

# Intraductal xenografts show lobular carcinoma cells rely on their own extracellular matrix and LOXL1

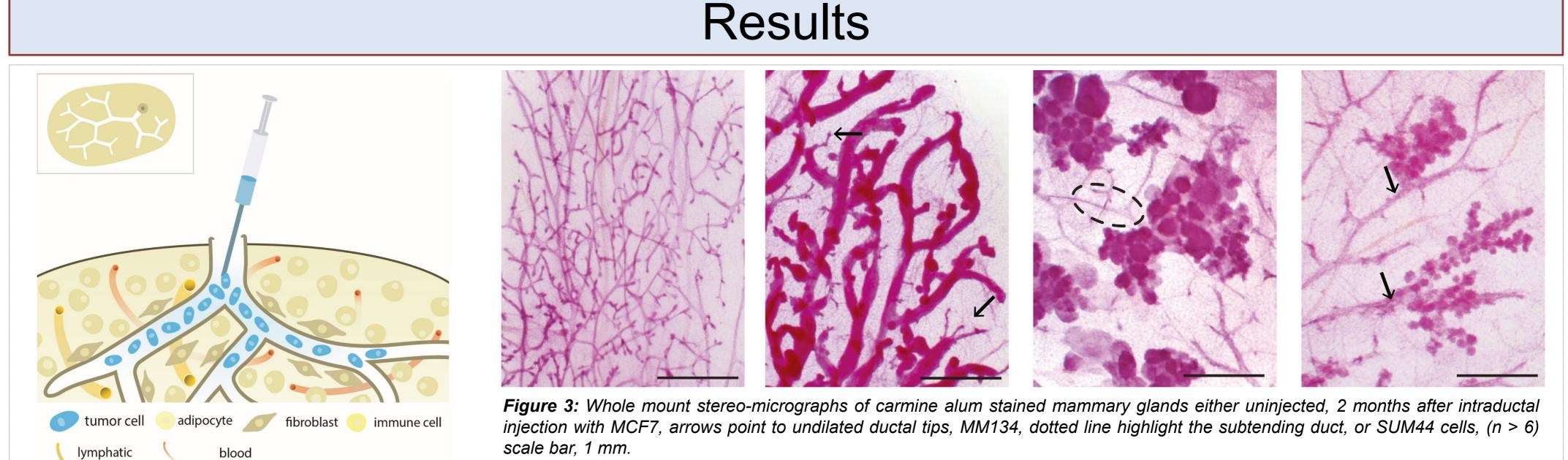
<u>George Sflomos<sup>1</sup></u>, Laura Battista<sup>1</sup>, Patrick Aouad<sup>1</sup>, Fabio De Martino<sup>1</sup>, Valentina Scabia<sup>1</sup>, Athina Stravodimou<sup>2</sup>, Ayyakkannu Ayyanan<sup>1</sup>, Assia Ifticene-Treboux<sup>2</sup>, RLS<sup>3</sup>, Philipp Bucher<sup>1</sup>, Maryse Fiche<sup>3,4</sup>, Giovanna Ambrosini<sup>1</sup> & Cathrin Brisken<sup>1</sup>

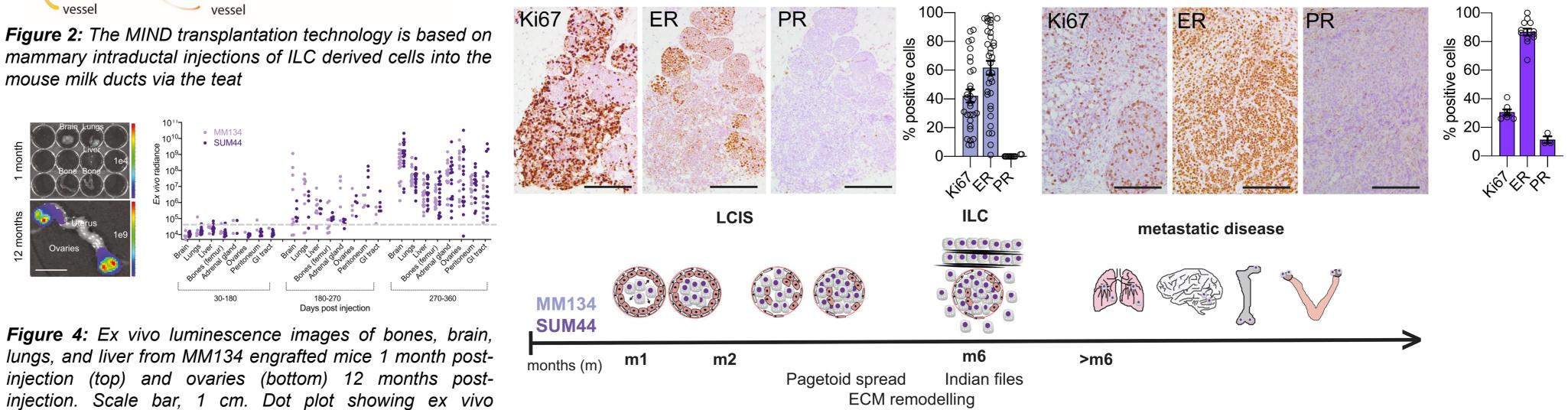
<u>https://www.epfl.ch/labs/brisken-lab/</u> - Name of the presenter: George SFLOMOS (georgios.sflomos@epfl.ch)

**Overview - Abstract** 

Invasive lobular carcinoma (ILC) is the frequent special histological most subtype of breast cancer, typically characterized by loss of E-cadherin. It has clinical features distinct from other estrogen receptor-positive (ER+) breast cancers but the molecular mechanisms underlying its characteristic biology are poorly understood

because we lack experimental models to study them. Here, we recapitulate the human disease, including its metastatic pattern, by grafting ILC-derived breast cancer cell lines, SUM-44 PE and MDAMB-134-VI cells, into the mouse Using patient-derived milk ducts. intraductal xenografts from lobular and non-lobular ER+ HER2+ tumors to compare global gene expression, we identify extracellular matrix modulation as a lobular carcinoma cell-intrinsic trait. Analysis of TCGA patient datasets shows matrisome signature is enriched lobular carcinomas with in overexpression of elastin, collagens, and the collagen modifying enzyme LOXL1. Treatment with the pan LOX inhibitor BAPN and silencing of LOXL1 expression decrease tumor growth, invasion, and metastasis by disrupting ECM structure resulting in decreased ER signaling. We conclude that LOXL1 inhibition is a promising therapeutic strategy for ILC.







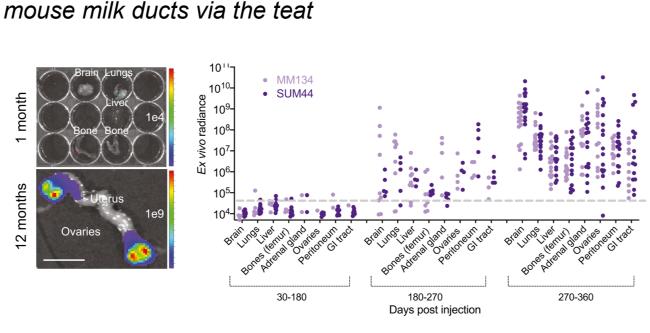


Figure 4: Ex vivo luminescence images of bones, brain, lungs, and liver from MM134 engrafted mice 1 month postinjection (top) and ovaries (bottom) 12 months postinjection. Scale bar, 1 cm. Dot plot showing ex vivo bioluminescence of different organs from mice xenografted with MM134 and SUM44 cells plotted over organ and time of analysis.

T105 (36/37)

T123 (06/07)

T124 (32/35)

T125 (23/26)

T130 (08/10)

T133 (05/06)

T135 (07/07)

T136 (06/08)

T137 (10/12)

T138 (02/04)

T139 (11/15)

T141 (13/16)

T143 (01/02)

T144 (06/06)

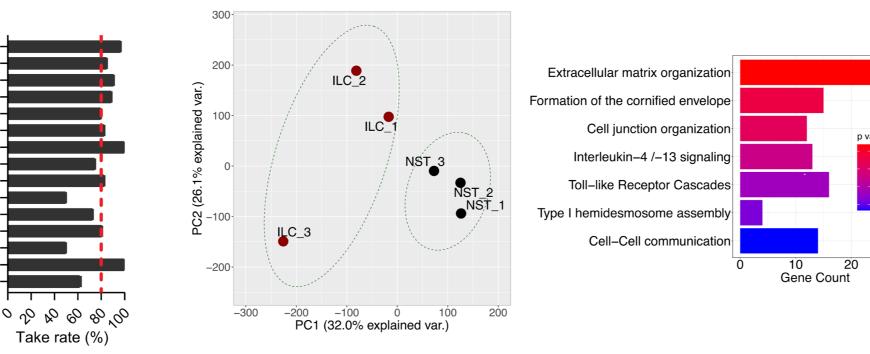
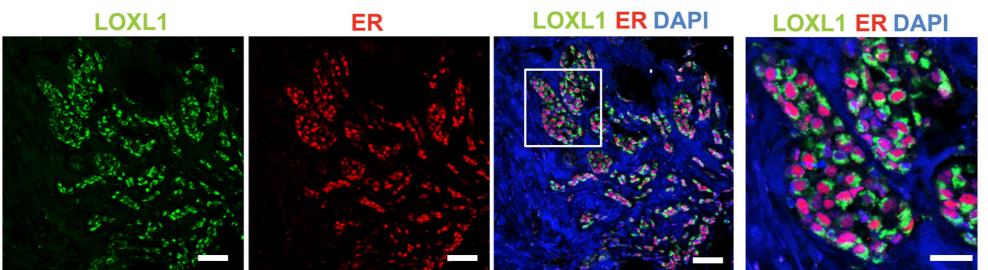


Figure 6: Right: Bar graph showing take rates in % of PDXs from the treatment naive patient ILCs. In parentheses number of injected glands (n) with growth over total n of injected glands. Red dotted line shows average take rate. Middle: Principal component analysis plot of global gene expression profiles of ILC and non-ILC ER+ HER2 (NST) PDX cells purified by FACS sorting based on GFP expression, n=3. Right: Barplot showing Reactome pathway enrichment analysis of differentially upregulated genes.



*Figure 5:* Representative micrographs of IHC for Ki67, ER, and PR on histological sections of MM134 and SUM44 xenografts 5 months after intraductal injection counterstained with hematoxylin. Scale bars, 200 um. Bar plots represent means SEM of measurements and indicate the percentage of positive cells for > 1,000 cells counted on three glands.

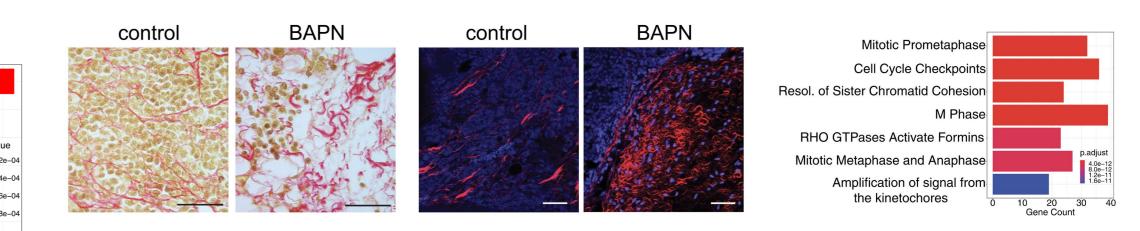


Figure 8: Left: Representative micrographs showing picrosirius red staining of sections from MM134 xenografts treated with PBS (left) or BAPN (right), n = 4. Scale bars, 100 um. Middle: Representative second-harmonic generation (SHG) image on SUM44 xenografts treated with vehicle (left) or BAPN (right), n = 3. Collagen fibers in red and DAPI nuclear stain (blue). Scale bar, 50 um. Right: Barplot showing reactome pathway enrichment analysis of differentially down-regulated genes. GSEA plots showing decreased early and late estrogen response and MYC targets. P-values are computed by nonparametric permutation tests.

Figure 9: LOXL1 knockdown and A its effects on ILC progression. A. Bar plot showing LOXL1 transcript levels as measured by semi qRT–PCR normalized to 36B4 SUM44:RFPLuc 100 ime after engraftment (day of scramble and shLOXL1 expressing ILCs cells in vitro. B. Scheme describing experimental approach used to generate shLOXL1 expressing and ILC xenograft models. ILC:RFP-luc2 cells were transduced Time after engraftment (d with GFP+ sh-scramble or GFP+ shLOXL1 expressing lentiviruses, selected by FACS and injected into the into contralateral 3rd thoracic and the 4th inguinal gland. Xenografted mice were monitored growth tumor by for bioluminescence imaging.



Figure 1: Experimental Design - A Simplified Flow Chart. Dissociated surgical specimen of ILCs is *lentiviral infected with GFP-luc2 and injected into* the milk ducts. Retransplanted tumors were follow up and treated with endocrine therapies. Along with the clinical samples, MDA-MB-134VI (model for ILC) and MCF7 (model for IDC) breast cancer cell lines used for the development of in vivo xenografts.

Keywords: Lobular Carcinoma, Microenvironment, Preclinical Models, Patient-derived Xenograft

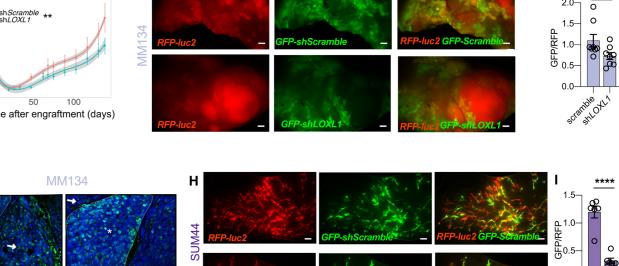


Sflomos G., et al., Cancer Cell, 2016

2. Ciriello G., et al., Cell 2015

- 3. Desmedt C., et al., Journal of Clinical Oncology 2016
- 4. Michaut, M., et al., Scientific reports 2016
- 5. Subramanian, Tamayo, et al., PNAS 2015
- 6. Szklarczyk D. et al., NAR 2017

*Figure 7:* Representative immunofluorescence image of primary ILC (*n* = 3) stained with anti-LOXL1 (green) and anti-ER (red) antibodies counterstained with DAPI (blue). Scale bars; 50 um and right inset 30 um.



## Conclusions

Here, lobular breast cancer cells either from cell lines or from patient tumors are grafted directly to the milk ducts of immunocompromised female mice. We show that in these models, the tumor cells grow, invade, and metastasize in a similar way as they do in patients. Molecular analysis of purified lobular carcinoma cells from intraductal xenografts reveals that these cells actively modulate their extracellular environment. Blocking an enzyme that is critical for this modulation interferes with tumor growth and progression, suggesting that this can be exploited for new therapies.

### Perspectives

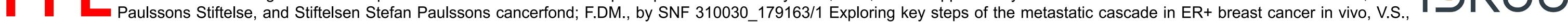
The new models for lobular carcinoma we have developed and characterized will improve our understanding of the disease. The finding that the lobular tumor cells are highly dependent on the proteins that surround them and that they themselves secrete proteins and enzymes that control this matrix opens new strategies for therapy.

# Acknowledgements



We thank R. Iggo for critical comments on the manuscript and J. Dessimoz at the EPFL histology core facility, O. Burri and A. Seitz at the EPFL bioimaging and optics platform (BIOP), B. Mangeat at the EPFL gene expression core facility (GECF), M. Garcia V. Glutz and A. Mozes (FCCF) and the Lausanne Genomic Technologies Facility (GTF) for technical assistance. We are grateful to the patients and their families who participated in this study. G.S., V.S., were supported by Biltema ISREC Foundation Cancera Stiftelsen, Mats





### P.A. by Swiss Cancer League KFS-3701-08-2015 Lobular carcinoma of the breast:insights from a new PDX model, and L.B by KFS-4738-02-2019-R Different facets of ER signaling Fondation Recherche Cancer

