UNIL | Université de Lausanne
Centre de compétences en bioinformatique

EPFL
BRISKEN LAB

The Breast Cancer Epigenomics Track Hub

Online exploration and visualization tool for public cancer data

Giovanna Ambrosini[1,2], Cathrin Brisken[1] and Philipp Bucher[1]

[1]The Swiss Institute for Experimental Cancer Research (ISREC), School of Life Sciences, EPFL, CH-1015, Lausanne Switzerland
[2]Bioinformatics Competence Center (BICC), UNIL/EPFL Lausanne

Introduction: The Breast Cancer Hub (BC-Hub) and viewer is a tool that provides a new way to explore cancer-related epigenetic data using the UCSC genome browser as a visualization platform. The hub is a collection of public high-resolution tracks from different sources such as research groups at EPFL and the GEO repository, tracks from the UCSC genome browser database and public track hubs (e.g. the Cancer Genome Atlas Hub).

Results: By comparing ChIP-seq data tracks from primary breast tumor material, we can reveal plasticity in steroid hormone receptor binding capacity as well as strong genomic cross-talk of hormone receptor action and interplay in human tumors. In particular, we observe that hormone response in estrogen-responsive breast cancer cell lines is significantly different from the one in human tumors, revealing the importance of studying hormone therapy effects in patient derived tumors rather than in cell lines. Besides, comparison of estrogen receptor (ER) binding under estrogen stimulation in normal ER^+ mature luminal mammary epithelial cells and ER^+ breast tumors, reveal differential recruitment of estrogen receptor in tumor versus normal.

Conclusions: The Breast Cancer hub is a powerful tool to visually explore cancer epigenetic profiles from cell lines, primary tumors, metastases and patient-derived xenografts. Being able to classify tumors based on chromatin binding profiles may have valuable implications for prognosis and tailored therapeutic interventions.

BC-Hub Home page: https://ccg.epfl.ch/bchub/.

WHY THE UCSC GENOME BROWSER ?

- Combine views from thousands of data tracks
- Easy way for integrating data from different experiments
- Zoom-in into specific genomic regions of interest
- Organize your own data via Track Hubs
- Track hubs are easy to create and manage
- Track sets offer a convenient way to bundle thematically related data from different sources

HOSTED DATA

Breast Cancer ChIP-seq and CNV tracks for:

- ✓ Cell lines
- ✓ Cell line-derived xenografts
- ✓ Patient-derived xenografts (PDXs)
- ✓ Primary tumor samples
- ✓ Circulating tumor cells
- ✓ Metastasis

THE VIEWER & THE TRACK CLUSTERING TOOL

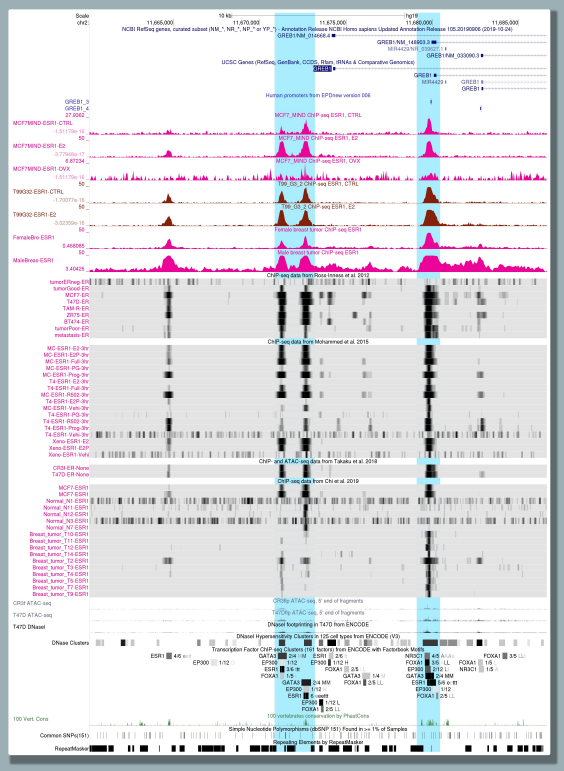

Figure 1. Extended promoter region of GREB1 gene with ChIP-seq data shown in both full and dense display modes. Samples are presented in the default order.

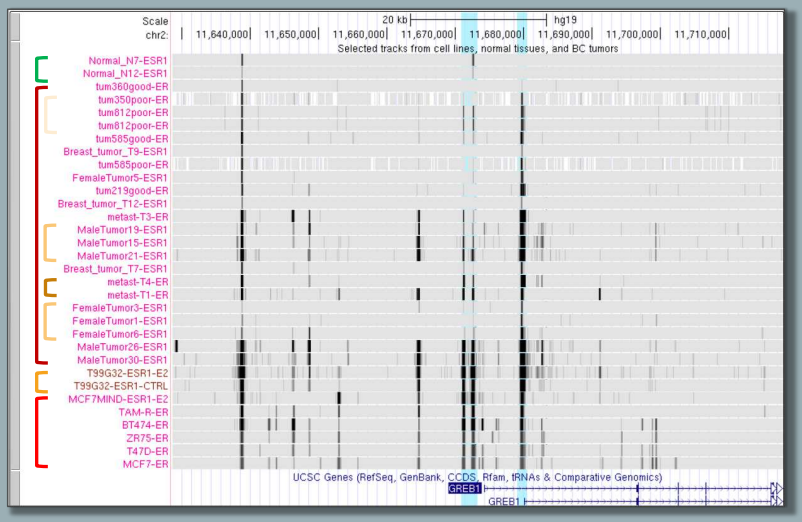

Figure 2. Extended promoter region of GREB1 gene with ChIP-seq data shown in dense display mode. Samples were reordered by hierarchical clustering.

- Cell lines cluster together
- No consistent trend for tumor samples
- Different recruitment mechanisms for ESR1 between, normal, tumor and cell lines

Data from *Severson et al. 2018*, *Mohammed et al. 2015*, *Takaku et al. 2018*, *Ross-Inness et al. 2012*, *Chi et al. 2019*, and *Brisken Lab* unpublished.

BC-Hub Tool
https://ccg.epfl.ch/bchub/