

LincRNAs: new epigenetic regulators of oncogenic pathways

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We recently reported the identification of a new class of large intergenic ncRNAs (lincRNAs) that are highly conserved in mammalian genomes. The "guilt by association method" that we developed to identify their functions pointed to a relationship between lincRNAs with chromatin remodeling complexes, particularly in the context of cancer. Moreover, we have profiled these lincRNAs across multiple cancer types and discovered numerous lincRNAs that are misregulated in cancer. For example, we show that p53 directly and temporally induces several chromatin-associated lincRNAs in response to DNA damage. Remarkably, these lincRNAs serve to regulate many key genes in the p53 pathway. Together, these results point to a general mechanism of lincRNA mediated regulation in key cancer processes, via the guidance of chromatin remodeling complexes.