Single Cell Topological and Transcription Analysis of Antimetastatic Effects of CARM1 Inhibitors

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CARM1 is a methyltransferase that methylates the BAF155 in the SWI/SNF protein complex, leading to cell proliferation and migration via the c-MYC pathway. SKI-73. EZM 2302, and TP-064 are three small molecule inhibitors that have shown promise in blocking CARM1. This study uses bioinformatics techniques to assess the effectiveness of these three inhibitors by examining the expression patterns of key genes withing a clustering map. scRNA data was collected from invasive cells, leukemia cells treated with DMSO, and cells treated with each inhibitor. This data was processed using SPRING, a kinematics-based interface tool that clusters cells based on their gene expression. Genes with differential expression were analyzed using Spearman Correlation to find genes with similar expression patterns. While a number of genes showed differential expression when exposed to SKI-73, the EZM2302, and TP-064 treated samples showed little to no change at the transcription level. These three inhibitors likely experienced off-target effects, binding to proteins other than CARM1. As a result, they have little effect on invasive cancer cells at the transcription level.