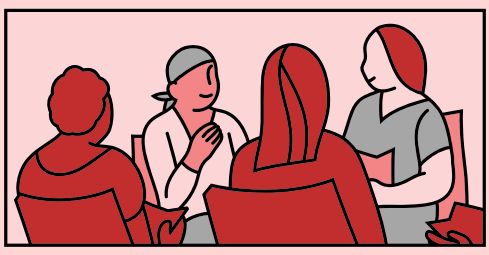

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Breast Cancer Biomarker Analysis

#1

What is a biomarker in cancer treatment?

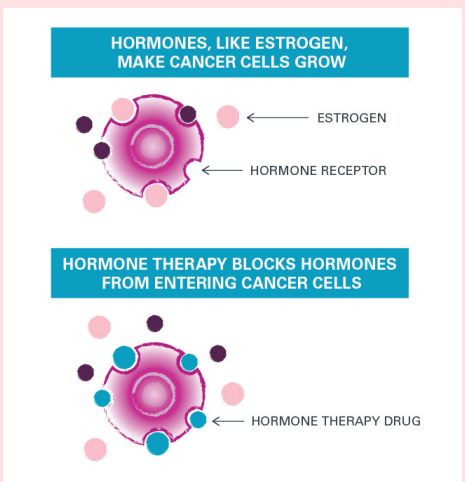
In an oncology context, biomarkers are genes, proteins, and other substances that can provide information on a person's cancer. Biomarker testing can help with not just diagnosis of cancer but also treatment and tracking disease progression.

Some common types of Biomarkers are:
Type 0 - natural history marker for measuring disease progression overtime
Type 1 - drug activity biomarker to indicate effectiveness of drug treatment
Type 2 - surrogate end point marker to predict effect of therapeutic intervention

2

Estrogen Receptor in Breast Cancer

- **There are multiple biomarkers associated with Breast Cancer. We chose to analyze the Estrogen Receptor (ER) because it is the most important biomarker in breast cancer.**
- **ER-positive tumors respond highly to endocrine therapy (estrogen feeds the growth of the tumor), while ER-negative tumors don't. Knowing if a breast cancer is ER(+) or not can help healthcare providers whether or not to administer anti-estrogen therapy**
- **According to the literature, we theorize that ER(+) samples should show a higher pattern of estrogen expression than ER(-) sample**



Source: Nebraska Medicine

3

Data and Analysis Method

- **We used the Gene Expression Omnibus (GEO) and analyzed a dataset pertaining to ER(+) expression. GEO is a public repository of arrays, sequencing, and functional genomic data**
- **We used GSE17040: " Functional ER alpha transcriptional regulatory network for cell cycle in an ER(+) breast cancer subgroup." There are 57 samples, 46 ER(+) and 11 ER(-).**
- **The data takes from both cell line and clinical samples. The platform used is GPL887 Agilent-012097 Human 1A Microarray (V2) G4110B (Feature Number version)**
- **"Analyze with GEO2R" to automatically run statistical analysis --> Locate the estrogen receptor gene (estrogen receptor 1 - ESR1) among all of the genes sampled --> Analyze expression level and statistical significance**
- **Download "Series Matrix File" to access full dataset --> Locate ER gene --> Make box plot to visualize ER(+) vs ER(-)**

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4 Results

- **For ESR1 (ID 5561), the log fold change is 4.04669853, and the adjusted P-value is 2.03E-08 (<0.05). The log fold change indicates the expression level of an ER group relative to the other. The P-value indicates statistical significance (adjusted t-test)**
- **The result means that the ER(+) variant has an expression level around 4 times higher than the ER(-), and that this difference is statistically significant**
- **This finding corroborates with the hypothesized pattern: ER(+) expresses estrogen at a statistically higher level than ER(-)**

VOLCANO PLOT

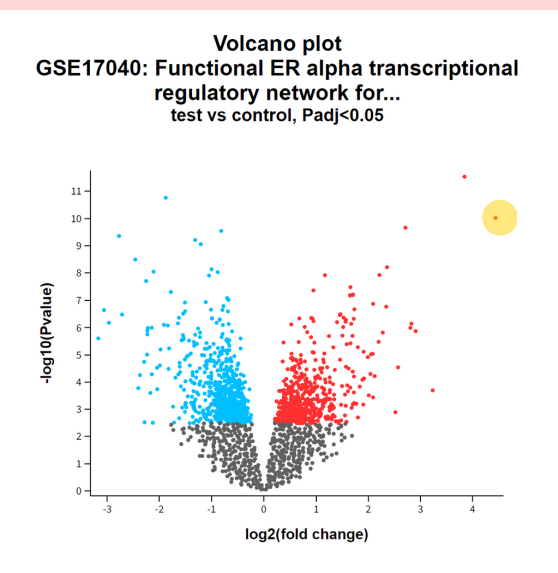

Figure 1: Genes that are significantly down-regulated (blue) or up-regulated (red). ESR1 is among the up-regulated gene (highlighted in yellow).

BOX PLOT

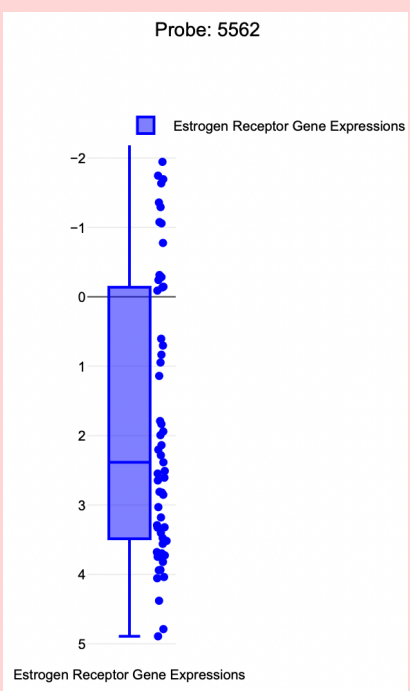

Figure 2: This showcases ER (+) which Confirms that this probe of has lower gene expression. This plots has a negative skewness meaning that this negative distribution has a lot of low gene expression levels

5 Discussion

- **This project is an entry exercise into analysis of a publicly available genomic dataset. There are opportunities to explore and analyze at higher levels of complexities**
- **A future project could look at estrogen expression in pre-endocrine therapy vs. post-endocrine therapy**
- **Besides estrogen receptor, progesterone receptor is also an important biomarker in breast cancer. Breast cancers with either ER positive, PR positive, or both, are known as hormone receptor-positive cancers. Interestingly, PR(+) occurs almost only concurrently with ER(+) (very rare PR(+), ER(-) occurrences.) ER(+), PR(+) tumors respond better to endocrine therapy than ER(+), PR(-) tumors. (Weigel 2010). A future analysis could investigate this relationship**
- **ER positive cancers that have a low number of cells with estrogen receptors may respond differently to treatment**

6 Acknowledgment

- **Thank you to our coach Dr. Hermioni Zouridis for her technical knowledge, guidance, and encouragement throughout the project**
- **Thank you Nvolve Founder Faye O'Brien and the Nvolve community for faciliating an educational experience for aspiring women in STEM and medicine**

Citations

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