Knockdown of long noncoding RNAs in breast cancer


Dharmacon, now part of GE Healthcare, 2650 Crescent Drive, Suite #100, Lafayette, CO 80026, USA

Abstract

Traditionally, genetics has held a protein-centric view with RNA seen as an intermediate step between DNA and protein. Recently, the emerging evidence of pervasive transcription throughout the genome has challenged this view. Long noncoding RNAs (lncRNA) are selectively expressed during different stages of breast cell cycle as well as transcribed differently in specific cell types, which emphasizes their importance in regulating cell specification. lncRNAs can work on every stage of transcription from chromatin remodeling, controlling transcription to post-transcriptional processing through various mechanisms such as directly binding to transcription activation sites, acting as decoys for transcript suppressors/activators or as guiding/scaffold molecules for chromatin remodeling complexes.

Increasing numbers of studies have associated disease with lncRNAs. lncRNA expression profiling shows that lncRNAs are differentially expressed in breast cell lines and normal breast tissues from TCGA. The samples are grouped based on the lncRNA expression profiling showing that lncRNAs are differentially expressed in breast cancer. The results are then validated in additional assays (wound healing).

Introduction

lncRNAs show differential expression between tumor and normal samples

References