Assignment 1

Absract:

Now we use long,non coding RNAs(lncRNAs)which are in the next generation sequencing technologies in breast cancer research . lncRNA are a type of RNA, defined as being transcripts with lengths exceeding 200 nucleotides that are not translated into protein .Their important roles in the regulation of cancer-related pathways in addition to deregulation of their expression in a number of cancers have suggested that they can be used as markers for cancer detection and prognosis, as well as targets for cancer treatment. They get a subset of 18 cell line from previously publish RNA-seq dataset of 675 cancer cell and analyses it by detailed comparison of differentially expressed lncRNAs in each breast cancer sub-type with normal-like breast epithelial cells. They use Gene Expression Profiling Interactive Analysis (GEPIA2) and data from The Cancer Genome Atlas (TCGA) and The Genotype-Tissue .Expression (GTEx) project to identify lnsRNAs with invasive breast cancer.

Introduction:

Breast cancer is the most common cancer diagnosed in women. Because of RNA sequencing (RNA-seq) ,We discovered that a lot of cells produce RNA that don't produce protien. Non coding RNAs have important roles like potential disease modifiers and could be exploited as biomarkers and/or therapeutic targets . There are some types of non coding RNAs. Abundant and functionally important types of non-coding RNAs include transfer RNAs (tRNAs) and ribosomal RNAs (rRNAs), as well as small RNAs such as microRNAs, siRNAs, piRNAs, snoRNAs, snRNAs, exRNAs, scaRNAs and the long ncRNAs such as Xist and HOTAIR . We will focus on lncRNA and how lncRNAs are altered contribute to cancer, along with discovering their normal physiological roles. To understand which lncRNAs are specifically be linked to breast cancer, it is important to examine their expression profiles in various cell lines .The classification of invasive breast lesions into molecular subtypes based on the presence or absence of receptors for hormones,oestrogen (ER) and progesterone (PR) along with human epidermal growth factor-2 (HER2/ERBB2).These difference have the basis of the molecular classification of breast cancer into four major groups:(1) luminal A (2) luminal B, HER2 enriched and basal-like (3) Luminal A involves cancer cells that are ER and/or PR positive, HER2-negative and low levels of the cell cycle-regulated protein Ki-67 (4) Luminal B cancers exhibit lower ER/PR expression, with variable HER2 levels and high levels of protein Ki-67

There are also preinvasive forms of breast cancer - ductal carcinoma in situ (DCIS) and lobular carcinoma in situ (LCIS) – distinguished by their sites of origin within the ducts or the lobules of the breast

Breast cancer cell lines are useful in knowing the details of biological processes involved with cancer initiation and progression and also split to types as breast cancer tumours (1) basal A cluster (2)basal B cluster and they don't appear in in primary tumours. To determine lncRNAs, We use classification of breast cancer cell lines

By usingGene Expression Profiling Interactive Analysis (GEPIA2) [37] and data from The Cancer Genome Atlas (TCGA) [38] and The Genotype-Tissue Expression (GTEx) project ,they

determined novel, uncharacterised lncRNAs, LOC101448202, LOC105372471 and .LOC105372815

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