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Abstract Topic: - Epigenetics

Abstract Title: - Chromosome dynamics orchestrates transcription termination via epigenetic alterations.

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Aims: - To study the role of DNA methylation close to the transcription termination regions and its impact in the cell dynamics

Methods: - Methylation DNA immunoprecipitation (MeDIP),

Whole Trancriptome Analysis (WTA),

Chromatin Immunoprecipitation (ChIP), CRISPR/CAS9, Closed Chromosome Confirmation (3C), Molecular Biology, Targeted Bisulfite Sequencing, Mass-spectrometry

Results: - We observed CpG island between the two polyA sites of the gene differentially methylated. Based on the results from transcriptome analysis, we observed the shift in the polyA site usage for the transcription termination depending on the status of DNA methylation of the CpG island between the two polyA sites. This observation further identifies the association of several transcription factor and the components from the meiosis complex leading to alteration in chromosome architecture leading to shorter transcript formation. The same observation could be reversed upon removal of the transcription factor binding site via CRISPR. Further the identified targets shows the similar sensitivity to DNA methylation shift upon the heat shock. Further detailed evaluation identified more factors that are essential for the shift in DNA methylation. Entire observation could be reevaluated in the TCGA data base and correlates over 11 cancer types.

Conclusions: - We conclude that the shift in the DNA methylation can alter the transcription fate based on the factors associated with the particular genomic loci. Therefore, DNA methylation based variation in the genomic landscape across several physiological conditions should be evaluated.

Keywords: - We observed CpG island between the two polyA sites of the gene differentially methylated. Based on the results from transcriptome analysis, we observed the shift in the polyA site usage for the transcription termination depending on the status of DNA methylation of the CpG island between the two polyA sites. This observation further identifies the association of several transcription factor and the components from the meiosis complex leading to alteration in chromosome architecture leading to shorter transcript formation. The same observation could be reversed upon removal of the transcription factor binding site via CRISPR. Further the identified targets shows the similar sensitivity to DNA methylation shift upon the heat shock. Further detailed evaluation identified more factors that are

essential for the shift in DNA methylation. Entire observation could be reevaluated in the TCGA data base and correlates over 11 cancer types