

Review of: "Predictive value of m5C regulatory gene expression in pancreatic adenocarcinoma"

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This study provides interesting perspective regarding the roles of m5C regulatory genes in pancreatic cancer based on bioinformatical methods. The study is logically arranged and methods are well-founded. While the manuscript describes an interesting topic, it is insufficiently discussed and leaves a number of questions unanswered.

1. This study analyzed the association of m5C regulatory gene changes with alterations to TP53, BRCA1, CDKN2A, and ATM in PAAD (**Table 1**). As we know, KRAS, TP53, SMAD4, and CDKN2A are the well-founded driver genes for PAAD. However, SMAD4 and KRAS were not included in this analysis.
2. As far as we know, the TCGA cohort included 185 PAAD patients. In **Figure 1A**, the authors analyzed 363 PAAD patients, which should be more elaborated.
3. Legend of **Figure 1D** seems to be incorrect.
4. In Figure 3, the authors should give more information about 'high/low stage T'. How the high or low was defined?