HRonBC: a web-tool tailored for analysis of transcriptomics and nucleome data for Hormone Replacement on Breast Cancer

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Hormone replacement (HR) therapy with estrogen (E2) alone or in combination with progesterone is used by women to compansate for the lack of these hormones during menopause. Despite the fact that HR has beneficial effects, long-term menopausal HR use has been associated with a higher risk of breast cancer. Drospirenone (Drsp), a fourth generation progestin derived from Spironolactone, is used together with estrogen (E2) and provides symptomatic relief in menopause. Drsp is also known to antagonize the Mineralocorticoid Receptor (MR) for which Aldosterone (Aldo) is a ligand modulating blood pressure. However, high throughput molecular comparisons between Drsp:E2 and other Progestin:E2 treatments in breast cancer cells are lacking. With the emerging NGS technology including RNA-seq, Chip-seq, and Hi-C, there are many datasets available on HR therapy in breast cancer cell lines to compare with each other; hence we first developed an R Shiny based web-tool called HRonBC where we collated such datasets. HRonBC, which is able to compare up to four HR-focused, two-group RNAseq datasets simultaneously, performs functional analysis for the selected gene sets through annotation by different terms as well as ChIP-Seq and/or Hi-C data. Accordingly, coverage and peak information of the selected genes from RNAseq data are displayed from the user-selected ChIP-Seq data while the Hi-C derived contact matrix of the relevant chromosome regions can be visualized. We also integrated into HRonBC the data from RNAseq and ChIP-seq experiments performed in our labs using breast cancer cells when exposed to different combinations of Drsp, E2, and/or Aldo.HRonBC has enabled us to seamlessly compare our data against other existing HR datasets in literature.

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