transcriptionFactorREST

REST acts as a transcriptional repressor of neuronal genes in non-neuronal cells. In some contexts, REST has been reported as a transcriptional activator. We aimed at defining the role of REST in IDH mutation related phenotype in glioma because REST was 1) described as a factor involved in a blockage of cell differentiation and 2) an important oncogenic factor, and knowing that 3) IDH mutations are oncogenic drivers in glioma that cause significant changes in epigenome, leading to block of differentiation. A pair of REST silenced IDH mutant and IDH WT U87 cell lines were used as a model. Whole genome and transcriptome analyses revealed different patterns of REST binding and its proximal TF motifs in IDH mutated and WT cells, and identified the genes downstream of REST related to ECM organization and cell differentiation. This study shows that the REST role in gliomas is dependent on IDH mutation status.

This project contains all R scripts used to produce all the results related to the paper: **'Comprehensive analysis of the transcription factor REST regulatory networks in IDH-mutant and IDH-wild type glioma cells and gliomas'**

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Installation

To rerun some parts of the analysis please make sure you downloaded input data by running the following bash scripts:

- './data/download.data.sh'
- './RData/RDatadownload.RData.sh'

Usage

The project cosists of several folders that contain R source code to run some parts of the analysis described in the paper.

Project Structure

- DiffMeth (Author: Michał Dramiński)
- BW (Author: Bartosz Wojtas)
- SurvivalAnalysis (Author: Adria-Jaume Roura)

Version

- Version: 1.0.0
- Date: 09.06.2022

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