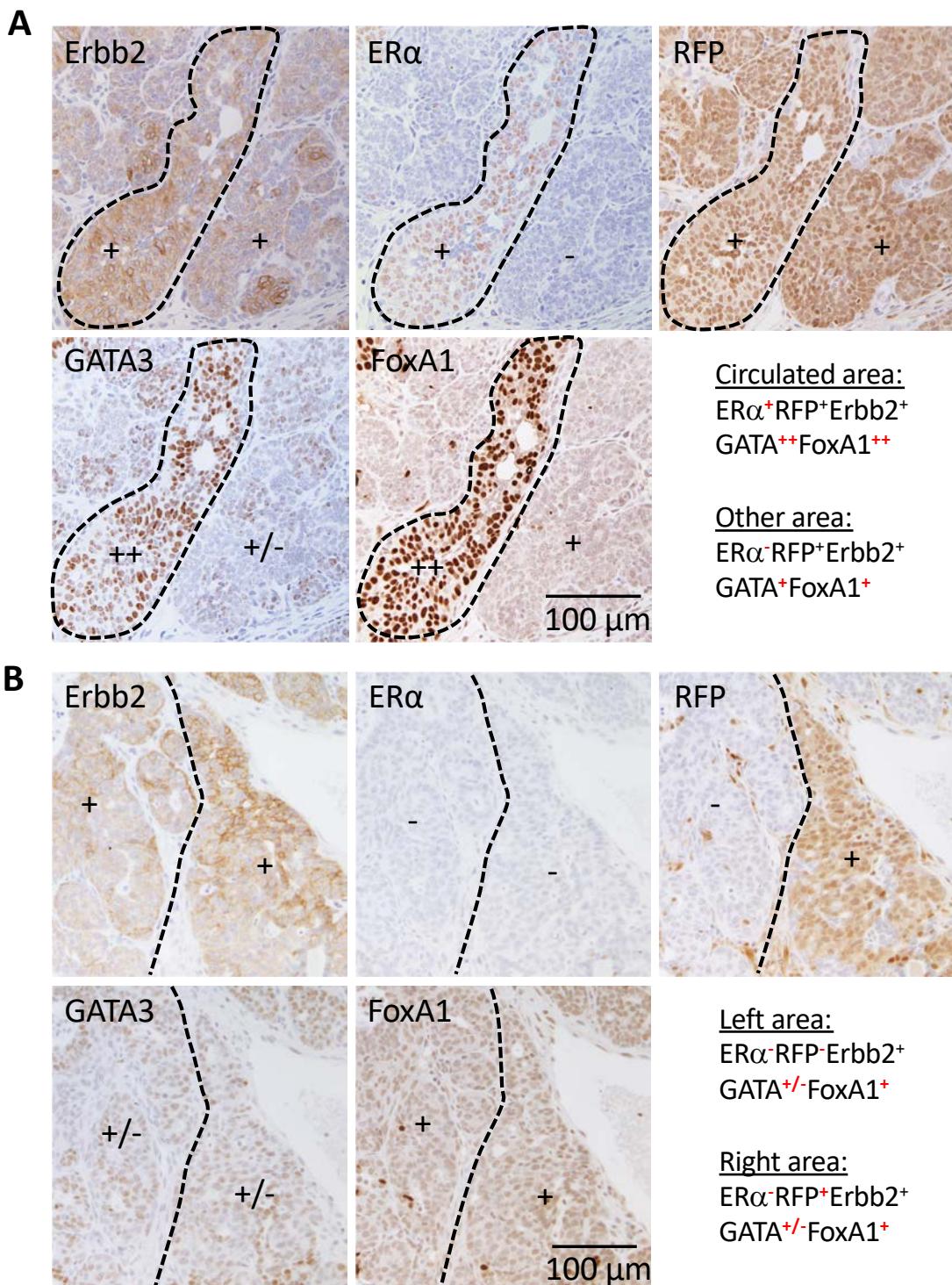


Figure. S4. The expression levels of GATA3 and FoxA1 proteins are high in ER α ⁺RFP⁺Erbb2⁺ tumor cells but low in ER α ⁻RFP⁺Erbb2⁺ and ER α ⁻RFP⁻Erbb2⁺ tumor cells. **A.** IHC for Erbb2, ER α , RFP, GATA3, and FoxA1 in a tumor region with ER α ⁺RFP⁺Erbb2⁺ (circulated area) and ER α ⁻RFP⁺Erbb2⁺ (outside of the circulated area) tumor cell areas. **B.** Ditto, but now in tumor regions with ER α ⁻RFP⁺Erbb2⁺ (lower right) and ER α ⁻RFP⁻Erbb2⁺ (left) tumor cell areas. “+”, “-”, and “+/-” indicate areas with tumor cells positive, negative and both positive and negative to the indicated protein in each panel.

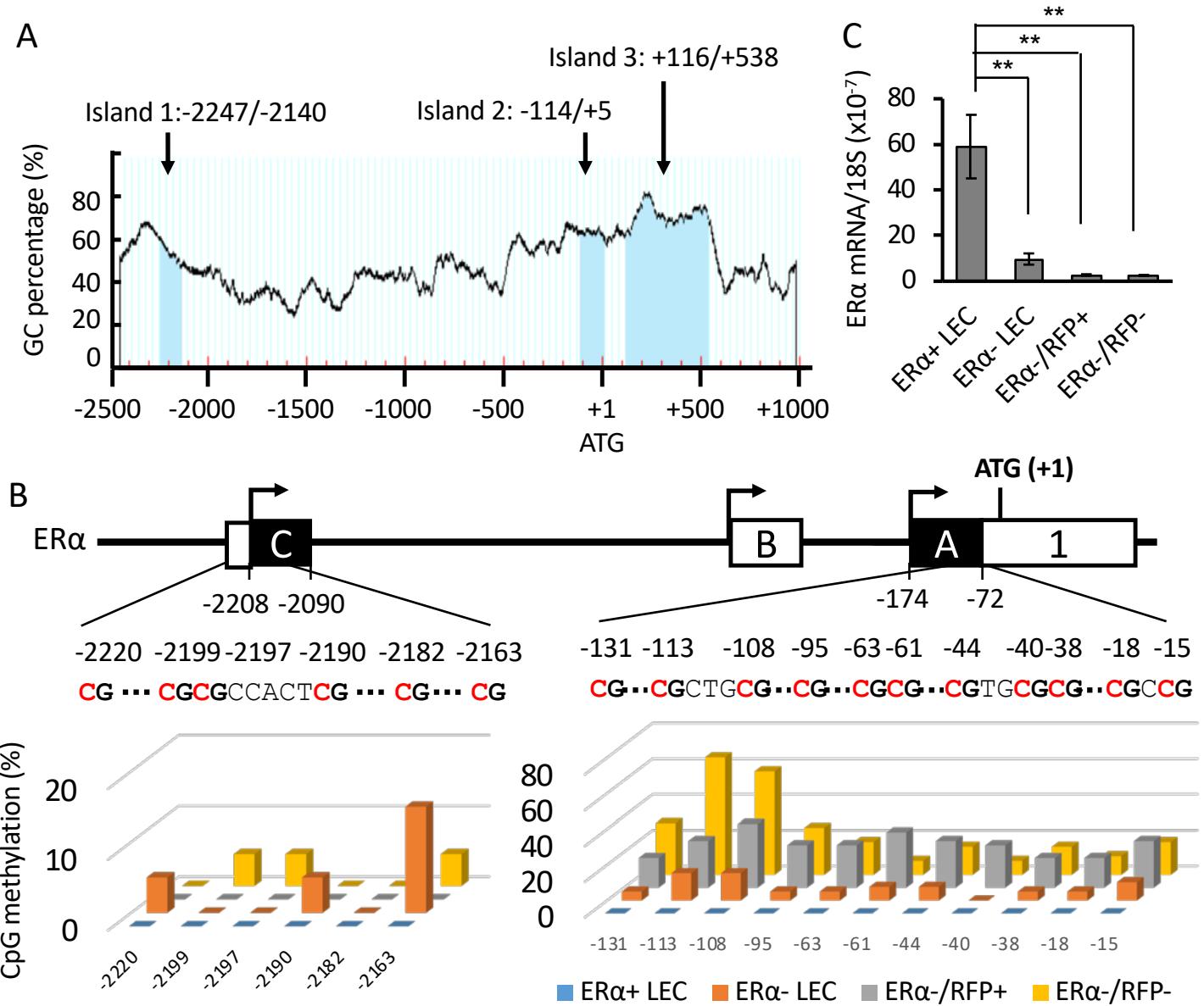


Figure. S5. DNA methylation near ER α promoter regions in ER α - mouse tumor cells. **A.** Three CpG islands near mouse ER α promoters A and C were predicted as described in Supplemental Methods. **B.** DNA methylation near ER α promoters A and C. The CpG island 1 near promoter C and the island 2 near promoter A are shown. Island 3 is in intron 1. DNA samples were isolated from purified normal ER α $^+$ and ER α - mouse MGECs, and ER α -RFP $^+$ Erbb2 $^+$ and ER α -RFP-Erbb2 $^+$ cell-derived tumors. For each group, DNA samples from MGECs of 5 mammary glands or cells of 5 tumors were equally mixed and used for analysis. For CpG island 1, 20 clones from normal ER α $^+$ MGEC DNA, 20 clones from normal ER α - MGEC DNA, 17 clones from ER α -RFP $^+$ Erbb2 $^+$ tumor DNA, and 22 clones from ER α -RFP-Erbb2 $^+$ tumor DNA were sequenced. For CpG island 2, 20 clones from normal ER α $^+$ MGEC DNA, 39 clones from normal ER α - MGEC DNA, 42 clones from ER α -RFP $^+$ Erbb2 $^+$ tumor DNA, and 39 clones from ER α -RFP-Erbb2 $^+$ tumor DNA were sequenced. For CpG island 3, 15 clones from normal ER α $^+$ MGEC DNA, 15 clones from normal ER α - MGEC DNA, 24 clones from ER α -RFP $^+$ Erbb2 $^+$ tumor DNA, and 24 clones from ER α -RFP-Erbb2 $^+$ tumor DNA were sequenced. The methylation profiles of CpG Islands 1 and 2 are presented in the left and right bar graphs. No methylation was detected in CpG island 3. The methylation percentage of each indicated CpG site was calculated by: (the number of methylated clones/total clones) $\times 100$. **C.** Relative expression levels of ER α mRNA in normal ER α $^+$ and ER α - LECs from 3 mice, and 5 ER α -RFP $^+$ Erbb2 $^+$ cell-derived tumors, and 5 ER α -RFP-Erbb2 $^+$ cell-derived tumors. Endogenous ER α mRNA and 18S rRNA were measured by RT-qPCR, and the relative ER α mRNA expression levels were normalized to 18S rRNA expression levels. **, $p < 0.01$ by One-Way ANOVA test.

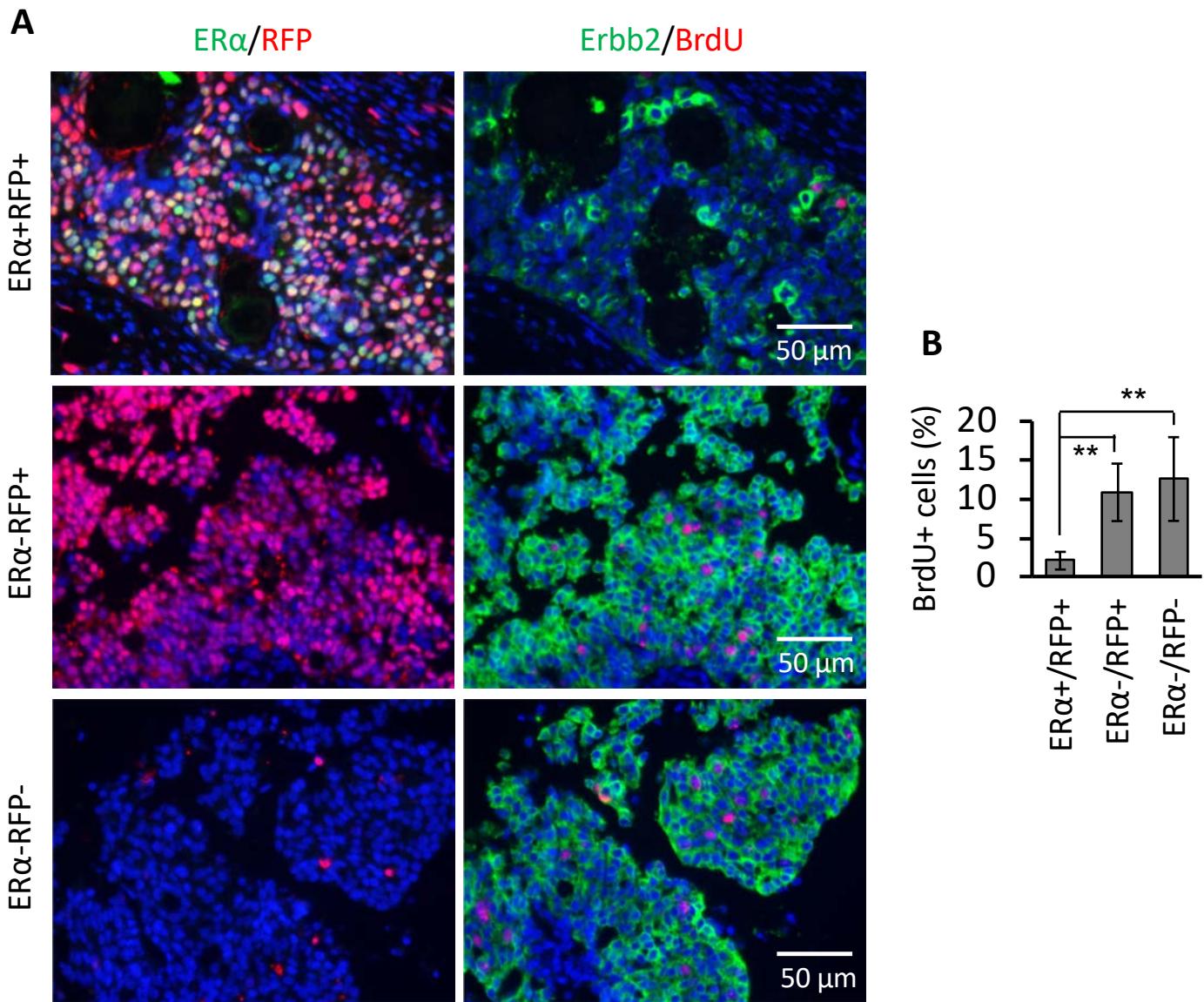


Figure S6. ER α -RFP $^+$ Erbb2 $^+$ and ER α -RFP $^-$ Erbb2 $^+$ tumor cells are much more proliferative than ER α $^+$ RFP $^+$ Erbb2 $^+$ tumor cells. A. ER Cre RFP-T mice bearing advanced mammary gland tumors at week 27 after viral infection were injected with 5 μ l/g body weight of BrdU solution (RPN201, GE Healthcare) at 2 hours before sacrifice. Tumor sections were prepared for double IF staining for ER α and RFP to identify ER α $^+$ RFP $^+$, ER α -RFP $^+$ and ER α -RFP $^-$ tumor cell regions. Adjacent sections were used for double IF staining for Erbb2 and BrdU to identify Erbb2 $^+$ BrdU $^+$ and Erbb2 $^+$ BrdU $^-$ tumor cells in the regions consisting of ER α $^+$ RFP $^+$, ER α -RFP $^+$ and ER α -RFP $^-$ tumor cells. B. The percentage of Erbb2 $^+$ BrdU $^+$ cells was determined by counting the numbers of Erbb2 $^+$ BrdU $^+$ cells and the total numbers of each indicated tumor cell type. Data were collected from 6 independent samples and presented as average \pm SD. The numbers of Erbb2 $^+$ BrdU $^+$ tumor cells in each cell type category were determined from counting 903 ER α $^+$ RFP $^+$ Erbb2 $^+$, 2530 ER α -RFP $^+$ Erbb2 $^+$ and 2468 ER α -RFP $^-$ Erbb2 $^+$ tumor cells. **, P < 0.01 by One-Way ANOVA test.

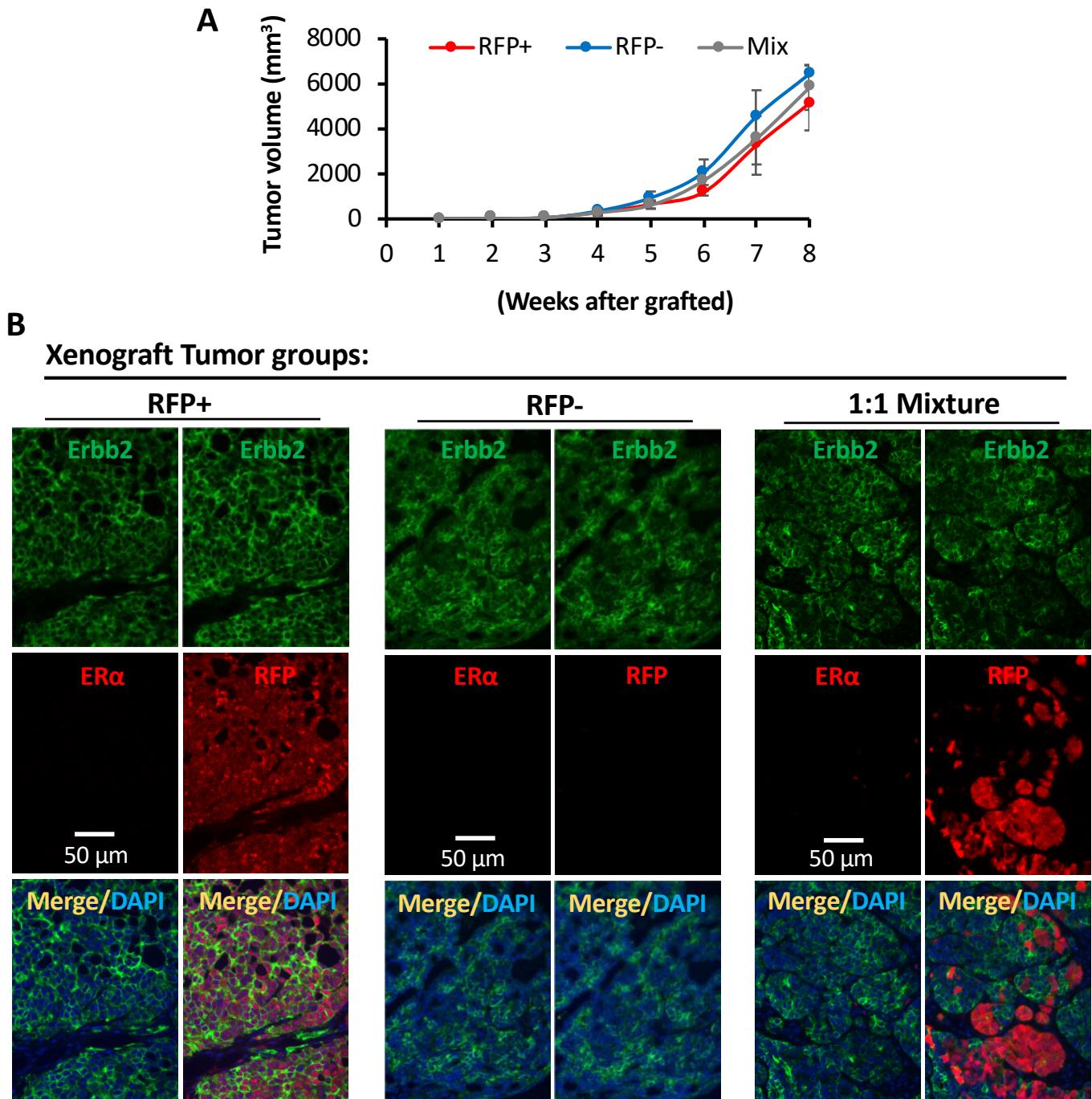


Figure S7. Xenograft tumor growth in SCID mice and validation of expected tumor cell types.

A. Growth curves of the xenograft tumors derived from inoculated RFP⁺, RFP⁻ and mixed RFP⁺ & RFP⁻ tumor cells in 8, 6 and 6 female SCID mice, respectively. Tumor formation was detected by palpation. Tumor length (L) and width (W) were measured weekly to calculate tumor volume using the formula $0.5 \times L \times W^2$. There were no significant differences in the growth rates of these tumors. **B.** Xenograft tumors in SCID mice were collected and adjacent sections were used for double IF staining for Erbb2/ER α and for Erbb2/RFP. As expected, ER α ⁻RFP⁺Erbb2⁺, ER α ⁻RFP⁻Erbb2⁺, and their mixture tumor cells were identified in the xenograft tumors derived from RFP⁺, RFP⁻ and the mixture of both tumor cells. ER α ⁺RFP⁺Erbb2⁺ tumor cells were not found in these xenograft tumors, indicating that ER α does not regain expression once it ceased being expressed in ER α ⁻RFP⁺Erbb2⁺ tumor cells.

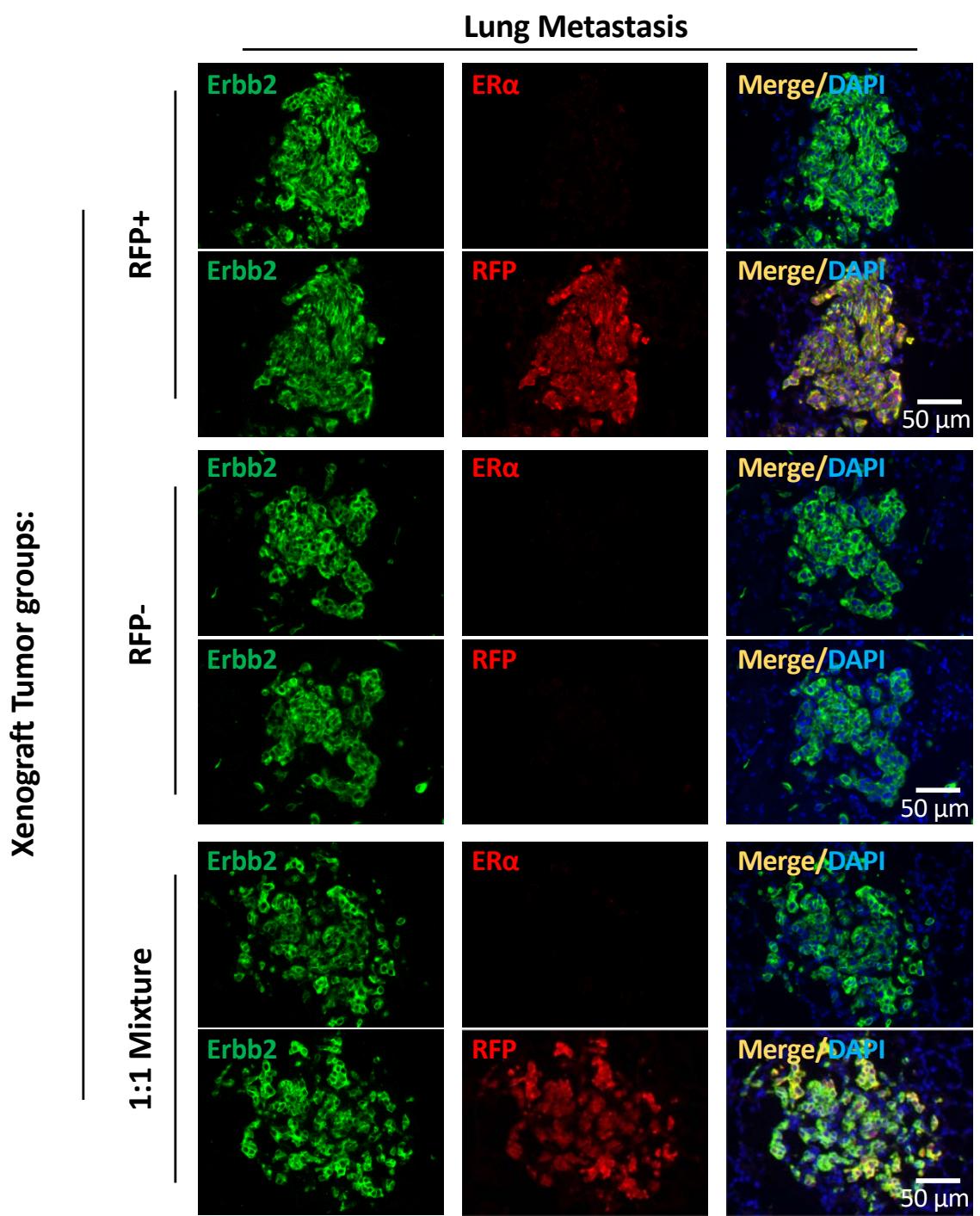


Figure S8. ER α ⁺RFP⁺Erbb2⁺ tumor cells were not detected in lung metastases. Lungs were collected from SCID mice bearing xenograft tumors derived from RFP+, RFP- and the mixture of both tumor cells as described in Figure S7. Each whole lung was sectioned. Each set of two adjacent sections with a 50 μ m interval between each set were used for double IF staining for Erbb2/ER α and for Erbb2/RFP. ER α ⁺RFP⁺Erbb2⁺ tumor cells were not found in all examined lung sections prepared from 8, 6, and 6 mice with RFP+, RFP-, and the mixed RFP+ and RFP- tumor cell-derived xenografts, respectively.

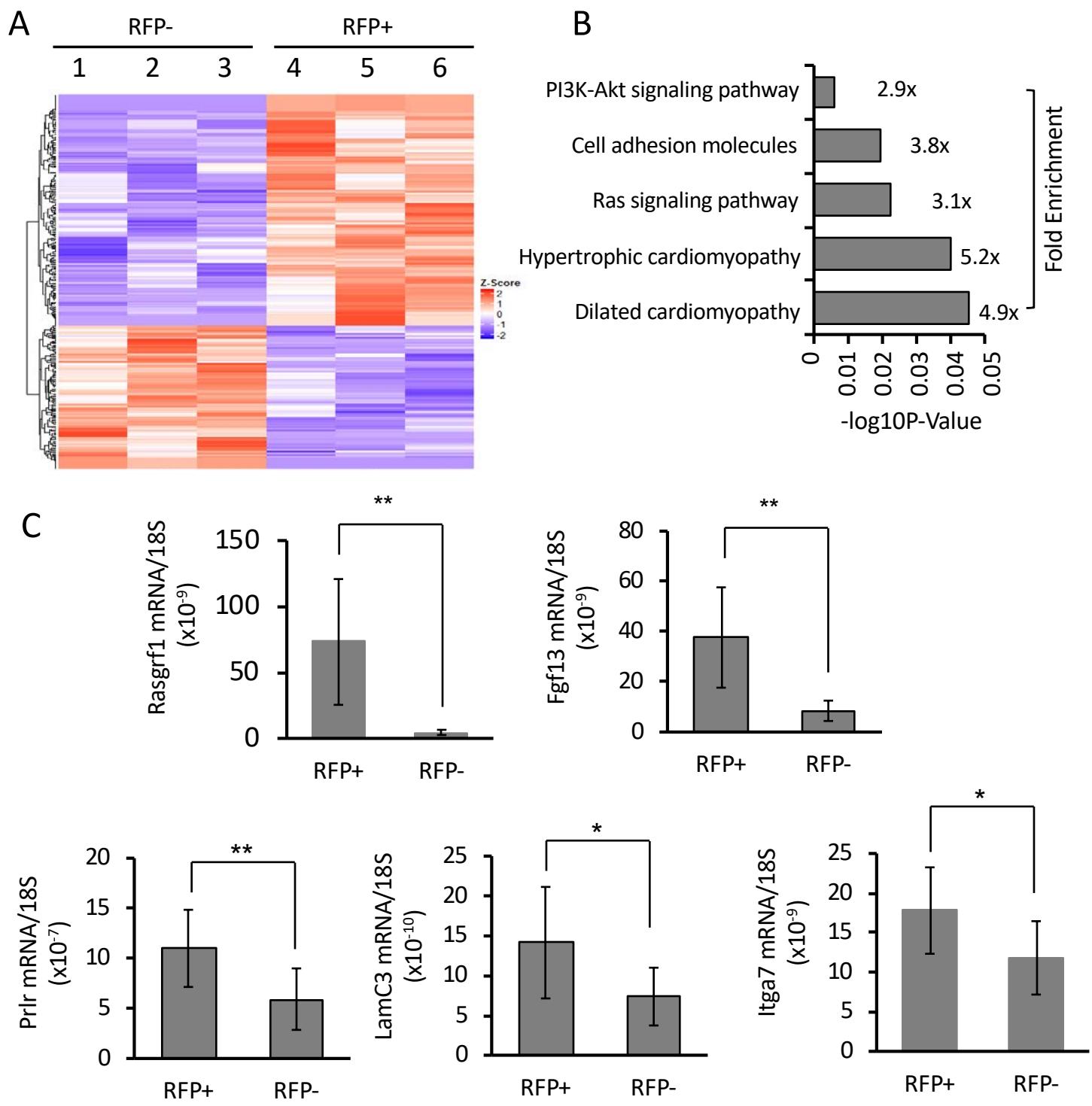


Figure. S9. RNA-Seq analysis of ERα-RFP+Erbb2+ and ERα-RFP-Erbb2+ tumor cells. **A.** The heatmap showing 230 upregulated and 143 downregulated mRNA transcripts identified by RNA-Seq profiling in ERα-RFP+Erbb2+ (RFP+) cells versus ERα-RFP-Erbb2+ (RFP-) cells. Six independent RNA samples isolated from purified cells of different tumors were analyzed. Data analysis is described in Supplementary Methods. Please see Supplementary Table S1 for entire gene list. **B.** KEGG pathways enriched with the differentially expressed genes. The top 5 significantly enriched pathways are shown. Pathway enrichment analysis was performed as described in Supplemental Methods with a cutoff p value of -log10P-value < 0.05. **C.** RT-qPCR assays of relative Rasgrf1, Fgf13, Prlr, LamC3, and Itga7 mRNA expression levels in ERα-RFP+Erbb2+ (RFP+) and ERα-RFP-Erbb2+ (RFP-) tumor cells. Three samples in each group and three replicates for each sample were assayed. Relative expression levels of these mRNAs were normalized to the expression levels of the endogenous 18S rRNA. *, p < 0.05, and **, p < 0.01 by two-tailed Student's t test.

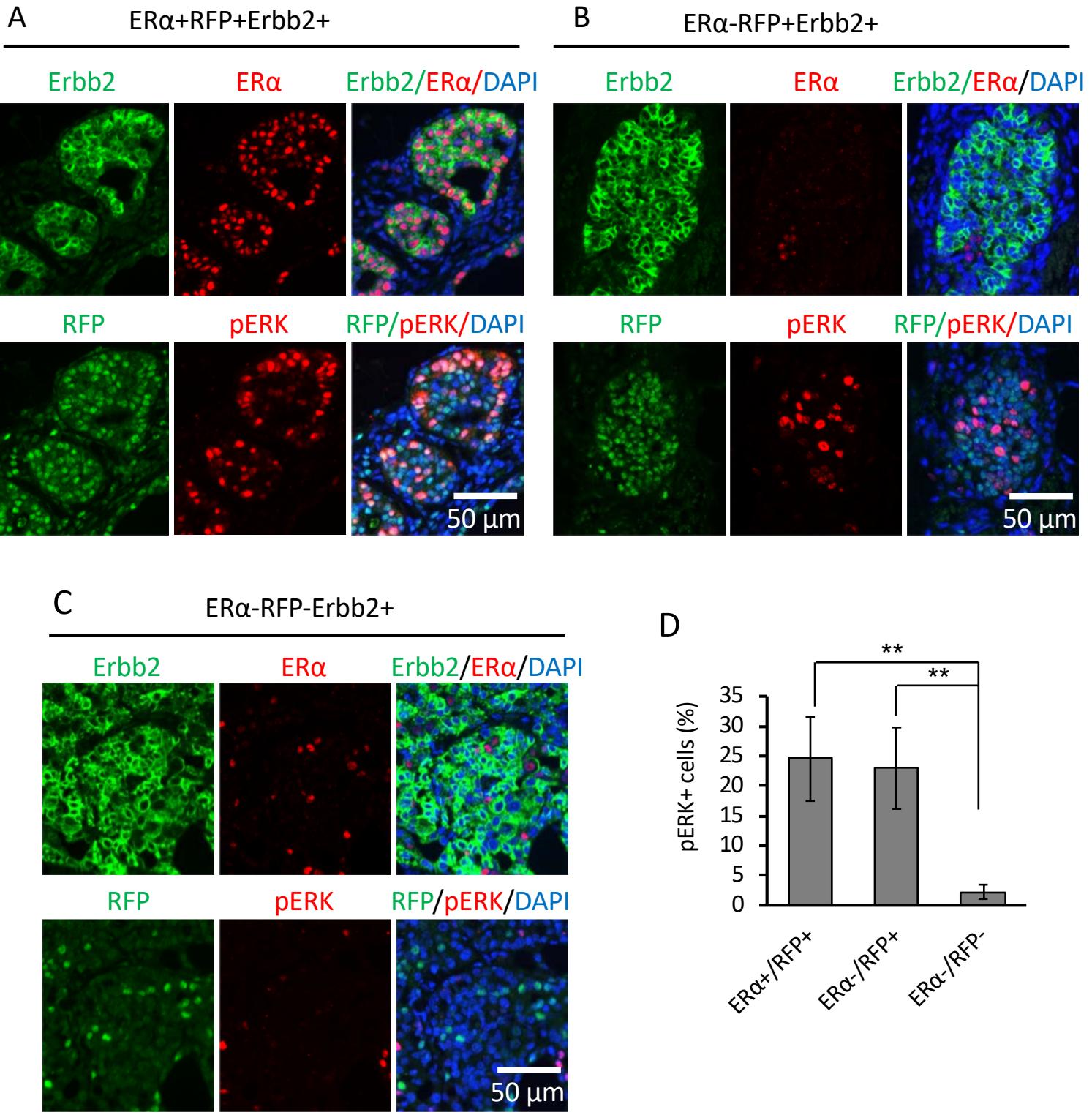


Figure. S10. pERK1/2 is highly expressed in ER α +RFP+Erbb2+ and ER α -RFP+Erbb2+ tumor cells of 13-week tumors. **A-C.** At week 13 after viral infection, mammary glands were collected and sectioned. Adjacent sections were used for double IF staining for Erbb2/ER α (Panels A & B) and RFP/p-ERK1/2 (Panel C). Erbb2+ staining identifies tumor cells. ER α staining reflects ER α expression status in tumor cells. In Panel A, ER α + and RFP+ tumor cells are colocalized in the same cell cluster, and most of these cells have high p-ERK1/2 staining signal. In Panel B, most Erbb2+ tumor cells are RFP+ but ER α - cells, and many RFP+ cells have high p-ERK1/2 staining signal. In Panel C, most Erbb2+ tumor cells are ER α - and RFP- cells, and the majority of these cells do not have detectable p-ERK1/2 staining signal. **D.** The percentages of p-ERK1/2+ cells in each of the indicated cell populations. The p-ERK1/2+ cells out of 6308 ER α +RFP+/Erbb2+ cells, 5987 ER α -RFP+Erbb2+ cells, and 6220 ER α -RFP-Erbb2+ cells from 6 independent samples were examined and counted. **, p < 0.01 by two-tailed Student's test.

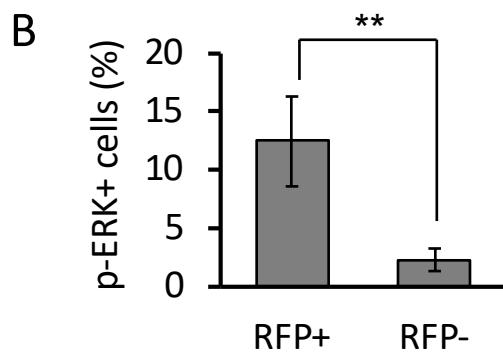
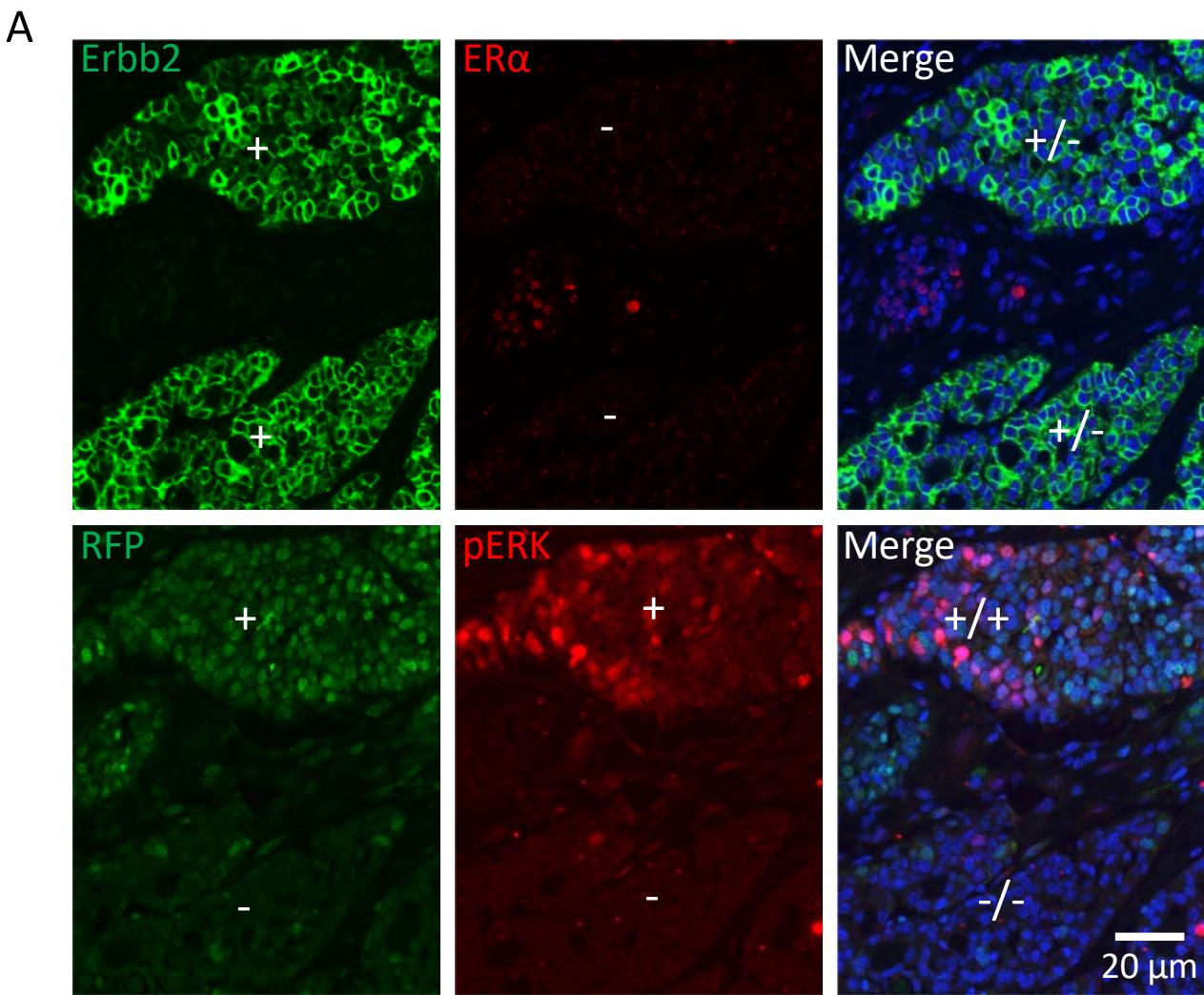


Figure S11. p-ERK1/2 is highly expressed in ER α -RFP $^+$ Erbb2 $^+$ tumor cells in advanced large tumors.

A. At week 27 after viral infection, tumor tissues ($1\text{ cm} \times 1\text{ cm} \times 0.3\text{ cm}$) were collected from different regions of each tumor. Adjacent sections prepared from 27-week tumors were used for double IF staining of Erbb2 and ER α (upper panels) and RFP and p-ERK1/2 (lower panels). In each panel, the upper region contains Erbb2 $^+$, ER α -, RFP $^+$ and p-ERK1/2 $^+$ cells, while the lower region contains mostly Erbb2 $^+$, ER α -, RFP $^-$ and p-ERK1/2 $^-$ cells. **B.** The percentages of p-ERK1/2 $^+$ cells in ER α -RFP $^+$ Erbb2 $^+$ (RFP $^+$) and ER α -RFP $^-$ Erbb2 $^+$ (RFP $^-$) cells. Sections prepared from six tumors were assayed. The numbers of p-ERK1/2 $^+$ cells out of 32678 ER α -RFP $^+$ Erbb2 $^+$ (RFP $^+$) tumor cells and 72221 ER α -RFP $^-$ Erbb2 $^+$ (RFP $^-$) tumor cells were counted. **, $p < 0.01$ by two-tailed Student's t test.

Table S1. Differentially expressed transcripts in ER-RFP+Erbb2+ and ER-RFP-Erbb2+ tumor cells.

Expressed genes were determined using DESeq2. The cut off thresholds for differentially expressed transcriptions are p < 0.05 and p-adjusted (FDR, corrected for multiple hypotheses testing) < 0.1. TMP means " transcripts per million RNA molecules".

		RNA samples of ER-RFP-Erbb2+ Cells			RNA samples of ER-RFP+Erbb2+ Cells			Average	Average	Fold Change	
Gene ID	Gene Symbol	Sample 1	Sample 2	Sample 3	Sample 4	Sample 5	Sample 6	Samples 1-3	Samples 4-6	ER-RFP+Erbb2+ vs. ER-RFP-	P-value
NM_177567	BC049762	0.0000	0.0000	0.0000	0.1361	0.1479	0.1378	0.0000	0.1406	#DIV/0!	0.0000
NR_029585	Mir199a-1	0.0000	0.0000	0.0000	1.7164	1.8658	1.7384	0.0000	1.7736	#DIV/0!	0.0000
NM_001164437	Tmem212	0.0000	0.0000	0.0000	0.1676	0.1822	0.1697	0.0000	0.1732	#DIV/0!	0.0000
NM_008455	Klkb1	0.0000	0.0000	0.0000	0.0488	0.0530	0.0494	0.0000	0.0504	#DIV/0!	0.0000
NM_146101	Habp2	0.0000	0.0000	0.0000	0.0582	0.0632	0.0589	0.0000	0.0601	#DIV/0!	0.0000
NM_001271578	Sec1	0.0000	0.0000	0.0000	0.0973	0.1058	0.0985	0.0000	0.1005	#DIV/0!	0.0000
NR_015587	9330111N05Rik	0.0000	0.0000	0.0000	0.0854	0.0928	0.0865	0.0000	0.0882	#DIV/0!	0.0000
NR_040754	4930546K05Rik	0.0000	0.0000	0.0000	0.0340	0.0369	0.0344	0.0000	0.0351	#DIV/0!	0.0000
NR_104382	Abcg8	0.0000	0.0000	0.0000	0.0396	0.0431	0.0401	0.0000	0.0410	#DIV/0!	0.0000
NM_001286005	Abcg8	0.0000	0.0000	0.0000	0.0352	0.0382	0.0356	0.0000	0.0364	#DIV/0!	0.0000
NM_183281	2310005G13Rik	0.0000	0.0000	0.0000	0.0392	0.0426	0.0397	0.0000	0.0405	#DIV/0!	0.0000
NM_011036	Reg3b	0.0000	0.0000	0.0000	0.1583	0.1721	0.1603	0.0000	0.1636	#DIV/0!	0.0000
NR_024599	Gm11346	0.0000	0.0000	0.0000	0.1078	0.1171	0.1091	0.0000	0.1113	#DIV/0!	0.0000
NM_007939	EphA8	0.0000	0.0000	0.0000	0.0255	0.0277	0.0258	0.0000	0.0263	#DIV/0!	0.0000
NM_026180	Abcg8	0.0000	0.0000	0.0000	0.0328	0.0356	0.0332	0.0000	0.0339	#DIV/0!	0.0000
NM_177923	H2-M10.2	0.0000	0.0000	0.0000	0.1214	0.1319	0.1229	0.0000	0.1254	#DIV/0!	0.0000
NM_020284	Ctsr	0.0000	0.0000	0.0000	0.1800	0.1957	0.2735	0.0000	0.2164	#DIV/0!	0.0017
NR_028572	Snora43	0.0000	0.0000	0.0000	1.7288	0.9396	1.7509	0.0000	1.4731	#DIV/0!	0.0053
NM_001081428	Fam184a	0.0000	0.0000	0.0000	0.0304	0.0661	0.0616	0.0000	0.0527	#DIV/0!	0.0093
NM_001037919	Gm6460	0.0000	0.0000	0.0000	0.5854	0.3182	0.2964	0.0000	0.4000	#DIV/0!	0.0126
NM_178915	Tmem179	0.0000	0.0000	0.0000	0.0506	0.0550	0.1026	0.0000	0.0694	#DIV/0!	0.0140
NM_008574	Smcp	0.0000	0.0000	0.0000	0.1352	0.1469	0.2738	0.0000	0.1853	#DIV/0!	0.0140
NM_010856	Myh6	0.0000	0.0000	0.0000	0.0200	0.0217	0.0405	0.0000	0.0274	#DIV/0!	0.0140
NM_001164171	Myh6	0.0000	0.0000	0.0000	0.0198	0.0215	0.0400	0.0000	0.0271	#DIV/0!	0.0140
NR_040626	9230105E05Rik	0.0000	0.0000	0.0000	0.0534	0.1161	0.0541	0.0000	0.0745	#DIV/0!	0.0231
NR_008011	Fgf4r	0.0000	0.0000	0.0000	0.0382	0.0830	0.0387	0.0000	0.0533	#DIV/0!	0.0231
NM_001093776	Myt1l	0.0000	0.0000	0.0000	0.0169	0.0368	0.0171	0.0000	0.0236	#DIV/0!	0.0231
NM_001093778	Myt1l	0.0000	0.0000	0.0000	0.0167	0.0363	0.0169	0.0000	0.0233	#DIV/0!	0.0231
NM_008174	Grm8	0.0000	0.0000	0.0000	0.0653	0.1420	0.0662	0.0000	0.0912	#DIV/0!	0.0231
NM_026296	4930548H24Rik	0.0000	0.0000	0.0000	0.0842	0.1830	0.0853	0.0000	0.1175	#DIV/0!	0.0231
NM_008666	Myt1l	0.0000	0.0000	0.0000	0.0167	0.0363	0.0169	0.0000	0.0233	#DIV/0!	0.0231
NR_033522	1600029O15Rik	0.0000	0.0000	0.0000	0.0664	0.1444	0.0673	0.0000	0.0927	#DIV/0!	0.0231
NM_001093775	Myt1l	0.0000	0.0000	0.0000	0.0167	0.0363	0.0169	0.0000	0.0233	#DIV/0!	0.0231
NR_033217	BC030870	0.0000	0.0000	0.0000	0.4874	1.1480	0.5760	0.0000	0.7371	#DIV/0!	0.0236
NM_001162537	9330159F19Rik	0.0000	0.0000	0.0000	0.0639	0.0694	0.0216	0.0000	0.0516	#DIV/0!	0.0269
NM_008241	Foxg1	0.0000	0.0000	0.0000	0.6523	0.3545	0.2065	0.0000	0.4044	#DIV/0!	0.0368
NM_001160112	Foxg1	0.0000	0.0000	0.0000	0.4824	0.2622	0.1527	0.0000	0.2991	#DIV/0!	0.0368
NM_013601	Msx2	0.0000	0.0532	0.0639	0.2223	0.6041	0.5629	0.0390	0.4631	11.8669	0.0258
NM_175138	Dnaic1	0.0000	0.0000	0.0554	0.1929	0.3146	0.1466	0.0185	0.2180	11.7999	0.0202
NM_007911	Efnb3	0.0000	0.0000	0.0429	0.1495	0.1625	0.1136	0.0143	0.1418	9.9081	0.0034
NM_001205235	Nrxn2	0.0000	0.0190	0.0000	0.0397	0.0647	0.0803	0.0063	0.0615	9.7272	0.0147
NM_020253	Nrxn2	0.0000	0.0189	0.0000	0.0395	0.0644	0.0800	0.0063	0.0613	9.7272	0.0147
NM_001205234	Nrxn2	0.0000	0.0173	0.0000	0.0361	0.0588	0.0731	0.0058	0.0560	9.7272	0.0147
NM_022030	Sv2a	0.0000	0.0294	0.0000	0.0613	0.1334	0.0621	0.0098	0.0856	8.7468	0.0425
NM_013777	Akr1c12	0.1176	0.0000	0.0000	0.3904	0.4244	0.1977	0.0392	0.3375	8.6075	0.0209
NM_010200	Fgf13	0.0580	0.0921	0.1106	0.4329	0.9411	0.8282	0.0869	0.7341	8.4499	0.0139
NM_001039655	Rasgrf1	0.0000	0.0000	0.1381	0.2403	0.5224	0.3651	0.0460	0.3759	8.1678	0.0244
NM_001290415	Fgf13	0.0719	0.1142	0.1371	0.4773	1.1024	0.9668	0.1077	0.8488	7.8778	0.0178
NM_001166464	Spock1	0.0000	0.0733	0.0879	0.5740	0.3328	0.3488	0.0537	0.4185	7.7879	0.0115
NM_001166465	Spock1	0.0000	0.0735	0.0882	0.5756	0.3337	0.3498	0.0539	0.4197	7.7879	0.0115
NM_001146295	Celf4	0.0000	0.0509	0.0612	0.1596	0.4049	0.2156	0.0374	0.2600	6.9594	0.0438
NM_018777	Cldn6	0.4808	1.6039	0.2751	2.6328	7.3715	6.3835	0.7866	5.4626	6.9447	0.0357
NM_001290414	Fgf13	0.0579	0.1379	0.1103	0.4320	0.8871	0.7779	0.1020	0.6990	6.8518	0.0127
NM_153576	Cxcl17	0.0000	0.3027	0.1817	0.6324	1.3748	1.2810	0.1615	1.0960	6.7883	0.0200
NR_004417	Snord73a	2.1295	3.3831	0.0000	7.0677	17.2861	12.5270	1.8375	12.2936	6.6903	0.0283

NM_016867	Gipc2	1.8330	1.0920	1.0924	3.7072	12.6060	10.4939	1.3391	8.9357	6.6728	0.0479
NR_106038	Mir7070	0.0000	2.6750	0.0000	5.5884	4.5560	7.0751	0.8917	5.7398	6.4371	0.0136
NM_001164631	Mum1l1	0.3809	0.4676	0.4622	1.3216	3.9350	3.1136	0.4369	2.7901	6.3860	0.0381
NM_001164633	Mum1l1	0.3720	0.4567	0.4514	1.2907	3.8432	3.0409	0.4267	2.7249	6.3860	0.0381
NM_001164632	Mum1l1	0.3668	0.4503	0.4451	1.2726	3.7892	2.9981	0.4207	2.6866	6.3860	0.0381
NM_001164630	Mum1l1	0.3778	0.4501	0.4503	1.3843	3.7194	2.9365	0.4260	2.6801	6.2907	0.0304
NM_175541	Mum1l1	0.3842	0.4578	0.4579	1.4079	3.7828	2.9864	0.4333	2.7257	6.2907	0.0304
NR_110348	Syt12	0.0619	0.2457	0.1180	0.4106	1.0600	1.0916	0.1418	0.8541	6.0218	0.0356
NM_178739	Dcaf12l1	0.0000	0.0328	0.0393	0.1368	0.1116	0.1733	0.0240	0.1406	5.8508	0.0058
NM_001190718	Dcaf12l1	0.0000	0.0329	0.0395	0.1374	0.1120	0.1739	0.0241	0.1411	5.8508	0.0058
NM_011084	Pik3c2g	0.0000	0.0324	0.0389	0.1693	0.0736	0.1715	0.0238	0.1381	5.8095	0.0294
NM_207683	Pik3c2g	0.0000	0.0261	0.0313	0.1363	0.0593	0.1380	0.0191	0.1112	5.8095	0.0294
NM_183278	Fam25c	2.7619	0.9403	1.8812	7.8573	11.7439	12.6002	1.8611	10.7338	5.7673	0.0046
NM_011245	Rasgrf1	0.0000	0.0272	0.0653	0.1137	0.2162	0.2015	0.0308	0.1771	5.7433	0.0171
NM_001301164	Car7	0.0745	0.1184	0.0000	0.1855	0.5378	0.3758	0.0643	0.3663	5.6967	0.0483
NR_028385	Gm10190	0.0000	0.0682	0.0000	0.0713	0.1549	0.1444	0.0227	0.1235	5.4313	0.0442
NM_028589	1700125H20Rik	0.1485	0.1180	0.0000	0.2465	0.5358	0.6241	0.0888	0.4688	5.2772	0.0363
NM_028629	Kprp	0.1061	0.0000	0.1012	0.3962	0.1914	0.4459	0.0691	0.3445	4.9856	0.0319
NR_002865	Rnu11	0.0000	1.0651	1.2785	4.4500	3.6279	3.3803	0.7812	3.8194	4.8893	0.0040
NM_001033499	Sh2d1b2	0.0000	0.2883	0.3461	1.5056	0.6547	0.9150	0.2114	1.0251	4.8479	0.0410
NM_053105	Klh1	0.0000	0.1421	0.0341	0.3562	0.2581	0.2104	0.0587	0.2749	4.6810	0.0235
NM_001166466	Spock1	0.0930	0.1724	0.2660	0.9775	0.8388	0.6253	0.1771	0.8139	4.5943	0.0050
NM_009262	Spock1	0.0929	0.1723	0.2659	0.9768	0.8383	0.6249	0.1770	0.8133	4.5943	0.0050
NM_001166463	Spock1	0.0931	0.1726	0.2664	0.9787	0.8399	0.6261	0.1774	0.8149	4.5943	0.0050
NM_133862	Fgg	0.6656	6.5707	6.6184	11.3603	30.1860	21.8932	4.6182	21.1465	4.5789	0.0463
NM_011855	Tenm1	0.0520	0.0550	0.0000	0.1581	0.1875	0.1310	0.0357	0.1588	4.4540	0.0070
NM_001005424	Gm996	0.0000	0.0491	0.0000	0.0513	0.0837	0.0779	0.0164	0.0710	4.3346	0.0465
NM_013519	Foxc2	0.7442	0.4223	0.9631	3.5287	2.3973	3.0378	0.7099	2.9879	4.2091	0.0033
NM_018857	Msln	13.7616	12.9438	12.9918	79.9868	33.9638	45.9722	13.2324	53.3076	4.0286	0.0438
NM_023047	Dpysl5	0.0288	0.1833	0.0550	0.2632	0.4162	0.3151	0.0890	0.3315	3.7231	0.0208
NM_020013	Gfg21	0.0000	0.2429	0.1458	0.5075	0.5517	0.3855	0.1296	0.4816	3.7163	0.0151
NR_001277	Snord33	3.5318	5.6110	0.0000	8.7915	9.5565	14.8404	3.0476	11.0628	3.6300	0.0331
NM_023557	Slc44a4	0.0000	0.2943	0.1766	0.4099	0.6127	0.6227	0.1570	0.5484	3.4935	0.0237
NM_008024	Foxl1	0.1957	0.0000	0.0466	0.3247	0.3089	0.2056	0.0808	0.2797	3.4629	0.0465
NM_008272	Hoxc9	0.0842	0.1338	0.1607	0.5592	0.4559	0.2832	0.1262	0.4327	3.4279	0.0214
NR_106037	Mir7069	0.0000	1.8553	2.2271	3.8758	4.2131	5.8883	1.3608	4.6591	3.4238	0.0237
NM_175350	Catsperd	0.0000	0.0448	0.0538	0.1405	0.1018	0.0949	0.0329	0.1124	3.4177	0.0221
NM_178621	Phyhipl	0.3528	0.4804	0.7690	2.5092	1.2274	1.6096	0.5341	1.7821	3.3367	0.0354
NM_001162846	Phyhipl	0.3722	0.5069	0.8113	2.6475	1.2950	1.6982	0.5635	1.8802	3.3367	0.0354
NM_001159647	Cntr1	0.1245	0.1780	0.0949	0.5370	0.2470	0.4812	0.1325	0.4217	3.1838	0.0348
NM_007727	Cntr1	0.1266	0.1810	0.0966	0.5461	0.2512	0.4893	0.1347	0.4289	3.1838	0.0348
NM_001159648	Cntr1	0.1277	0.1825	0.0974	0.5509	0.2533	0.4935	0.1359	0.4326	3.1838	0.0348
NM_001253782	Prlr	1.2078	3.9444	5.6307	7.3493	13.1938	11.9548	3.5943	10.8326	3.0139	0.0300
NM_001253781	Prlr	0.3328	1.2337	1.8335	2.2091	4.3357	3.6980	1.1333	3.4143	3.0126	0.0409
NR_028480	Gm12238	1.1678	0.9276	0.0000	1.9379	2.1066	1.9628	0.6985	2.0024	2.8669	0.0223
NM_177781	Trpa1	0.0000	0.0270	0.0648	0.0846	0.0919	0.0856	0.0306	0.0874	2.8563	0.0399
NR_009406	Tnni3	0.0000	0.4188	0.3351	0.7291	0.7925	0.5907	0.2513	0.7041	2.8018	0.0326
NM_001024698	Cpa2	0.3279	0.0000	0.2084	0.4534	0.4929	0.5511	0.1788	0.4991	2.7920	0.0327
NM_001159568	Meis2	0.7487	0.1982	0.3867	1.5530	0.7878	1.3632	0.4445	1.2347	2.7775	0.0483
NM_001136072	Meis2	0.7369	0.1951	0.3806	1.5286	0.7754	1.3418	0.4376	1.2153	2.7775	0.0483
NM_010825	Meis2	0.7521	0.1991	0.3884	1.5601	0.7914	1.3694	0.4466	1.2403	2.7775	0.0483
NM_001159567	Meis2	0.7337	0.1943	0.3789	1.5219	0.7720	1.3359	0.4356	1.2099	2.7775	0.0483
NM_013724	Nrk	1.3160	0.4878	0.7320	2.7663	1.8991	2.3778	0.8453	2.3477	2.7774	0.0129
NR_007933	Eno3	12.3703	4.3351	5.5509	23.9999	15.9976	21.7851	7.4188	20.5942	2.7760	0.0189
NM_001276285	Eno3	13.1994	4.6257	5.9230	25.6085	17.0698	23.2453	7.9160	21.9745	2.7760	0.0189
NM_001136062	Eno3	13.3064	4.6632	5.9710	25.8161	17.2082	23.4337	7.9802	22.1527	2.7760	0.0189
NM_001159570	Meis2	0.6676	0.1614	0.3875	1.3968	0.7330	1.1952	0.4055	1.1083	2.7334	0.0455
NM_001159569	Meis2	0.6648	0.1607	0.3858	1.3910	0.7299	1.1902	0.4038	1.1037	2.7334	0.0455
NM_011324	Scnn1a	0.5796	0.7234	0.3158	0.8931	1.7922	1.7394	0.5396	1.4749	2.7334	0.0411
NR_024325	9130024F11Rik	0.1554	0.0926	0.1111	0.2578	0.3153	0.3917	0.1197	0.3216	2.6872	0.0093
NR_011542	Tcea3	0.1161	0.3690	0.4429	0.7708	0.9426	0.6831	0.3093	0.7988	2.5825	0.0173
NM_001195760	S100a2	3.6776	2.1910	0.4383	6.1029	4.1462	5.7948	2.1023	5.3480	2.5439	0.0437
NM_001289498	Egflam	0.3559	1.2485	1.2725	1.7962	2.9422	2.3675	0.9589	2.3686	2.4701	0.0345
NM_001289496	Egflam	0.3555	1.2472	1.2712	1.7944	2.9392	2.3651	0.9580	2.3662	2.4701	0.0345
NM_178748	Egflam	0.3572	1.2534	1.2775	1.8032	2.9537	2.3768	0.9627	2.3779	2.4701	0.0345

NM_172922	Ankk1	0.4852	0.2569	0.1028	0.6710	0.8266	0.5890	0.2817	0.6955	2.4694	0.0343
NM_176957	Nckap5	0.0000	0.1163	0.1397	0.2025	0.2202	0.2051	0.0853	0.2093	2.4525	0.0466
NR_029741	Mir24-2	1.3533	2.1500	6.4523	8.9832	8.5443	6.8238	3.3185	8.1171	2.4460	0.0489
NR_002455	Snord34	4.3880	5.2284	4.1842	10.9228	9.8944	12.9066	4.6002	11.2413	2.4436	0.0021
NM_001201330	5730507C01Rik	0.2848	0.0905	0.1086	0.3781	0.4624	0.3351	0.1613	0.3919	2.4292	0.0334
NM_001033157	5730507C01Rik	0.2931	0.0931	0.1118	0.3892	0.4759	0.3449	0.1660	0.4033	2.4292	0.0334
NM_001159697	Efcc1	0.2630	0.3343	0.1505	0.6110	0.6167	0.5746	0.2492	0.6008	2.4105	0.0031
NR_038016	Gm16998	0.7064	0.2806	0.4490	1.0745	1.1680	1.1872	0.4787	1.1433	2.3885	0.0067
NR_040534	Gm10548	0.0551	0.1313	0.0525	0.1371	0.1987	0.2314	0.0796	0.1891	2.3749	0.0444
NM_201531	Kcnf1	0.3024	0.1921	0.2595	0.6523	0.4636	0.6607	0.2513	0.5922	2.3562	0.0090
NM_011430	Sncg	63.5005	22.4709	45.0832	113.0926	78.1496	113.0463	43.6848	101.4295	2.3218	0.0255
NM_023814	Tbx18	0.1857	0.3196	0.1476	0.3338	0.6141	0.5202	0.2176	0.4894	2.2488	0.0494
NM_001164524	Serpinb9c	0.2270	0.4207	0.5050	0.8161	0.8188	0.9537	0.3842	0.8629	2.2458	0.0070
NM_175140	Chst8	0.2416	0.4319	0.4032	1.0025	0.6538	0.7615	0.3589	0.8060	2.2455	0.0198
NR_028537	Snord99	5.1716	6.1621	7.3971	15.0188	13.9935	13.0383	6.2436	14.0169	2.2450	0.0008
NM_177914	Dgkk	1.8665	2.2409	1.8405	4.3822	3.7688	5.1871	1.9826	4.4460	2.2425	0.0046
NM_023755	Tfcpl2l1	0.2343	0.5708	0.7597	1.1147	1.2962	1.0896	0.5216	1.1668	2.2371	0.0180
NR_027772	Airn	0.7012	1.1141	1.0030	2.3274	1.8974	2.0626	0.9394	2.0958	2.2309	0.0028
NM_001081328	Chsy3	0.4476	0.6222	0.5335	1.2071	1.1775	1.1912	0.5345	1.1919	2.2302	0.0002
NM_001081349	Slc43a1	0.3422	0.2265	0.2175	0.5205	0.4630	0.7669	0.2621	0.5835	2.2262	0.0340
NM_001039042	Klk13	0.8411	0.3341	0.4010	0.9305	1.1379	1.4136	0.5254	1.1607	2.2092	0.0400
NM_008985	Ptprn	4.6288	2.6031	3.7498	5.6082	8.8672	9.7766	3.6606	8.0840	2.2084	0.0338
NM_011453	Serpinb9c	0.2305	0.4272	0.5128	0.7649	0.8314	0.9684	0.3901	0.8549	2.1914	0.0107
NM_172855	Galnt5	0.0446	0.1063	0.1276	0.1850	0.1609	0.2623	0.0928	0.2028	2.1845	0.0494
NR_033304	Lypd6	0.0396	0.0629	0.0377	0.0985	0.1071	0.0997	0.0467	0.1018	2.1783	0.0030
NM_177139	Lypd6	0.0414	0.0658	0.0395	0.1031	0.1121	0.1045	0.0489	0.1066	2.1783	0.0030
NM_001085509	Myom3	0.0260	0.0206	0.0248	0.0646	0.0468	0.0436	0.0238	0.0517	2.1740	0.0143
NM_001163064	AU041133	0.3299	0.3930	0.3670	0.6842	0.9917	0.6930	0.3633	0.7896	2.1737	0.0142
NM_001282148	Gm15816	0.0853	0.2033	0.0814	0.2832	0.2309	0.2868	0.1233	0.2670	2.1644	0.0308
NR_028122	2310001K24Rik	0.9464	0.7518	0.3008	1.3088	1.4227	1.5907	0.6664	1.4408	2.1622	0.0204
NM_001171187	Mal	11.2071	5.4208	7.6711	22.8793	13.2107	16.3187	8.0996	17.4696	2.1568	0.0473
NM_010762	Mal	10.5294	5.1757	7.2071	21.5821	12.4588	15.3318	7.6374	16.4576	2.1549	0.0472
NM_024474	Col26a1	0.1606	0.1276	0.1021	0.2221	0.3380	0.2699	0.1301	0.2767	2.1268	0.0176
NR_035422	Mir1191	6.0335	2.3964	8.6299	12.5157	13.6048	10.1409	5.6866	12.0871	2.1255	0.0369
NM_027268	Scrn1	1.2223	0.5826	0.8547	2.2989	1.3965	1.9175	0.8865	1.8709	2.1104	0.0373
NM_053141	Pcdhb16	0.1649	0.1746	0.2620	0.5472	0.4213	0.3002	0.2005	0.4229	2.1092	0.0458
NM_001083809	Slc43a1	0.3506	0.2321	0.2229	0.5334	0.4217	0.7366	0.2685	0.5639	2.0998	0.0430
NM_024497	Slc43a1	0.3565	0.2360	0.2266	0.5423	0.4287	0.7490	0.2731	0.5734	2.0998	0.0430
NM_030028	Tmem190	0.9901	1.1798	2.1243	2.8754	2.6791	3.3283	1.4314	2.9609	2.0686	0.0187
NM_053146	Pcdhb21	0.0534	0.0848	0.1527	0.1772	0.1926	0.2244	0.0970	0.1981	2.0422	0.0357
NM_007855	Twist2	3.2007	3.2439	3.9992	6.9599	6.7692	7.5129	3.4813	7.0807	2.0339	0.0005
NM_001256224	Wnt5a	8.0339	3.2063	5.2182	9.2746	11.3068	12.6225	5.4861	11.0680	2.0174	0.0307
NM_001159652	Gpr62	0.3655	0.5226	0.1394	0.6672	0.7912	0.6143	0.3425	0.6909	2.0172	0.0472
NR_028573	Snora24	4.4555	2.6544	8.4972	10.1666	10.0466	11.2330	5.2024	10.4821	2.0149	0.0405
NM_001286404	Ghrl	0.5712	0.2269	0.5447	0.7110	1.0304	0.9601	0.4476	0.9005	2.0118	0.0370
NM_009524	Wnt5a	7.1837	2.8532	4.5984	8.2234	10.0189	11.1797	4.8784	9.8074	2.0104	0.0318
NM_212487	Krt78	0.2530	0.1675	0.1608	0.3849	0.4184	0.3544	0.1938	0.3859	1.9913	0.0053
NM_178793	Ccbe1	23.4784	13.4818	13.2260	37.2881	28.2730	34.0362	16.7287	33.1991	1.9846	0.0184
NM_016719	Grb14	9.2162	3.8654	4.7104	13.1529	9.7755	12.2682	5.9307	11.7322	1.9782	0.0406
NM_198052	Tbx3	1.7278	1.0836	1.1562	2.4397	2.9528	2.2672	1.3225	2.5532	1.9306	0.0132
NM_001291483	Mdk	2.3738	2.2628	4.3763	5.9090	5.4241	5.9848	3.0043	5.7726	1.9215	0.0175
NM_001291455	Dpysl3	11.7238	12.3751	14.5280	32.6229	21.0294	20.4150	12.8756	24.6891	1.9175	0.0437
NM_015775	Tmprss2	1.3743	4.1847	3.9751	5.1694	6.9414	6.1596	3.1780	6.0901	1.9163	0.0487
NM_011535	Tbx3	1.7785	1.1153	1.1901	2.5112	2.9549	2.3337	1.3613	2.5999	1.9099	0.0114
NM_001136086	Dpysl3	12.0071	12.7245	14.9845	32.9875	21.6845	20.9483	13.2387	25.2068	1.9040	0.0402
NM_009468	Dpysl3	11.6058	12.3416	14.5346	31.9070	21.0079	20.2706	12.8273	24.3952	1.9018	0.0402
NR_027924	2010204K13Rik	1.7531	1.3926	1.5045	2.6183	3.0043	3.0938	1.5500	2.9055	1.8744	0.0017
NM_001001650	Prss48	0.1526	0.1212	0.1455	0.2532	0.2752	0.2565	0.1398	0.2616	1.8720	0.0005
NM_138661	Pcdha9	0.1898	0.2369	0.1551	0.4499	0.2690	0.3645	0.1939	0.3612	1.8622	0.0435
NM_010784	Mdk	2.2857	1.9224	3.9744	5.3549	4.7295	5.0846	2.7275	5.0563	1.8538	0.0240
NM_001039543	Mlf1	1.9956	3.2695	1.4272	4.1396	4.3873	3.8782	2.2307	4.1350	1.8536	0.0279
NM_007796	Ctla2a	33.1163	17.5932	22.2254	43.8423	37.8596	53.3561	24.3116	45.0193	1.8518	0.0325
NM_001145799	Ctla2a	34.0590	18.0939	22.8580	45.0002	38.9372	54.8749	25.0036	46.2708	1.8506	0.0327
NR_027925	2010204K13Rik	2.6376	2.0952	2.2636	3.7205	4.5201	4.6548	2.3321	4.2985	1.8432	0.0041
NM_175654	Hist1h4d	1.5740	1.8754	1.1256	2.9385	2.8393	2.6455	1.5250	2.8077	1.8411	0.0054

NM_010801	Mlf1	2.0761	3.4013	1.4847	4.3065	4.4472	4.0346	2.3207	4.2627	1.8368	0.0285
NM_011836	Lamc3	0.5616	1.2026	0.9547	1.5804	1.9822	1.4160	0.9063	1.6595	1.8311	0.0400
NM_138663	Pcdha12	0.1929	0.2408	0.1577	0.4116	0.2983	0.3706	0.1971	0.3602	1.8269	0.0164
NM_001012335	Mdk	2.8037	2.3582	4.8752	6.5686	5.6527	6.0984	3.3457	6.1066	1.8252	0.0281
NR_027290	Uckl1os	0.9328	1.2540	0.6158	1.5480	1.8769	1.6885	0.9342	1.7045	1.8245	0.0206
NM_001204931	Reep6	0.4490	0.7133	0.9277	1.1177	1.4849	1.1949	0.6967	1.2658	1.8170	0.0329
NM_001291481	Mdk	3.1359	2.6375	5.4528	7.1937	6.3223	6.8209	3.7421	6.7790	1.8116	0.0283
NM_001291482	Mdk	3.0848	2.5946	5.3640	7.0765	6.2193	6.7098	3.6811	6.6686	1.8116	0.0283
NM_001012336	Mdk	2.8134	2.3662	4.8919	6.4538	5.6720	6.1193	3.3572	6.0817	1.8116	0.0283
NM_008398	Itga7	3.6742	2.8900	2.2326	5.0810	4.4185	6.1451	2.9322	5.2149	1.7785	0.0250
NM_001037918	Lipt1	0.5587	1.0356	1.1544	1.6999	1.5118	1.6434	0.9162	1.6184	1.7663	0.0210
NM_030139	Zfp449	0.3099	0.1846	0.2586	0.3857	0.4193	0.5209	0.2510	0.4420	1.7605	0.0249
NM_139292	Reep6	0.4310	0.6847	0.9589	1.0728	1.4253	1.1469	0.6915	1.2150	1.7570	0.0484
NM_001252347	Rundc3a	3.7081	2.6056	2.4479	5.4040	5.2311	4.7142	2.9205	5.1164	1.7519	0.0080
NR_102374	Dmr	2.1453	2.0449	2.4547	2.8480	4.6438	4.1465	2.2150	3.8794	1.7515	0.0388
NM_016759	Rundc3a	4.6481	3.2188	3.0116	6.6256	6.5572	5.8592	3.6262	6.3473	1.7504	0.0088
NM_009960	Pcdha11	0.1929	0.2408	0.1577	0.4116	0.2734	0.3474	0.1971	0.3442	1.7458	0.0344
NM_198884	B4galnt3	1.6138	1.1266	1.8187	2.7999	2.5142	2.5892	1.5197	2.6344	1.7335	0.0074
NM_021488	Ghrl	0.5190	0.4123	0.4949	0.6460	0.9362	0.8723	0.4754	0.8182	1.7210	0.0217
NM_009957	Pcdha7	0.1944	0.2426	0.1589	0.4147	0.2755	0.3267	0.1986	0.3390	1.7066	0.0414
NM_001003671	Pcdhac1	0.1914	0.2389	0.1564	0.4084	0.2713	0.3217	0.1956	0.3338	1.7066	0.0414
NM_138662	Pcdha3	0.1938	0.2419	0.1584	0.4135	0.2747	0.3258	0.1980	0.3380	1.7066	0.0414
NM_198117	Pcdha2	0.1890	0.2359	0.1545	0.4032	0.2678	0.3176	0.1931	0.3295	1.7066	0.0414
NM_054072	Pcdha1	0.1931	0.2411	0.1579	0.4121	0.2738	0.3246	0.1974	0.3368	1.7066	0.0414
NM_007767	Pcdha6	0.1934	0.2414	0.1580	0.4126	0.2741	0.3250	0.1976	0.3372	1.7066	0.0414
NM_007766	Pcdha4	0.1905	0.2377	0.1557	0.4064	0.2699	0.3201	0.1946	0.3321	1.7066	0.0414
NR_030432	Mir761	11.4320	9.0810	5.4505	15.8093	15.4665	12.8096	8.6545	14.6951	1.6980	0.0381
NM_001033346	Lrrc55	0.2497	0.1983	0.3809	0.4972	0.4504	0.4196	0.2763	0.4557	1.6494	0.0381
NM_177391	Fam109b	0.4748	0.4190	0.4527	0.7003	0.8089	0.7093	0.4488	0.7395	1.6476	0.0016
NM_009181	St8sia2	4.5529	4.5154	3.0056	6.5496	6.0747	7.1090	4.0247	6.5778	1.6344	0.0124
NM_175223	Dnali1	0.3471	0.4411	0.5957	0.6336	0.7513	0.8751	0.4613	0.7533	1.6330	0.0440
NM_172824	Ccdc14	0.5641	0.5601	0.5043	0.9069	0.8268	0.8593	0.5429	0.8643	1.5922	0.0004
NM_010636	Klf12	1.6415	1.2437	1.5652	2.4726	2.0272	2.5467	1.4835	2.3488	1.5833	0.0130
NR_045182	4932702P03Rik	2.0986	2.0004	2.2013	3.1344	3.0285	3.7036	2.1001	3.2889	1.5660	0.0055
NM_028448	Cenpv	6.5820	3.7823	4.9409	7.4368	7.3261	9.1798	5.1017	7.9809	1.5643	0.0464
NM_001286347	Eml1	2.6479	3.9664	4.9778	6.0578	5.9025	6.0400	3.8640	6.0001	1.5528	0.0342
NM_001043335	Eml1	2.4366	3.6499	4.5805	5.5743	5.4315	5.5580	3.5557	5.5213	1.5528	0.0342
NM_001286346	Eml1	2.5898	3.8793	4.8684	5.9246	5.7728	5.9073	3.7791	5.8683	1.5528	0.0342
NM_001043336	Eml1	2.6837	4.0200	5.0450	6.1395	5.9822	6.1216	3.9162	6.0811	1.5528	0.0342
NM_001081099	Chc1	0.9122	0.9057	0.6523	1.0407	1.3369	1.4373	0.8234	1.2716	1.5444	0.0378
NM_153596	Tmem17	0.6342	0.8396	0.7055	0.8770	1.2393	1.2436	0.7264	1.1200	1.5417	0.0440
NM_001162909	Spaca6	2.8908	3.4445	3.1325	4.2522	5.8073	4.5275	3.1559	4.8623	1.5407	0.0279
NM_172614	Tmem44	0.6146	0.4882	0.5860	0.7366	0.8315	1.0330	0.5629	0.8670	1.5402	0.0333
NM_029264	Ttll10	0.5649	0.5485	0.6584	0.8854	0.8492	0.9495	0.5906	0.8947	1.5149	0.0025
NM_001048179	Ccl27a	2.7510	2.9799	3.3387	5.3954	3.6091	4.6238	3.0232	4.5428	1.5026	0.0493
NR_038028	B230208H11Rik	0.9308	1.1619	1.0144	0.5517	0.5997	0.8940	1.0357	0.6818	0.6583	0.0490
NR_110421	Eldr	0.5653	0.5132	0.5391	0.3351	0.4371	0.2715	0.5392	0.3479	0.6451	0.0193
NM_146016	Eml6	0.3943	0.3701	0.4272	0.3123	0.2748	0.1807	0.3972	0.2559	0.6443	0.0292
NM_019925	Gpr132	29.5665	30.2302	25.2494	22.3651	17.4570	14.7187	28.3487	18.1802	0.6413	0.0203
NM_007825	Cyp7b1	4.4123	3.0801	4.0161	2.2743	3.0149	2.0787	3.8362	2.4560	0.6402	0.0472
NM_001206390	Hk3	5.1631	6.6836	6.7011	4.6410	3.7944	3.3747	6.1826	3.9367	0.6367	0.0236
NM_001206391	Hk3	5.4039	6.9953	7.0137	4.8160	3.9714	3.5322	6.4710	4.1065	0.6346	0.0224
NM_027279	Mettl18	1.6884	1.8145	1.5153	1.0713	1.3437	0.7512	1.6727	1.0554	0.6309	0.0324
NM_009326	Tcea2	1.4941	1.2858	1.7809	0.8265	0.8984	1.1510	1.5203	0.9586	0.6306	0.0321
NM_001033245	Hk3	4.8133	6.3248	6.3914	4.3298	3.5299	3.1755	5.8432	3.6784	0.6295	0.0248
NM_001206392	Hk3	4.8595	6.4955	6.6388	4.3811	3.6244	3.2985	5.9980	3.7680	0.6282	0.0271
NM_001301094	Olr1	7.3686	9.0253	9.4289	7.2579	4.2449	4.4346	8.6076	5.3125	0.6172	0.0469
NM_001301096	Olr1	7.3780	9.1036	9.2866	7.1421	4.3033	4.3815	8.5894	5.2756	0.6142	0.0410
NM_001289708	Clec2i	1.5460	2.0979	1.4127	0.9621	0.9296	1.1909	1.6855	1.0275	0.6096	0.0432
NM_001123371	Pnp2	1.1840	0.9405	0.9032	0.4912	0.6407	0.6965	1.0092	0.6095	0.6039	0.0204
NM_009109	Ryr1	0.3205	0.3369	0.3146	0.2034	0.2466	0.1347	0.3240	0.1949	0.6014	0.0178
NM_001081124	Map7d2	0.1879	0.2089	0.2508	0.1559	0.1356	0.0947	0.2159	0.1287	0.5963	0.0278
NM_027948	1700003E16Rik	0.2825	0.2244	0.2021	0.1172	0.1274	0.1781	0.2364	0.1409	0.5962	0.0352
NM_029525	Prex2	0.2882	0.2810	0.3248	0.2174	0.1063	0.2092	0.2980	0.1776	0.5961	0.0345
NM_009042	Reg1	2.0713	1.9445	2.8729	1.2499	1.3587	1.4242	2.2963	1.3443	0.5854	0.0321

NM_177897	B4galnt4	0.8394	0.9632	1.0228	0.3483	0.7151	0.5879	0.9418	0.5504	0.5844	0.0313
NM_183312	Synm	0.3529	0.3059	0.3060	0.1864	0.2605	0.1079	0.3216	0.1849	0.5749	0.0431
NM_028518	Col20a1	0.3111	0.3844	0.3955	0.1721	0.2494	0.2034	0.3637	0.2083	0.5727	0.0110
NM_008598	Mgmt	9.5476	8.7077	8.7669	4.2544	5.1030	5.9434	9.0074	5.1003	0.5662	0.0022
NR_045821	6330418K02Rik	1.9542	2.1732	2.4224	1.1350	1.4101	1.1496	2.1833	1.2316	0.5641	0.0042
NR_028264	Dleu2	2.6499	3.8704	3.9125	2.2697	2.2359	1.3649	3.4776	1.9568	0.5627	0.0404
NR_045889	Gm10791	1.3132	1.8081	1.8366	0.7991	1.1055	0.8829	1.6527	0.9291	0.5622	0.0200
NM_010229	Flt3	0.5149	0.4405	0.6421	0.2629	0.2858	0.3329	0.5325	0.2939	0.5519	0.0187
NM_172776	Slc22a29	0.4591	0.4689	0.5003	0.2177	0.2366	0.3307	0.4761	0.2617	0.5496	0.0044
NR_105958	Mir6992	9.2994	6.3317	7.6007	3.3069	4.7929	4.4657	7.7439	4.1885	0.5409	0.0215
NR_027388	1700096K18Rik	0.3997	0.3175	0.3812	0.2488	0.0901	0.2519	0.3661	0.1969	0.5379	0.0454
NM_013566	Itgb7	3.7365	3.4843	3.4081	2.1568	1.4653	2.0934	3.5430	1.9052	0.5377	0.0025
NM_001099319	Gm12942	3.4326	4.2415	5.2128	1.5823	2.9814	2.3505	4.2956	2.3047	0.5365	0.0383
NM_001290316	Vsig10l	0.6309	0.8018	0.6417	0.3141	0.3035	0.4948	0.6914	0.3708	0.5363	0.0182
NM_001014995	Fam189b	0.7574	1.0529	1.1736	0.7070	0.5123	0.3580	0.9946	0.5258	0.5286	0.0425
NM_177191	Sycp2	0.3055	0.2427	0.2428	0.2113	0.0919	0.1070	0.2637	0.1367	0.5185	0.0418
NM_026793	Myct1	0.6774	0.5381	0.8447	0.4756	0.2350	0.3503	0.6867	0.3536	0.5150	0.0416
NM_011268	Rgs9	0.6990	0.5090	0.8331	0.2900	0.2627	0.4895	0.6804	0.3474	0.5106	0.0479
NM_001085501	Ppp1r3d	1.0223	1.6594	1.5257	0.8482	0.8018	0.4856	1.4025	0.7118	0.5076	0.0373
NR_033457	Gm6225	0.3407	0.2030	0.3249	0.1414	0.1537	0.1432	0.2895	0.1461	0.5045	0.0304
NM_008005	Fgf18	1.1298	0.7479	0.8080	0.3906	0.3397	0.5539	0.8952	0.4280	0.4781	0.0258
NR_102395	Fgf18	1.0963	0.7257	0.7840	0.3790	0.3296	0.5374	0.8687	0.4154	0.4781	0.0258
NM_010612	Kdr	1.0626	0.9074	1.2919	0.8376	0.3594	0.3572	1.0873	0.5181	0.4765	0.0432
NM_023612	Esm1	0.9640	1.2033	1.3132	0.8570	0.5589	0.2315	1.1602	0.5491	0.4733	0.0425
NR_045640	Gm20199	0.2174	0.1727	0.2073	0.0301	0.1307	0.1218	0.1991	0.0942	0.4730	0.0397
NR_106138.1	Mir7676-2	51.3823	70.4997	73.4936	31.0066	35.8114	23.5531	65.1252	30.1237	0.4626	0.0109
NR_106137.1	Mir7676-1	51.3823	70.4997	73.4936	31.0066	35.8114	23.5531	65.1252	30.1237	0.4626	0.0109
NM_019790	Tmeff2	0.3903	0.7234	0.7444	0.2159	0.3129	0.3280	0.6194	0.2856	0.4611	0.0497
NM_133222	Eltd1	1.0933	1.2326	1.4124	0.7901	0.5089	0.4149	1.2461	0.5713	0.4585	0.0098
NM_001081199	Mamdc4	0.2178	0.2595	0.2769	0.0903	0.1637	0.0915	0.2514	0.1152	0.4582	0.0104
NM_001082547	Gm5483	24.1926	18.1033	25.7435	14.8370	7.2735	8.5449	22.6798	10.2185	0.4506	0.0195
NM_008653	Mybpc3	0.2791	0.2217	0.2329	0.1737	0.0944	0.0586	0.2446	0.1089	0.4453	0.0239
NR_046069	Gm2848	0.5927	0.9415	0.7535	0.4917	0.3564	0.1660	0.7626	0.3380	0.4433	0.0372
NR_037959	1600010M07Rik	0.9403	1.1204	1.1208	0.7802	0.4240	0.1976	1.0605	0.4673	0.4406	0.0300
NM_001033636	Prex2	0.3101	0.3167	0.2746	0.1838	0.0799	0.1303	0.3005	0.1313	0.4371	0.0067
NM_133720	Cysltr2	0.4821	0.5745	0.5364	0.4001	0.2174	0.0675	0.5310	0.2283	0.4300	0.0387
NM_001162412	Cysltr2	0.4979	0.5933	0.5539	0.4131	0.2245	0.0697	0.5484	0.2358	0.4300	0.0387
NM_021715	Chst7	0.9896	0.7861	1.2581	0.7116	0.2975	0.2772	1.0112	0.4288	0.4240	0.0416
NM_001033248	Gm266	0.3575	0.5680	0.5682	0.0989	0.2150	0.3005	0.4979	0.2048	0.4113	0.0326
NR_040265	2310001H17Rik	2.6073	3.3456	4.3986	2.3298	0.7236	1.1798	3.4505	1.4111	0.4089	0.0446
NM_001101486	Fam71f2	3.2015	2.3475	3.2876	1.4304	1.3327	0.8278	2.9455	1.1970	0.4064	0.0078
NM_019577	Ccl24	65.1565	81.8298	60.6305	28.8958	29.9918	25.2067	69.2056	28.0314	0.4050	0.0034
NM_181390	Mustn1	1.4738	1.1707	1.2883	0.5095	0.3323	0.7225	1.3110	0.5215	0.3978	0.0053
NM_001267846	Fign	0.0443	0.0234	0.0281	0.0122	0.0133	0.0124	0.0319	0.0126	0.3960	0.0378
NM_001267847	Fign	0.0443	0.0235	0.0282	0.0123	0.0133	0.0124	0.0320	0.0127	0.3960	0.0378
NM_021716	Fign	0.0445	0.0236	0.0283	0.0123	0.0134	0.0125	0.0321	0.0127	0.3960	0.0378
NR_015553	9430076C15Rik	0.3346	0.5316	0.5014	0.1983	0.2156	0.1205	0.4559	0.1782	0.3908	0.0150
NM_001170976	Dbnd1	0.4310	0.3423	0.4109	0.0894	0.0972	0.2716	0.3948	0.1527	0.3869	0.0207
NM_001165965	Fndc7	0.1191	0.1182	0.1703	0.0741	0.0537	0.0250	0.1359	0.0509	0.3749	0.0191
NM_177091	Fndc7	0.1131	0.1123	0.1617	0.0704	0.0510	0.0238	0.1290	0.0484	0.3749	0.0191
NM_009892	Chil3	43.0933	42.6021	36.4263	11.6325	17.4820	15.5771	40.7072	14.8972	0.3660	0.0007
NM_010452	Hoxa3	0.1708	0.2262	0.2715	0.0945	0.0514	0.0957	0.2228	0.0805	0.3614	0.0120
NM_021381	Prokr1	0.1428	0.1418	0.2383	0.0592	0.0644	0.0600	0.1743	0.0612	0.3512	0.0242
NM_080437	Celsr3	0.0878	0.0498	0.1076	0.0312	0.0113	0.0422	0.0817	0.0282	0.3453	0.0496
NM_147218	Abca6	0.1658	0.3074	0.2108	0.0917	0.0748	0.0697	0.2280	0.0787	0.3453	0.0242
NR_040266	2310001H17Rik	3.2400	4.3555	3.5649	2.4816	0.4496	0.8378	3.7201	1.2563	0.3377	0.0251
NR_040268	2310001H17Rik	3.3142	4.4552	3.6465	2.5384	0.4599	0.8570	3.8053	1.2851	0.3377	0.0251
NM_172603	Phf11a	0.4278	0.4248	0.5099	0.2662	0.1929	0.0000	0.4541	0.1530	0.3370	0.0232
NM_001048176	Cerk1	0.3293	0.5231	0.6280	0.1366	0.2228	0.1384	0.4935	0.1659	0.3362	0.0236
NM_001271019	Siglec5	1.5034	2.2451	1.4909	0.8981	0.7051	0.1011	1.7465	0.5681	0.3253	0.0272
NM_145581	Siglec5	1.4423	2.1539	1.4303	0.8616	0.6764	0.0970	1.6755	0.5450	0.3253	0.0272
NM_153101	Mrgpra2b	0.2298	0.3652	0.3288	0.1907	0.1037	0.0000	0.3079	0.0981	0.3187	0.0373
NM_001177471	Gm15056	4.1505	5.4949	6.5961	1.5306	2.0797	1.5502	5.4138	1.7202	0.3177	0.0072
NR_040374	A2300280O5Rik	0.2592	0.2883	0.2966	0.0430	0.0935	0.1307	0.2814	0.0891	0.3166	0.0023
NM_007567	Bsn	0.0273	0.0217	0.0260	0.0075	0.0082	0.0076	0.0250	0.0078	0.3120	0.0006

NM_010225	Foxf2	0.2448	0.1458	0.1167	0.0508	0.0552	0.0514	0.1691	0.0525	0.3103	0.0397
NM_183183	Gprin3	0.2803	0.3339	0.3563	0.0388	0.1685	0.0785	0.3235	0.0953	0.2945	0.0069
NM_009217	Sstr2	0.7562	1.8020	1.0816	0.3137	0.3410	0.3972	1.2132	0.3506	0.2890	0.0497
NR_015489	2900041M22Rik	0.2155	0.3423	0.4109	0.0894	0.0000	0.1811	0.3229	0.0902	0.2792	0.0399
NM_010780	Cma1	8.7475	12.0798	14.1159	7.7048	0.7283	0.4524	11.6477	2.9618	0.2543	0.0378
NM_205810	Mrgprb1	0.2422	0.1374	0.2310	0.0287	0.0624	0.0582	0.2035	0.0498	0.2445	0.0116
NR_024323	4930426L09Rik	0.2923	0.4644	0.2788	0.0000	0.0879	0.1638	0.3452	0.0839	0.2430	0.0266
NM_009464	Ucp3	0.1183	0.2819	0.2256	0.0982	0.0534	0.0000	0.2086	0.0505	0.2421	0.0471
NM_007753	Cpa3	8.9693	12.8246	15.9651	7.3595	0.8989	0.2513	12.5863	2.8366	0.2254	0.0327
NM_013805	Cldn5	0.7158	0.9748	1.0726	0.3394	0.1845	0.0859	0.9211	0.2033	0.2207	0.0052
NM_017385	Ear7	0.6188	0.7373	1.1802	0.2567	0.2791	0.0000	0.8454	0.1786	0.2113	0.0259
NM_053111	Ear6	0.4068	0.4847	0.7757	0.1688	0.1834	0.0000	0.5557	0.1174	0.2113	0.0259
NM_010779	Mcpt4	15.2118	24.1670	26.5000	12.7432	0.9235	0.2458	21.9596	4.6375	0.2112	0.0312
NM_001042606	Sstr2	0.8632	1.9714	0.9260	0.1791	0.2920	0.2720	1.2535	0.2477	0.1976	0.0495
NM_028392	Ppp2r2b	0.2090	0.1660	0.2657	0.0000	0.1256	0.0000	0.2135	0.0419	0.1961	0.0279
NM_021272	Fabp7	0.5701	0.6038	0.5436	0.1577	0.1714	0.0000	0.5725	0.1097	0.1916	0.0013
NM_010781	Tpsb2	10.9136	15.4354	17.8944	7.3990	0.8403	0.2237	14.7478	2.8210	0.1913	0.0178
NR_015543	2810055G20Rik	0.1379	0.1825	0.3067	0.0381	0.0414	0.0386	0.2090	0.0394	0.1885	0.0284
NM_031187	Tpsab1	7.9029	14.2937	16.5788	6.0529	0.8773	0.3065	12.9251	2.4122	0.1866	0.0296
NR_033521	Tpsab1	8.6114	15.5753	18.0652	6.5956	0.9559	0.3340	14.0840	2.6285	0.1866	0.0296
NM_029360	Tm4sf5	0.4456	1.0618	0.8497	0.3697	0.0000	0.0000	0.7857	0.1232	0.1568	0.0388
NM_019779	Cyp11a1	0.3265	0.8429	0.6227	0.0677	0.0736	0.1372	0.5974	0.0928	0.1554	0.0290
NR_034045	Snora30	2.7066	2.1500	2.5809	1.1229	0.0000	0.0000	2.4792	0.3743	0.1510	0.0068
NM_146515	Olf99	0.3155	0.3759	0.3008	0.0000	0.0000	0.1326	0.3307	0.0442	0.1336	0.0045
NM_001242943	Gm14436	0.0719	0.0571	0.1371	0.0000	0.0000	0.0302	0.0887	0.0101	0.1135	0.0415
NM_001242944	Gm14306	0.2236	0.1776	0.4265	0.0000	0.0000	0.0940	0.2759	0.0313	0.1135	0.0415
NM_001285937	Zdbf2	0.0343	0.0364	0.0328	0.0000	0.0000	0.0096	0.0345	0.0032	0.0930	0.0008
NM_001267872	Zdbf2	0.0346	0.0366	0.0330	0.0000	0.0000	0.0097	0.0347	0.0032	0.0930	0.0008
NM_028673	Zdbf2	0.0344	0.0365	0.0328	0.0000	0.0000	0.0096	0.0346	0.0032	0.0930	0.0008
NM_001285936	Zdbf2	0.0342	0.0362	0.0326	0.0000	0.0000	0.0096	0.0343	0.0032	0.0930	0.0008
NM_153508	Clstr3	0.0361	0.0287	0.0345	0.0000	0.0000	0.0000	0.0331	0.0000	0.0000	0.0001
NR_110990	Pla2g10	0.0950	0.0755	0.0906	0.0000	0.0000	0.0000	0.0870	0.0000	0.0000	0.0001
NR_027377	Gm17769	0.0565	0.0449	0.0539	0.0000	0.0000	0.0000	0.0517	0.0000	0.0000	0.0001
NR_033602	Gm5779	0.1597	0.1268	0.1522	0.0000	0.0000	0.0000	0.1462	0.0000	0.0000	0.0001
NM_011987	Pla2g10	0.1016	0.0807	0.0969	0.0000	0.0000	0.0000	0.0931	0.0000	0.0000	0.0001
NR_049190	Mir5617	2.5404	2.0180	2.4224	0.0000	0.0000	0.0000	2.3270	0.0000	0.0000	0.0001
NR_125720	4930445N18Rik	0.1634	0.1298	0.1558	0.0000	0.0000	0.0000	0.1497	0.0000	0.0000	0.0001
NM_008227	Hcn3	0.0444	0.0353	0.0423	0.0000	0.0000	0.0000	0.0407	0.0000	0.0000	0.0001
NR_037986	Gm16880	0.1208	0.0959	0.1152	0.0000	0.0000	0.0000	0.1106	0.0000	0.0000	0.0001
NM_001291009	Pla2g10	0.0963	0.0765	0.0918	0.0000	0.0000	0.0000	0.0882	0.0000	0.0000	0.0001
NM_172430	Sphkap	0.0222	0.0177	0.0212	0.0000	0.0000	0.0000	0.0204	0.0000	0.0000	0.0001
NM_177544	Ang4	0.2084	0.3310	0.1987	0.0000	0.0000	0.0000	0.2460	0.0000	0.0000	0.0045
NM_008954	Pspn	0.3055	0.4853	0.2913	0.0000	0.0000	0.0000	0.3607	0.0000	0.0000	0.0045
NM_001142539	Gm9992	0.0909	0.1444	0.0867	0.0000	0.0000	0.0000	0.1073	0.0000	0.0000	0.0045
NM_001141925	Bean1	0.0912	0.0724	0.1304	0.0000	0.0000	0.0000	0.0980	0.0000	0.0000	0.0046
NM_001141922	Bean1	0.0854	0.0678	0.1222	0.0000	0.0000	0.0000	0.0918	0.0000	0.0000	0.0046
NM_001141924	Bean1	0.0912	0.0725	0.1305	0.0000	0.0000	0.0000	0.0981	0.0000	0.0000	0.0046
NM_176844	Chrna5	0.0529	0.0840	0.1009	0.0000	0.0000	0.0000	0.0793	0.0000	0.0000	0.0049
NM_019991	Prl2a1	0.4993	0.6611	0.3174	0.0000	0.0000	0.0000	0.4926	0.0000	0.0000	0.0077
NR_033550	Gm10248	0.0530	0.1264	0.1012	0.0000	0.0000	0.0000	0.0935	0.0000	0.0000	0.0122
NR_045876	F630206G17Rik	0.0604	0.0480	0.1153	0.0000	0.0000	0.0000	0.0746	0.0000	0.0000	0.0226
NM_001127576	Gm1564	0.0949	0.1005	0.0302	0.0000	0.0000	0.0000	0.0752	0.0000	0.0000	0.0291
NR_038017	Gm15915	0.1595	0.2534	0.4562	0.0000	0.0000	0.0000	0.2897	0.0000	0.0000	0.0297
NR_040445	1700017G19Rik	0.1187	0.0472	0.0566	0.0000	0.0000	0.0000	0.0742	0.0000	0.0000	0.0298
NR_029908	Mir215	2.6091	1.0363	3.7319	0.0000	0.0000	0.0000	2.4591	0.0000	0.0000	0.0347
NM_001290735	Osbpl6	0.1141	0.2719	0.1088	0.0000	0.0000	0.0000	0.1649	0.0000	0.0000	0.0368
NR_037977	Gm53	0.2347	0.5593	0.2238	0.0000	0.0000	0.0000	0.3393	0.0000	0.0000	0.0368
NR_037973	Gm20597	0.0264	0.0629	0.0252	0.0000	0.0000	0.0000	0.0382	0.0000	0.0000	0.0368

Supplementary References

1. Xu Y, *et al.* (2017) Breast tumor cell-specific knockout of Twist1 inhibits cancer cell plasticity, dissemination, and lung metastasis in mice. *Proc Natl Acad Sci U S A* 114(43):11494-11499.
2. Lee DK, Liu Y, Liao L, Wang F, & Xu J (2014) The prostate basal cell (BC) heterogeneity and the p63-positive BC differentiation spectrum in mice. *Int J Biol Sci* 10(9):1007-1017.
3. Li LC & Dahiya R (2002) MethPrimer: designing primers for methylation PCRs. *Bioinformatics* 18(11):1427-1431.
4. Liao Y, Smyth GK, & Shi W (2014) featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. *Bioinformatics* 30(7):923-930.
5. Love MI, Huber W, & Anders S (2014) Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biol* 15(12):550.
6. Huang da W, Sherman BT, & Lempicki RA (2009) Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. *Nat Protoc* 4(1):44-57.