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PEER-REVIEW REPORT

Name of journal: World Journal of Gastrointestinal Oncology

Manuscript NO: 84710

Title: Proteomics-based identification of proteins in tumor-derived exosomes as candidate biomarkers for colorectal cancer

Provenance and peer review: Unsolicited Manuscript; Externally peer reviewed

Peer-review model: Single blind

Reviewer's code: 03004840

Position: Editorial Board

Academic degree: MSc, PhD

Professional title: Academic Research, Postdoc, Senior Researcher

Reviewer's Country/Territory: Turkey

Author's Country/Territory: China

Manuscript submission date: 2023-03-26

Reviewer chosen by: AI Technique

Reviewer accepted review: 2023-04-04 06:54

Reviewer performed review: 2023-04-17 21:05

Review time: 13 Days and 14 Hours

	[] Grade A: Excellent [] Grade B: Very good [Y] Grade C:
Scientific quality	Good
	[] Grade D: Fair [] Grade E: Do not publish
Novelty of this manuscript	 [] Grade A: Excellent [Y] Grade B: Good [] Grade C: Fair [] Grade D: No novelty
Creativity or innovation of this manuscript	 [] Grade A: Excellent [Y] Grade B: Good [] Grade C: Fair [] Grade D: No creativity or innovation



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Scientific significance of the conclusion in this manuscript	 [] Grade A: Excellent [Y] Grade B: Good [] Grade C: Fair [] Grade D: No scientific significance
Language quality	[] Grade A: Priority publishing [Y] Grade B: Minor language polishing [] Grade C: A great deal of language polishing [] Grade D: Rejection
Conclusion	 [] Accept (High priority) [] Accept (General priority) [Y] Minor revision [] Major revision [] Rejection
Re-review	[Y]Yes []No
Peer-reviewer statements	Peer-Review: [Y] Anonymous [] Onymous Conflicts-of-Interest: [] Yes [Y] No

SPECIFIC COMMENTS TO AUTHORS

The authors conducted a proteomic profiles of colorectal cancer (CRC) tissue exosomes and suggested the six exosomal proteins, NHP2, OLFM4, TOP1, SAMP, TAGL and TIF1B as promising diagnostic markers and effective therapeutic targets for CRC. The overall level of the paper is good, well written and important issues are emphasized. The hypothesis is clear and the results were reported in an organized way. However, it could be significantly improved by expanding on a few topics and providing more details. Below are suggestions for improving the manuscript. Selection of the candidate proteins could be an important issue for the readers. What is the filtration strategy of selected candidate genes? The authors are requested to provide the more details for the selection filter criterias instead of " based on the results and other findings" expression. The authors are requested to add the "Statistical analysis" part to the materials and methods section. Did the authors use tools for gene ontology and pathway analysis? All bioinformatic analysis was conducted using the R platform? Authors should indicate the bioinformatic analysis clearly in the "Bioinformatic analysis" part of the materials and methods section. What was the recorded video time duration and rate of frames



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per second information for the Brownian motion of the particles in the NTA analysis. Authors should add this information to the related part of materials and methods section. It would be informative for the readers. How much protein did the Authors use for the WB analysis? Authors are requested to give this information in the western blot analysis part of the materials and methods section. Authors are asked to analyze these six proteins in terms of prognostic importance such as overall survival analysis.