Transcriptional Response to Shear Stress in HUVEC Cells: A Comparison with Enhancer Count

Spencer D. Francis[a]

[a]*Brown University, Physics Department, Providence, 02912, Rhode Island, United States*

Abstract

RNA transcription regulation is influenced by shear stress from fluid flow, leading to the upregulation or downregulation of certain genes. This study examines RNA transcription and gene expression in human umbilical vein endothelial cells (HUVECs) to characterize how enhancer counts affect shear-regulated transcription. Our analysis demonstrates that in HUVEC cells, genes with multiple enhancers are upregulated more significantly than single-enhancer genes, suggesting that multi-enhancer genes exhibit a stronger transcriptional response to shear stress.

Keywords: Transcriptomics, Shear Stress, Enhancers

1. Introduction

RNA transcription is a fundamental biological process that governs gene expression and protein synthesis. This process involves a complex network of regulatory mechanisms that enable cells to respond to environmental stimuli and physiological signals. Understanding these mechanisms is critical for advancements in medicine and biology, particularly in addressing disorders related to gene expression.

Transcription factors play a pivotal role in RNA transcription by binding to specific DNA sequences, known as enhancers, to promote or inhibit transcription. Enhancers are thus key regulatory elements in gene expression.

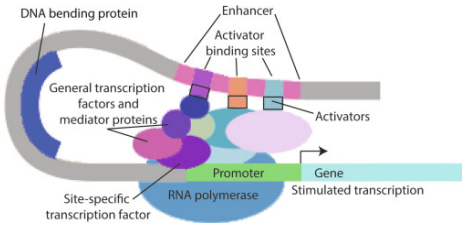

Figure 1: Diagram illustrating the process of RNA transcription. Image credit [1].

The transcriptional response is also influenced by mechanical forces, such as shear stress, exerted by fluid flow. Genes have been shown to alter their expression under shear stress [2]. Quantifying these changes often involves measuring fold changes, which compare gene expression levels under stressed and control conditions.

Previous studies ([2]) have suggested a link between enhancers and transcriptional responses to shear stress. This study uses that date to explore the relationship between the number of enhancers associated with a gene and its transcriptional response to shear stress.

2. Methods

HUVEC cells were cultured in a flow chamber, enabling observation under both control and shear stress conditions. Chromatin immunoprecipitation sequencing (ChIP-Seq) data was used to quantify gene expression levels. Data on enhancer locations in HUVEC cells was cross-referenced with gene annotations from Frankish [3] to determine the number of enhancers regulating each gene.

Python was employed for data analysis, leveraging libraries such as Pandas for data handling, Seaborn for vi-

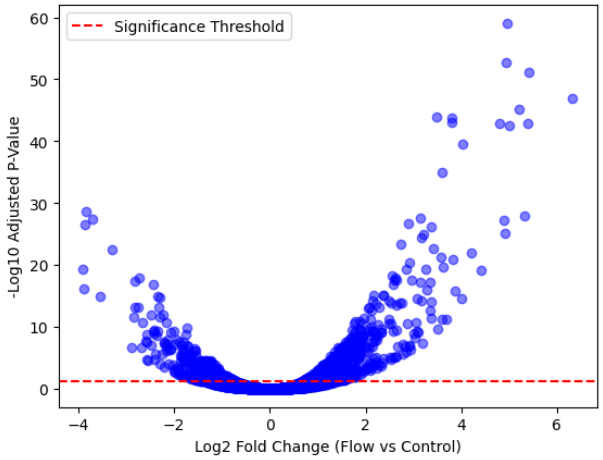

Figure 2: Volcano plot showing the fold change significance of genes. Genes with negative x-axis values are downregulated, while those with positive values are upregulated. The red line indicates the significance threshold (p = 0.05). Adapted from Tsaryk [2].

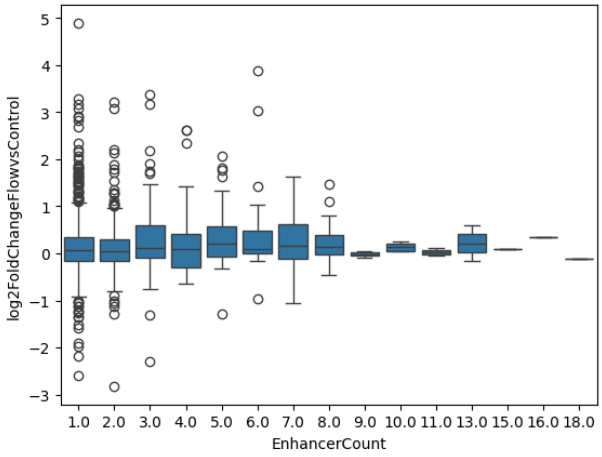

Figure 3: Boxplot showing the distribution of fold changes for genes with different enhancer counts.

sualization, and SciPy for statistical analysis. Bedtools facilitated the integration of genomic data.

3. Results and Analysis

Of the 1,704 genes studied, 1,029 were regulated by a single enhancer, while 675 had multiple enhancers. Figure 3 shows the distribution of fold changes for genes categorized by enhancer count.

Key findings include:

- Multi-enhancer genes were upregulated more significantly than single-enhancer genes. A t-test yielded $t = -1.76$, $p = 0.0779$.
- Multi-enhancer genes exhibited greater variability in fold change. Variance was 0.388 for single-enhancer genes and 0.426 for multi-enhancer genes. A Bartlett test indicated this difference was statistically significant ($\chi^2 = 1.51$, $p = 0.219$).

4. Conclusion

Our analysis underscores the critical role of enhancers in modulating transcriptional responses to shear stress. Multi-enhancer genes show stronger and more variable responses compared to single-enhancer genes. These findings support conclusions from Tsaryk [2], which highlighted the importance of enhancers in shear-stress response.

Future research should investigate the functional implications of upregulated and downregulated genes to elucidate the evolutionary and physiological significance of these responses.

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