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Identification of genes marked with H3K4me3 buffer domains: roles in cancer cell properties

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Background:

Tri-methylation of histone H3 lysine 4 (H3K4me3) is a major chromatin mark regulating gene transcription and it is mostly found around transcription start sites (TSS). Although this active chromatin mark is typically restricted to narrow regions of the promoter and the 5`region of the gene body, a small subset of genes have broad H3K4me3 regions (called H3K4me3 buffer domains). The function of these buffer domains is to ensure transcriptional consistency of the gene giving the cell the information about their identity.

Objective:

We are testing the hypothesis that genes marked by H3K4me3 buffer domains in colorectal and breast cancer cell lines are critical for gene programming of that cancer cell type, providing information about cancer cell's properties and malignancy, although these can be applied to any kind of disease. Identification of genes unique for each cell line will provide the knowledge necessary to understand cellular behaviour and would be useful for designing novel drug interventions to control the growth of these tumours.

Methods:

We performed ChIP-seq from colorectal cancer cell lines (HCT-116, RKO, HT-29 and CCD-841) and we analyzed previous ChIP-Seq data of breast cancer cell lines (MCF7, MDA-MB-231, MCF10A) and have identified genes that possibly play a crucial role in cell identity using bioinformatic tools

Results:

We have identified genes that possibly play a crucial role in cell identity. Among these genes are FOXA1 and GATA3 which have recently been reported to be essential in maintaining MCF7 properties.

Conclusion:

This demonstrates the significance of broad domains analysis as a useful tool to identify genes involved in cancer and their potential as drug targets