

## Utilization of Next Generation Sequencing in the Identification of Long Non-Coding RNAs as Potential Players in Breast Cancer Prevention

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### Abstract:

**Aim:** The advancement of new advances, for example, Next Generation sequencing (NGS), and techniques to improve the capacities of this innovation has been an unrest for the investigation of genomics and transcriptomics. NGS opens entryways for progress in an assortment of natural fields, including biomedical examination. NGS permits the sequencing of the entire genome and transcriptome in a gigantic scope, available cost, and it isn't restricted to past information. Genome sequencing has been applied for the improvement of an assortment of research zones, for example, portrayal of antiquated genomes, sequencing of various species, hazard evaluation of hereditary sicknesses, sub-atomic analysis of different sicknesses including malignant growth among other, prompting a street for customized medication. With NGS, definite investigations of the transcriptome have been made conceivable. Definite data about courier RNA, yet in addition ribosomal RNA, move RNA, little RNAs are presently available. Due to the way that this innovation needs no past information about the frameworks being contemplated contrasted with other high-throughput innovations (for example oligo-microarrays), NGS takes into account novel records to be found. Accordingly, elective joining, novel microRNAs, and non-coding districts which produce long non-coding RNAs (lncRNAs) would now be able to be investigated. Non-coding areas of the genome were initially portrayed as garbage, or a result of messy transcriptional apparatus. It was not until the ENCODE project that these

noncoding areas were demonstrated to be practical pieces of the genome. In fact, they have been appeared to have significant parts in quality guideline. LncRNAs have been named RNAs which are longer than 200 nucleotides (a length which was set self-assertively to recognize them from little RNAs) and don't seem to code for a protein (for example have no altogether huge open understanding casing). Notwithstanding compensating for most of the human genome, just under 180 lncRNAs have been clarified and the comprehension of their organic job is still a matter for dynamic exploration. LncRNAs have been depicted as significant central participants in cell separation and cell change. Nonetheless, up to this point, very few lncRNAs have been straightforwardly connected to bosom malignancy; H19 and HOTAIR are some of lncRNAs over communicated in bosom malignancy.

### Biography:

He has a client experiences lie primarily in manufacturing, energy and project development where he has represented some of Maine's largest manufacturers and energy generators as well as offshore wind, solar and hydroelectric power developers. He also has represented both water and electric utilities at state legislatures and regulatory agencies. Steve also participated in the preparation of multiple appellate briefs on decisions of the Maine PUC affecting the interests of his clients.