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*The Role of the miR-106b-25 miRNAs in Predicting Breast Cancer Outcomes in Differential Subtypes*

This study observed how the expressions of the miR-106b-25 miRNAs could be used to predict breast cancer patient outcomes. Based on previous work showing that the miR-106b-25 miRNAs are downstream of Six1 and induce breast cancer phenotypes, the hypothesis is that these miRNAs will be predictive of breast cancer patient outcome in human data sets. In addition, this study predicts that the miR-106b-25 miRNAs will have differential expression and outcome results in different breast cancer subtypes, and will specifically be enriched in Luminal B breast cancers, where Six1 is enriched and predictive of breast cancer outcome. I analyzed publicly available data-sets for relapse and survival rates based on the miRNA expressions. In order to simulate the results found in actual human tumors, I used real-time PCR to find the miRNA expressions of different cell-line subtypes. It was found that the expressions of the miR-106b-25 miRNAs are predictive of breast cancer patient outcomes. The highest expressions of the miRNAs are in Luminal B tumors. The expressions between cell-lines and human tumors are inconclusive. More study and more trials need to be performed in order to make definite conclusions.