**SUPPLEMENTARY MATERIALS AND METHODS**

***Isolation of hASC and mature adipocytes from adipose tissue***

A total of 3 abdominal and 3 breast fat samples were used in this work. Adipose tissues from abdominal or mammary fat were washed X 4 with PBS, digested with collagenase 1A 1g/L HANK´S solution with 1% BSA for 1 hour at 37ºC, and centrifuged at 1500 rpm for 5 minutes. Floating mature adipocytes and pelleted hASC were separated, washed with PBS, filtered by a 100 µm diameter membrane and cultured separately in DMEM plus 10% FBS. hASC were used between passage 5-10 and prior characterization by flow cytometry as in (1).

Abdominal fat samples were obtained from three women who underwent liposuction plastic surgery. Donor ages and BMI are as follows: 38 years old, BMI 28.5; 26 years old, BMI 32.7; and 33 years old, BMI 31.3. Breast fat samples were obtained from distant sites within the breast at the time of simple mastectomy for breast cancer. Donor ages and BMI are as follows: 62 years old, BMI 31.2; 63 years old, BMI 26.5; and 59 years old, BMI 33.1.

***Co-culture of adipose cells with cancer cells***

For co-culture, GFP-tagged malignant mammary epithelial cells (4 x 104/well in 6 well plates) were seeded onto adherent hASC, HMF, CAF23 or immature adipocytes. For mature adipocyte co-culture, adipocytes were suspended overtop adherent GFP-tagged malignant mammary epithelial cells (104/well in 6 well plates) in 2 ml media. After 7 days, epithelial and adipose cells were flow sorted. For transwell assays, immature adipocytes were differentiated and malignant mammary epithelial cells (104/well in 6 well plates) were seeded onto the upper chamber of a 3 µm diameter pore membrane transwell (BD Biosciences) and maintained in culture for 1 week.

***RNA isolation and real-time PCR***

RNA was isolated by QIAGEN miRNeasy mini kit from adipose cells and from malignant breast monocultures or after cell separation by FACS based on GFP expression from immature adipocytes co-cultures at day 7. cDNA was synthesized from the isolated RNA using iScript cDNA synthesis kit (Bio-Rad) for cytokines and ES-TFs expression studies, or NCode miRNA First-Strand cDNA synthesis kit (Invitrogen) for miR302b measurement, as indicated by manufacturer. QPCR was performed with a Bio-Rad iCYCLER using an iQ SYBR Green Supermix (Bio-Rad). See Supplementary Table S1 for details on primer sequences.

***Mammosphere assays***

Malignant mammary epithelial cells grown for 7 days as monoculture, co-cultured with immature adipocytes or in presence of indicated cytokines were isolated, resuspended in a single cell suspension and seeded in ultra low adhesion plates as in (2). Mammospheres >75µM were counted after 10-14 days and graphed as mean +/- SEM/number of cells seeded. For serial sphere assays, primary spheres were recovered after 7-14 days, gently trypsinized, counted and re-seeded without cytokine for two additional passages to generate secondary and tertiary spheres. To test Src inhibitor effects on sphere assay 1 µM AZD0530 (saracatinib) was added to the cultures at day 5 and cells were maintained for 48 hours more in presence of this drug prior performing the mammosphere assays.

***Colony formation assays***

MDA-MB-231 cells were mixed with soft agar at 103 cell/ml/well in 24 well plates +/- cytokines. Treatment with Src inhibitor was performed adding +/- PP1 1µM to the media for 1 hr at 37 0C before addition of cytokines. Medium was supplemented twice/week with fresh cytokine +/- drug inhibitor. Colonies were counted at 3 weeks.

***ALDH1 activity***

Flow cytometry for ALDH1 activity was assayed +/- 7 days of cytokine exposure using Aldefluor assay (STEMCELL Technologies) as in (3). Cells were analyzed by flow cytometry using a LSR Fortessa cytometer and FACSDiva software (BD Biosciences).

***Cell cycle analysis***

Cell cycle distribution was assayed after 48 hrs of cytokine or kinase inhibitor-treatment as in (4). Flow cytometry analysis was performed using a LSR Fortessa cytometer and FACSDiva software (BD Biosciences).

***Western blots***

Cells were treated with Src inhibitor PP1 (1µM) added 20 min prior to cytokine treatment. Cells were lysed after 2 hours for total and phosphorylated Src, 12 hours for SOX2, c-MYC and OCT4 or 18 hours for NANOG and KLF4 with RIPA Buffer (Cell Signaling) supplemented with 1x Protease and Phosphatase inhibitor cocktails (GBiosciences). All antibodies were purchased from Cell Signaling, Inc.

***Invasion assays***

Cells (105) were seeded in the upper chamber of a 1% gelatin-coated transwell membrane (Corning). At 15 h, cells were fixed in 90% ethanol (10 min) and stained with 1% crystal violet (10 min). Cells in the lower chamber were eluted with 10% acetic acid for 10 min and cell number was determined by OD at 595 nm.

***Lentivirus transfections***

Briefly, the lentiviral plasmids and viral packaging mix (System Biosciences) were co-transfected into 293T cells using lipofectamine transfection reagent (Invitrogen). Viral particles produced from 293T cells were collected and used to infect different malignant mammary epithelial cells. After viral infection, GFP+ cells were selected for stable integration of the transfects by FACS.

***miRNA Analysis***

MDA-MB-231 cells were treated with cytokines IL6, CCL5 or IP10 at 10ng/ml media for 7 days prior to harvesting of RNA for miRNA profiling. RNA quality was verified by Nanodrop 8000 Spectrophotometer (Thermo Scientific, Wilmington) and RNA integrity and the small RNA fraction assayed by a Bioanalyzer 2100 (Agilent, Santa Clara). Assays were performed by the UMSCCC Oncogenomics Core using mirCURY LNA Universal RT microRNA human Panel I+II (version 2.0). 20ng of total RNA per panel was reverse transcribed using miRCURY LNA™ Universal RT microRNA PCR, Polyadenylation and cDNA synthesis kit (Exiqon, Woburn, MA) per manufacturer’s instructions. cDNA was diluted, combined with SYBR Green Master Mix (Exiqon) and added to the Ready-to-Use PCR Panels. Human microRNA Ready-to-Use PCR Panels I and II hold 742 different miRNA targets and 6 reference gene assays (mirBase 13). The real-time PCR reactions were run according to the manufacturer’s instructions on an Applied Biosystems 7900HT real-time PCR instrument. The data was analyzed using Real Time Statminer (Integromics, Philadelphia, PA) and normalized using the global mean method and GeNorm (5;6).

**SUPPLEMENTAL REFERENCES**

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 (6) Mestdagh P, Van VP, De WA, Muth D, Westermann F, Speleman F, et al. A novel and universal method for microRNA RT-qPCR data normalization. Genome Biol 2009;10(6):R64.