Review of: "Increased Protein and Transcript Expression Levels of Lysine-Specific Demethylase 1 (LSD1) Signify Worse Prognosis in Triple-Negative Breast Cancer"

Xuequan Wang[1]

[1] Zhejiang Taizhou Hospital

Potential competing interests: No potential competing interests to declare.

The author made a relatively detailed analysis of the impact of LSD1 on triple negative breast cancer, but I think this article needs a lot of adjustment before it is published.

1.The author emphasized many aspects of epigenetics, but the article did not conduct an analysis of epigenetics.

2.This article detected the LSD1 gene influence on 879 hypoxia-, immune- and cancer-associated genes by NanoString counts using MAX Analysis System. But the samples collected in this article were all from 10 or 20 ago. Can such a long period of time ensure the stability of mRNA? If there is degradation of RNA, the length of storage time may lead to deviation in the expression difference analysis results.

3.It is best to indicate on the graph how many patients there are in each group for data, as the author does not have a relevant patient baseline table and reader does not know the specific information such as patient staging information.

4.The expression value in figure 4 needs to be specified, otherwise readers may not be very clear about what the negative expression value represent.

5.According to the literature about TCGA relative studies, there are more than 42 TNBC patients. Therefore, the number of patients analyzed in this paper is relatively small, which makes many analyses results not significant. Sufficient patients need to be re enrolled to improve the relevant analysis.

6.Can the difference analysis showed in the volcano be further validated by correlation analysis in other databases or different TNBC cohort.

7.The font size of the captions on many figures is relatively small, making it difficult for reviewers to read them clearly.

8.The functional enrichment in is not he overlap of the three database, its better to reanalyze after the number of patients in TCGA recounted.