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Comprehensive analysis of long non-coding RNAs in early stage breast cancer

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Abstract

Breast cancer is one of the most common cancers in India as well as worldwide. Among Indian females, the age adjusted incidence rate of breast cancer is as high as 25.8 per 100,000 women and mortality rate of 12.7 per 100,000 women. Accumulating evidence highlights the potential role of long non-coding RNAs (lncRNAs) in breast cancer development. LncRNAs are emerging as important players in tumorigenesis as they are known to participate in various cancerous processes including proliferation, apoptosis, and invasion. LncRNAs are reported to be dysregulated in a number of cancers, demonstrating both oncogenic and tumor suppressive roles, thus suggesting their aberrant expression may be a substantial contributor in cancer development. However, their mechanism of action is poorly understood. Several studies have been published describing lncRNA expression profile of various breast cancer subtypes in different stages of cancer; however, their aberrant expression has not been systematically investigated in early stages. We have carried out expression profiling using deep sequencing of total RNAs to identify lncRNA expression profile in ductal carcinoma *in situ* and early stage breast cancers. We identified 103 differentially expressed (DE) lncRNAs of which 21 lncRNAs showed progressive pattern based on transcripts per million (TPM) in unmatched normal, adjacent normal, ductal carcinoma in situ, and stage 1 breast cancers. We identified several novel lncRNAs including RP11-295M3.4, LINC01614, RP11-527N22.1, RP11-126H7.4 and RAMP-AS1 that have not been reported in breast cancer before. These findings provide insights into lncRNA expression landscape in early stage breast cancers.