Transcriptional regulation of breast cancer progression

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Gruppens kerneforskningsområder

Cancer cells develop from normal cells due to accumulation of multiple oncogenic mutations that ultimately lead to uncontrolled growth. The resulting primary tumour can then further spread to other distant organs in the body (e.g., lung, liver and brain) to form secondary tumours through a process termed metastasis. The development of these secondary tumours is the main cause of death for most cancer patients, yet we know remarkably little about this process.

We are specifically interested in understanding the biology of breast cancer, which is the most common type of cancer affecting women. Our research is centered around the transcription factors and coregulatory proteins that drive breast cancer progression by controlling the activity of our genes. Our overall goal is to provide fundamental insight into how growth and metastasis of breast cancer cells is controlled at the genomic level and use this information to identify new therapeutic opportunities to inhibit cancer progression.

Methods

1. Genomics and proteomics analyses, e.g., next-generation sequencing.
2. Genome editing approaches, i.e., 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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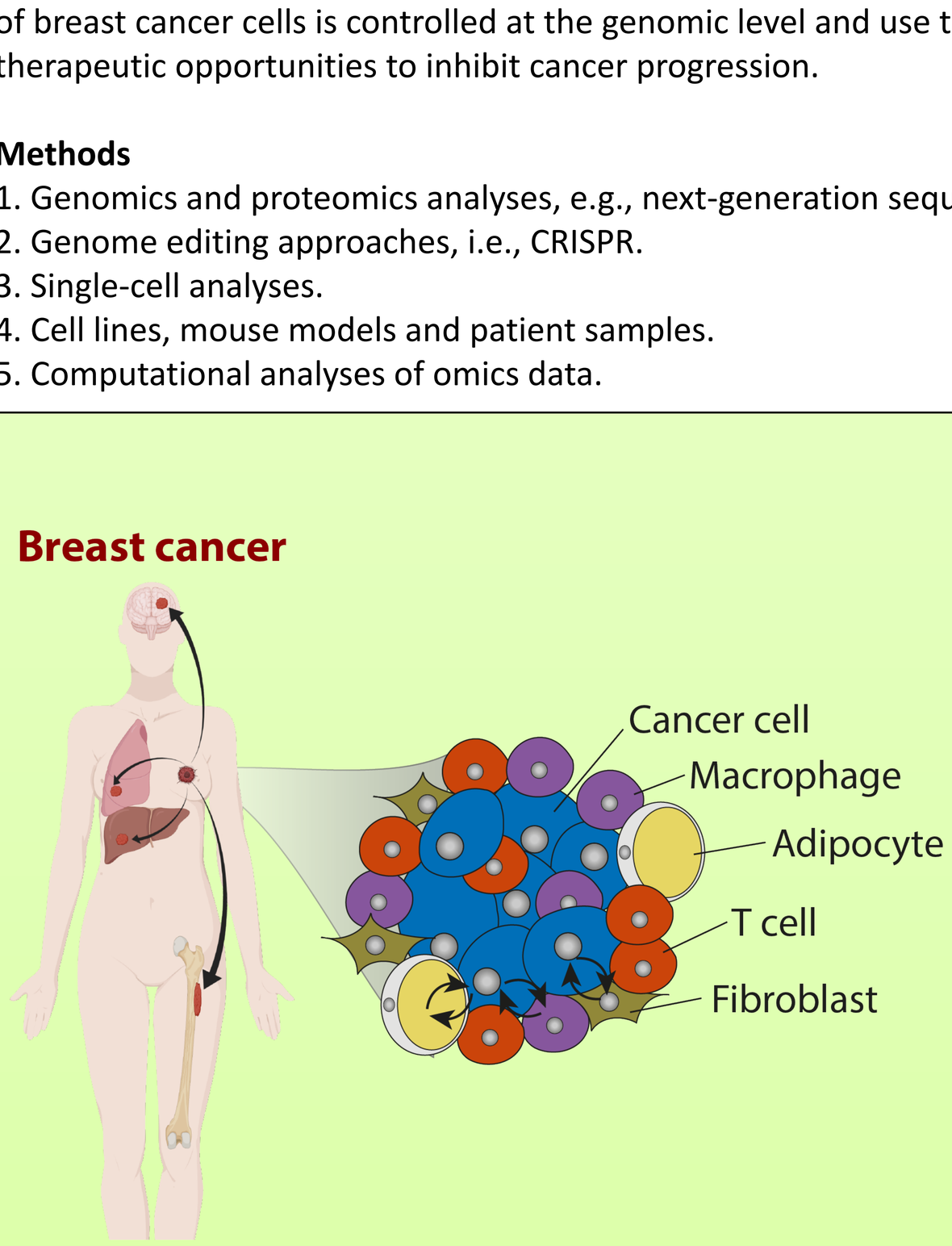
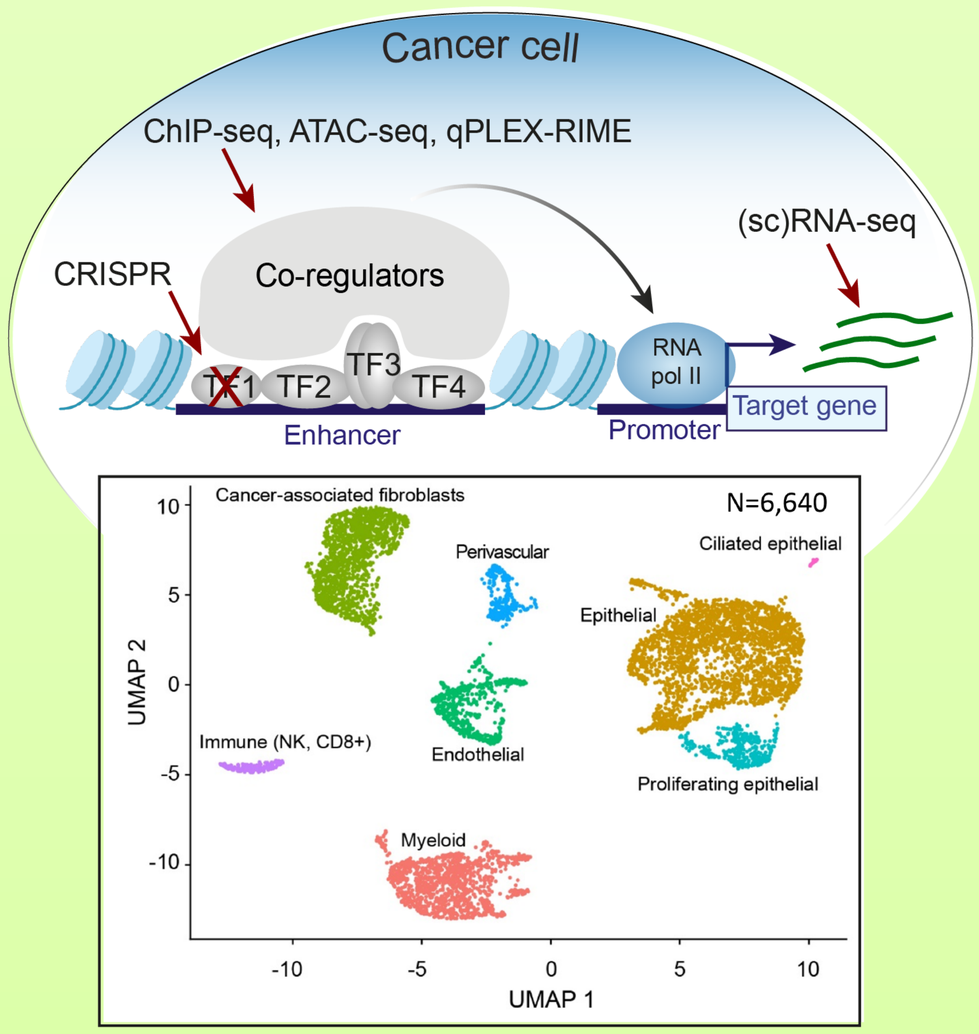
Functional Genomics & Metabolism

Breast cancer





Projekter	Beskrivelse
Transcriptional regulation of 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 mechanisms that control the aggressive nature of this breast cancer subtype. The long-term goal is to identify potential new 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 normal cells in the tumour ecosystem (e.g., immune cells, fat cells, and fibroblasts) and cancer cells. To understand how obesity impacts breast cancer cells and the whole breast tumour ecosystem, we are analysing patient tumours using new single-cell genomics approaches.
Transcriptional regulation at single-cell resolution	Our understanding of transcriptional regulation by transcription factors and coregulatory proteins is based on analysing millions of cells. Thus, we have limited information about the heterogeneity of these transcriptional complexes and how they regulate cell function in individual cells. In this project, we are applying and developing single-cell technologies to obtain a single-cell resolution picture of how transcriptional regulators work together to control cell function.