**Supplemental Methods and References**

**Syngeneic mouse models**

A-FABP deficient mice did not display any obvious phenotypic alterations regarding overall health, body weights, adipocyte size and fat composition (1), nor did they develop spontaneous tumors. Mouse E0771 cells were from CH3 BioSystems. MC38 and MMT060562 (MMT) cells were kindly provided by Dr. Jun Yan (University of Louisville, Louisville, KY). All cells were cultured under the same conditions as described previously (2). For syngeneic mouse models, mouse mammary tumor cells, including E0771 and MMT, were orthotopically implanted into the mammary fat pad of 6- to 8-week-old WT and A-FABP-/- mice. Mouse colon cancer MC38 cells were injected subcutaneously in the flanks of mice. Tumors size was measured as previously reported (2). For dynamic macrophage phenotypic analysis, E0771 bearing-mice were sacrificed on day 3, 12 and 24, respectively, and tumors, peripheral blood and spleens were removed for experiments. For macrophage depletion assays, female WT and A-FABP-/- mice were intraperitoneally injected with 100μl liposome/clodronates or control liposomes (FormuMax Scientific, Inc.) on day 0, 7 and 14. E0771 tumors cells (5×105) were orthotopically injected on day 10 and were monitored for tumor growth for 3 weeks. To analyze the phenotype and function of infiltrated immune cells in tumors, we minced the tumor mass and digested them in RPMI-1640 supplemented with 0.5mg/ml collagenase A, 0.2mg/ml type V, hyaluronidase, and 0.02 mg/mL DNase I. For adipocyte separation, subcutaneous adipose tissues were minced and digested in DMEM (Life Technologies) supplemented with 1mg/ml collagenase (Sigma) and 1% BSA for 30min at 37°C. After filtration through a 150µm screen, adipocytes were separated from the medium containing stroma-vascular fraction through centrifugation. Single cells from tumors or adipose tissues were collected for further analyses.

**Prognostic survival and gene expression analysis**

For analyzing the association of FABPs with the overall survival of breast cancer patients, we performed the analysis using PROGgene, an online tool to investigate prognostic implications of interesting genes in cancers (3). We used the TCGA breast cancer datasets and created the overall survival curve by providing the information, such as target gene name, selected cancer type, survival measurements, bifurcate gene expression, etc. For analyzing the expression of FABPs in the stroma of breast cancer tissues, we performed gene expression analysis using publicly assessable microarray data provided by Oncomine.org. Specifically, we analyzed FABPs expression in Finak breast database (GSE9014) by comparing normal tissues with invasive breast carcinoma (4). Survival was based on the expression of FABP family members and samples in the top 50% levels of each FABP member were defined as high expressers.

**Culture of macrophages**

For bone-marrow derived macrophages, the bone marrow collected from WT and A-FABP-/- mice was cultured in RPMI-1640 with 10ng/ml of M-CSF (Cell signaling technology) for 2 hours. Non-adherent cells were plated in RPMI 1640 containing 25% filtered supernatant of L929 fibroblasts with 10ng/ml M-CSF in low-attach plates (Corning). Cells were harvested on day 7 for further applications. In some experiments, CD11b+F4/80+ primary macrophages directly separated from the peripheral blood, the spleen or tumors using a flow sorter, or immortalized A-FABP+ and A-FABP- macrophage cell lines established as previously described (5, 6) , were used for phenotypic and functional assays.

**Macrophage transfection assays**

The siRNA oligos for NFκB were synthesized by Integrated DNA Technologies. The shRNAs against A-FABP(TRCN0000105185, TRCN0000059619, V2LHS\_131701) and their scrambled constructs (pLKO.1 or pGIPZ) were purchased from BMGC RNAi (University of Minnesota). The synthetic miR-29b and its scramble oligos were obtained from Dharmacon (GE Healthcare). WT and A-FABP-/- macrophage cell lines (1×106 cells/wells) were seeded into 6-well plates overnight before transfection. The NFκB siRNA oligos (100 nM) or A-FABP shRNA vectors (2 µg) and their respective controls were introduced into cells using Lipofectamine™ RNAiMAX or Lipofectamine™ 2000 (13778-150, 11668-019, Life Technologies) as our previous study (7). See detailed sequence information in the supplementary Table 1.

**Confocal microscopy**

Human breast tissues were collected in conjunction with a required surgery procedure. The collected tissues were embedded in optimal cutting temperature compound and stored at -80ºC. Frozen tissues were cut into 6-8µm thick sections and stained with hematoxylin and eosin (H&E). For fluorescent immunohistochemistry (IHC) staining, the sections were fixed with 4% paraformaldehyde buffer. After washing and blocking with 2.5% horse serum, the sections were then incubated with diluted primary antibodies over night at 4ºC. After incubating with secondary antibodies and DAPI, sections were visualized with confocal microscope (Nikon Instruments A1+ Confocal Microscopes). Anti-A-FABP antibody (Cat# MAB3150) was from R&D system. Anti-CD163 antibody (Cat# 326508) was from Biolegend. Anti-F4/80 antibody (Cat# ab100790) was from Abcam.

**miRNA microarray**

A total of 1×106 WT and A-FABP-/- macrophages were cocultured with 2×106 E0771 cells in a transwell plate for 24 hours, respectively. Total RNA was extracted from tumor-stimulated macrophages using miRNA isolation kit (Qiagen). 1µg of total RNA was labeled using the Genisphere FlashTag Biotin HSR kit (Hatfield, PA) and incubated with ATP and Poly A polymerase to add a polyA tail. A ligation reaction was then performed to attach to the miRNA population a multiple-biotin molecule containing a 3 DNA dendrimer. Labeled samples were processed according to the manufacturer’s instructions for the Affymetrix miRNA Array 4.0 (Santa Clara, CA) at the Mayo Clinic genome analysis core. The expression profiling data were submitted to the Gene Expression Omnibus (accession number: GSE109703).

**Colony formation assay**

1×103 E0771 tumor cells were cultured with supernatants collected from A-FABP+/+ and A-FABP-/- macrophages, respectively, for two weeks. The clones were fixed with 4% paraformaldehyde and then stained with 0.01% (w/v) crystal violet for 30 minutes. To observe if IL-6 promoted tumor colony formation, anti-IL-6 neutralizing antibody or control IgG was added in the culture. In some experiments, E0771 cells (5×103) were subjected to the methylcellulose colony formation assays in triplicate using methylcellulose medium (R&D Systems, Minneapolis, MN, USA), according to the manufacturer’s instructions. The actual numbers of colonies were counted under a microscope.

**Reference List**

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