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Genetic variants within long non coding RNA: Role in Cancer

Abstract:

Long non-coding RNAs (lncRNAs) constitute a diverse group of RNA molecules with pivotal roles in cellular regulation, challenging the conventional view of non-functional genome regions. This paradigm shift underscores their potential implications in diseases, particularly cancer. Single Nucleotide Polymorphisms (SNPs), prevalent genetic variations, have been linked to disease susceptibility, including Breast, Cervical, and Ovarian cancer. This thesis endeavors to unravel the functional significance of GWAS-associated SNPs within lncRNAs in breast, cervical, and ovarian cancers. Through comprehensive analyses and experimental validation, it aims to elucidate shared and distinct SNP-containing lncRNAs across female cancers, shedding light on their impact on cancer biology. First, I have developed an updated version of the LncRBase database, expanding its reach to include lncRNA from multiple species and enriched information on lncRNA associated features. Next, I have put forward ClinicLSNP, a database housing information on female cancer specific lncRNA-SNPs based on patient transcriptomic data analysis. Armed with this knowledge, I have delved into identifying shared SNP-associated lncRNAs influencing Breast, Cervical, and Ovarian cancers. Finally, by deducing Breast and Ovarian cancer specific lncRNA-SNP and their interacting gene partners, I have developed cancer risk prediction models for predicting the risk factor, particularly in patients with conditions that heighten cancer susceptibility. By bridging gaps in our understanding, this work aims to advance the field, potentially revealing therapeutic targets and diagnostic markers for improved cancer management and patient outcomes. Through this interdisciplinary approach, the thesis aims to contribute to the growing body of knowledge in cancer research and pave the way for personalized approaches to cancer treatment.

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