BOSTON UNIVERSITY ACADEMY

Title: Finding potential HOXB13 regulators in ER+/HER2- breast cancer

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Abstract:

Breast cancer is one of the most commonly diagnosed cancers and carries significant morbidity and mortality. There have been many advancements in cancer genomics that may give patients a better chance at treatment. HOXB13 has shown to be clinically effective at predicting ER+/HER2- breast cancer patient prognosis. I explored possible regulatory pathways of HOXB13 expression by writing a high-throughput Python-based algorithm and using it on data from the National Institute of Health's Cancer Genome Atlas (TCGA) breast cancer study. I looked into potential regulatory elements by checking its coexpression with other genes, promoter methylation, post-transcriptional modification by miRNA, and by enhancer regions near the HOXB13 locus. I found a potential enhancer region downstream of HOXB13, genes that are positively and negatively correlated to HOXB13, and potential miRNAs that target HOXB13. Finding pathways of HOXB13 regulation can lead to the identification of ways to alter its expression in breast cancer and therefore improve prognosis and treatment for patients.