



PEER-REVIEW REPORT

Name of journal: *World Journal of Clinical Cases*

Manuscript NO: 69324

Title: Development of a lipid metabolism-related gene model to predict prognosis in patients with pancreatic cancer

Reviewer's code: 05667363

Position: Peer Reviewer

Academic degree: MD

Professional title: Doctor

Reviewer's Country/Territory: Japan

Author's Country/Territory: China

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Reviewer chosen by: AI Technique

Reviewer accepted review: 2021-06-27 23:12

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Scientific quality	<input type="checkbox"/> Grade A: Excellent <input type="checkbox"/> Grade B: Very good <input checked="" type="checkbox"/> Grade C: Good <input type="checkbox"/> Grade D: Fair <input type="checkbox"/> Grade E: Do not publish
Language quality	<input checked="" type="checkbox"/> Grade A: Priority publishing <input type="checkbox"/> Grade B: Minor language polishing <input type="checkbox"/> Grade C: A great deal of language polishing <input type="checkbox"/> Grade D: Rejection
Conclusion	<input type="checkbox"/> Accept (High priority) <input type="checkbox"/> Accept (General priority) <input checked="" type="checkbox"/> Minor revision <input type="checkbox"/> Major revision <input type="checkbox"/> Rejection
Re-review	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No
Peer-reviewer statements	Peer-Review: <input checked="" type="checkbox"/> Anonymous <input type="checkbox"/> Onymous Conflicts-of-Interest: <input type="checkbox"/> Yes <input checked="" type="checkbox"/> No



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SPECIFIC COMMENTS TO AUTHORS

This study explored the differences in lipid metabolites between pancreatic cancer and paracancerous tissues and used the TCGA cohort model to identify lipid metabolism genes involved in pancreatic cancer malignancy. The author concluded that the lipid metabolites PC, PE, PEtOH, PMeOH, PS, and DGTS be significantly higher in cancer tissues, and a 4-gene signature model, including GALNT16, FADS3, CERS4, and ABO, was developed to predict the prognosis of pancreatic cancer. The writing, tables, figures are solid quality, and the observation is interesting, but I have the following concerns: 1: In the lipid metabolomics analysis using 9 cases of pancreatic cancer tissues, non-cancerous tissues (stroma, inflammatory cells, etc.) were also included in the analysis. How should we consider the influence of non-cancerous tissues? 2: Were all 9 cases analyzed not treated with preoperative chemotherapy? Even if there is a period between preoperative chemotherapy and surgery, preoperative chemotherapy may affect the metabolism. The association between the results of lipid metabolomics analysis using cancer tissues (PC, PE, PEtOH, PS, and DGTS) and the four genes from the TCGA cohort (GALNT16, FADS3, CERS4, and ABO) is unclear. Therefore, we believe that an additional description in DISCUSSION is necessary.