Abstract

Pancreatic cancer, specifically pancreatic ductal carcinoma (PDAC), is highly lethal, with a 5-year survival rate below 10% due to several compounding factors that lowers the chances of patients to have a good prognosis. This underscores the need for better prognostic markers due to the lack of approved factors aside from a single marker. Current research trends focus on lncRNA due to their specific expression as well as their function as a regulatory mechanism of several genes. By correlating them with copy number aberration (CNA), one of the hallmarks of cancer, it is hoped that this a good prognostic marker can be elucidated. It is hypothesized that there is possible prognostic biomarkers that can be discovered from CAN driven lncRNA. Through *in silico* analysis utilizing RNA-seq and copy number data, as well as literature review, four potential prognostic biomarkers were discovered alongside their functional pathway. This four lncRNA are found to be in two groups with CCAT1 being in a single network with correlated mRNA while FAM83A-AS1; CASC8; and PVT1 are in another. This discovery indicates potential prognostic targets alongside functional pathways highly correlating to PDAC prognostics that can be further explored and studied.

Keywords: Pancreatic Ductal Carcinoma; Long non-coding RNA; Copy Number; *in silico* analysis