Transcriptional and epigenetic regulation of breast cancer

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Gruppens kerneforskningsområder

Transcription is a key determinant of cell function, and deregulation of this process is a key driver of diseases such as cancer. Cancer cells often become dependent on these alterations in the transcriptional and epigenetic mechanisms driving gene expression, and they are consequently termed transcriptional and epigenetic addictions.

We are enthusiastic about uncovering the transcriptional and epigenetic mechanisms controlling cancer cell biology, particularly in the context of breast cancer. Our research is centered around the transcription factors and coregulatory proteins that work together to regulate the activity of our genes and thereby control breast cancer progression. Our overall goal is to provide fundamental insight into how breast cancer growth, metastasis and treatment resistance are controlled at the genomic level and use this information to identify new targeted therapeutic opportunities to inhibit progression of this disease.

Methods

1. Functional genomics and proteomics analyses, e.g., next-generation sequencing.
2. Genome editing approaches using CRISPR.
3. Single-cell analyses.
4. Cell lines, mouse models and patient samples.
5. Computational analyses of omics data.

Er du interesseret i at skrive projekt i gruppen, så kontakt :
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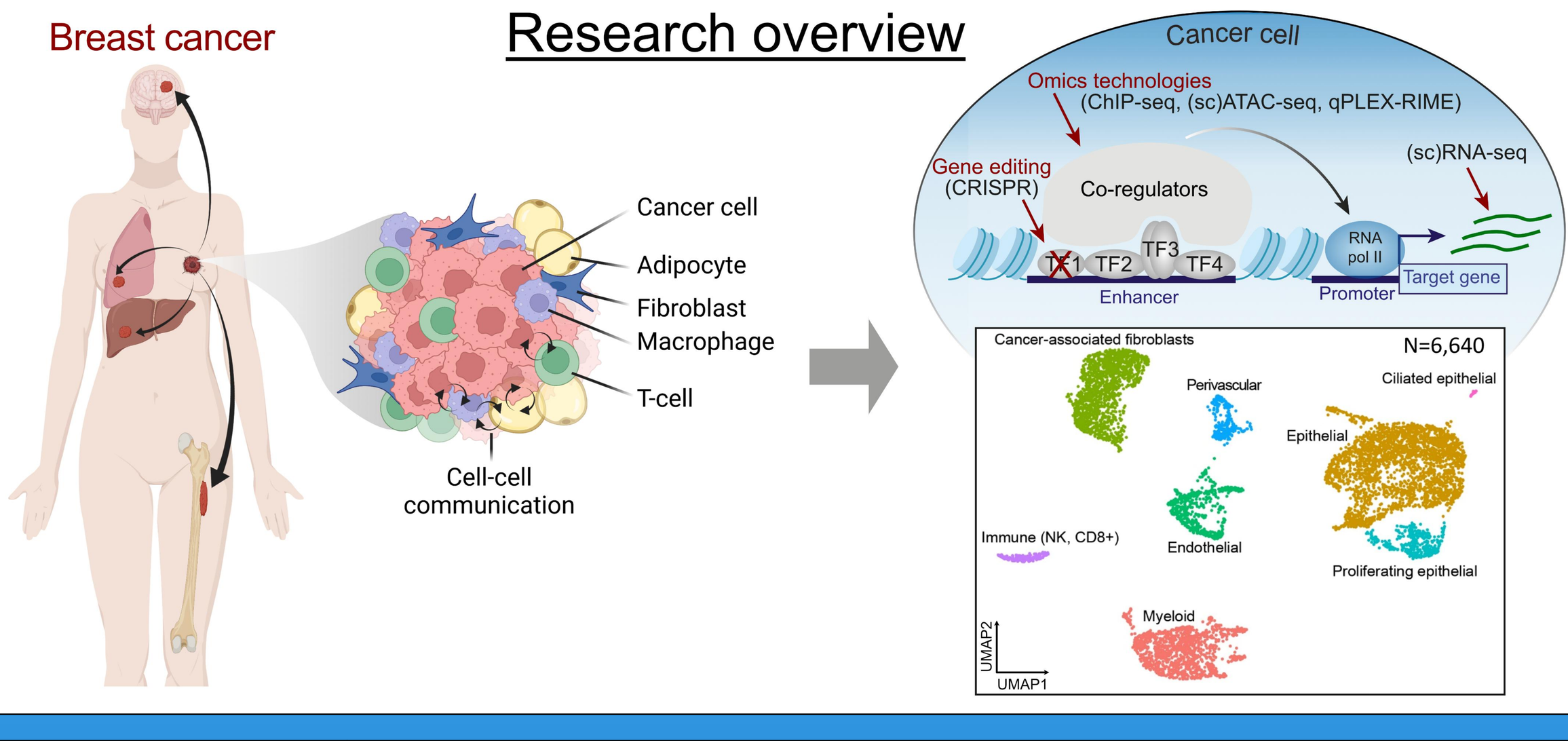
Functional Genomics & Metabolism

SDU

Research overview



Projekter	Beskrivelse
Transcriptional and epigenetic addictions in triple-negative breast cancer	Triple-negative breast cancer is a particularly aggressive and metastatic subtype of breast cancer with limited treatment options. In this project, we employ a range of omics technologies to understand the transcriptional and epigenetic mechanisms controlling the aggressive nature of this breast cancer subtype. The long-term goal is to identify potential new targeted treatment opportunities for this disease.
Obesity-driven breast cancer	Obesity has been linked to increased incidence and aggressiveness of breast tumours. This is likely mediated by altered paracrine signalling between cancer cells and the normal cells in the tumour microenvironment (e.g., immune cells, fat cells and fibroblasts). To understand how obesity impacts the transcriptional and epigenetic mechanisms controlling breast cancer biology, we are analysing patient tumours using new functional single-cell genomics approaches.
Basic mechanisms of transcriptional regulation	There are hundreds of transcription factors and coregulators that work together to precisely regulate transcription to fit the cellular need. In this project, our aim is to understand how these different transcriptional complexes work together to shape gene expression. This includes developing single-cell methods to uncover the heterogeneity of key transcriptional complexes controlling gene expression and cell function.