BRECT group descriptions

Jonas Bergh
The aim of the research group is to use tumour bank material and biobank material from prospective clinical studies for translational research studies, to analyse and predict the response and resistance to endocrine treatment modalities and chemotherapy regimens. We apply gene expression array analysis, microRNA analysis, single nucleotide polymorphism analysis and analysis of proteins in primary tumours, metastases and blood from breast cancer patients. This includes the investigation of genetic signatures and detailed studies of the roles of p53 and HER2/neu and linked pathways in breast cancer. The gene signatures are investigated in the epithelial and stroma cells, respectively, for prognostication and therapy prediction. Specifically, we study genetic signatures predicting sensitivity/resistance to tamoxifen and to pre- and post-operative chemotherapy regimens.

Staffan Strömblad’s research group
The Cell Biology of Cancer
We aim to improve our fundamental understanding on how cancer develops and progresses by elucidating the signaling pathways that governs critical cellular functions, including cell proliferation and cell migration. We focus on the role of p21-activated kinase 4 and of cell to extracellular matrix interactions. Our laboratory has in place a number of techniques, including in vitro models, transgenic mice, cancer mouse models, patient database bioinformatics and patient specimens, which are combined within our comprehensive yet molecularly detailed investigations, stretching also into testing Pak4 pharmacological targeting. We also utilize a systems microscopy approach, where live cell microscopy of migrating cancer cells is combined with mathematical analyses and modeling.

Marianne Farnebo
Our laboratory is investigating how cells repair their DNA and what factors that contribute to this essential process. Our overall goal is to unravel the complex details of cellular responses to DNA damage and whether these functions are altered in cancer and then build on this knowledge to develop novel strategies for prevention and treatment of cancer.

Guillem Genové
Research at the Genové group is focused on the tumor stroma and its interactions with the malignant cell. Specifically, our interest is in how pericytes alter the tumor microenvironment resulting in modulation of immune responses. From the other end, immune cells can influence tumor vascularization and render it permeable for tumor cell intravasation. Finally, we are studying how both pericytes and immune system may contribute to failed therapeutic approaches.

Per Hall
My primary scientific goal is to identify women at increased risk of breast cancer. This is done using the Karma cohort where we have collected blood, lifestyle factors, mammographic density and a couple of other variables. Women at an increased risk will be offered possibilities to influence the risk. Intervention ranges from increased physical activity to risk-reducing medications such as tamoxifen.
Charlotte Rolny
Tumor associated macrophages (TAMs) are classified as M2-macrophages (Møs) and promote tumor progression while anti-tumoral M1-Mø restrains tumor progression. We have shown that re-education of M2-Møs to an anti-tumoral M1-phenotype restrains tumor progression. We are now working on i) to understand underlying mechanism that dictates the Mø phenotype and ii) to find novel targets that promote an M1- Mø phenotype in order to develop new anti-cancer therapies.

Arne Östman
The AÖ group performs translational research on the roles of the tumor microenvironment on tumor initiation, growth, metastasis and treatment response. Ongoing projects use tissue culture models, animal models and analyses of clinical samples. The group has a particular interest in cancer-associated fibroblasts (CAFs) and vascular cells. Breast cancer-related studies investigate the roles of CAF subsets in DCIS progression, impact of CAFs on response to treatment and prognostic and response-predictive potential of novel marker-defined subsets of perivascular cells.

Erik Fredlund
Our research is focused on functional analysis of omics-type breast cancer data. By integrating multiple layers of high-throughput data with a strong knowledge of tumor biology we build hypotheses that can be tested using molecular biology methods. Currently, we are concentrating on developing methods for analysis of deregulated signaling pathways in cancer by merging mutational, copy-number, gene expression and quantitative proteomics data. We apply these methods to investigate response to targeted therapies as assessed using high-throughput imaging in vitro screening assays.

Rune Toftgård
Our research aims to understand the role of Hedgehog signaling in the initiation and maintenance of breast cancer and to identify tissue progenitor cell populations that serve as cells of origin and/or tumor inducing cells in breast cancer. To this end we utilize genetically modified experimental models and develop small molecule inhibitors of Hedgehog signaling.

Sten Linnarsson
Our research focuses on single-cell biology, in particular applying single-cell expression analysis to characterize the cell types and lineages of the mouse nervous system. We also pursue single-cell analysis of cancer genomes aiming to elucidate the cellular origin and evolution of human neoplasms. The long-term goal of our research is to map the stable cellular states (‘cell types’) that human organs are made of, and to understand the regulatory networks that induce and maintain them; both in normal tissues and in cancer.

Svetlana Bajalica Lagercrantz
The research aims to understand tumor development to achieve improved patient handling in clinical oncology including: Genetic predisposition in hereditary cancer syndromes with focus on breast cancer, and genetic markers for early detection and tumor spread in breast cancer. And tumor
progression from low malignant follicular lymphoma to high malignant diffuse large B-cell lymphoma (DLBCL)

**Urban Lendahl**
The Lendahl laboratory investigates the role of dysregulated Notch signaling in breast cancer. We have unveiled links to other signaling pathways, including hypoxia, and demonstrated that high Notch signaling induces a glycolytic switch in breast tumor cells. Furthermore, we have recently developed novel methodology, species-specific sequencing, as a novel tool to explore tumor-stroma interactions at the genome-wide transcriptomic level. Finally, recent, yet unpublished findings, unravel a completely new role for the DNA-binding protein CSL in the Notch signaling cascade in breast cancer.

**Jan Frisell**
The JF group performs translational research of tumor biology in young women, <35 years, with breastcancer, related to treatment and prognosis. The group has also a epidemiology research of older women, >70 years, with bad prognosis, related to given treatment and prognostic outcome. Other ongoing projects is randomized trial of mammography screening, where we are PI for national evaluation of the Swedish randomized trials. The group has also projects about sentinel node biopsy and its introduction in Sweden. SENOMAC is an international study, PI from out unit, including 3700 patients randomized to axillary clearance or not in node positive sentinel node cases. Oncoplastic surgery, a new surgical technique, we study oncological safety in reconstructive surgery as well as cosmetic outcome in breastcancer patients. We have also a randomized, national study of a new reconstructive technique with ADM.