

This manuscript highlights the interaction between miRNA and colon cancer, because the Colorectal cancer (CRC) account ~ 10% of all new cancer cases in 2022 and is the third-most prevalent cancer in the world, I think it is very important to try identifying a novel parameter that might cause the disease. Furthermore, identifying the miRNA that causes the disease can be considered as a promising diagnostic biomarker or a novel therapeutic. Thus, in my opinion this kind of paper is important. Considering this specific manuscript, I think the topic is important. Yet, before it is published, some revisions are required to improve the manuscript:

Although the authors validate the results with TCGA COAD, I'm not convinced about the control samples, which were used in the experiments. This is because they were taken from different tissues of the patient "Adjacent normal colonic mucosa of each tumour was used as the corresponding control", and as it is known that miRNA expression is tissue specific. Thus, it might not be a good control. The authors may consider taking samples from healthy individuals. In addition, the tissue samples, which were taken from the patients, were taken from different areas in the colon, and from tumors of different Grades. What is the evidence that the gene expression level is the same in the different tissues and in the different tumors Grades?