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PEER-REVIEW REPORT

Name of journal: World Journal of Clinical Cases

Manuscript NO: 60859

Title: Evaluation of a five gene signature associated with stromal infiltration for diffuse large B-cell lymphoma

Reviewer's code: 02544757
Position: Editorial Board
Academic degree: MD, PhD
Professional title: Professor
Reviewer's Country/Territory: Taiwan
Author's Country/Territory: China

Manuscript submission date: 2020-11-16
Reviewer chosen by: Ze-Mao Gong
Reviewer accepted review: 2020-12-30 15:15
Reviewer performed review: 2021-01-12 08:20
Review time: 12 Days and 17 Hours

Scientific quality	[ ] Grade A: Excellent [ ] Grade B: Very good [Y] Grade C: Good [ ] Grade D: Fair [ ] Grade E: Do not publish
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) [ ] Minor revision [Y] Major revision [ ] Rejection
Re-review	[Y] Yes [ ] No
Peer-reviewer statements	Peer-Review: [Y] Anonymous [ ] Onymous Conflicts-of-Interest: [ ] Yes [Y] No

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SPECIFIC COMMENTS TO AUTHORS

Through analyzing the e GSE60 dataset in DLBCL and using principal components analysis (PCA) plot, the authors identified five genes were closely associated with tumor stage and stromal infiltration in DLBCL. The author also found two genes, FN1 and SPARC, cooperatively expressed in DLBCL, which may be novel therapeutic targets for DLBCL. Although the current manuscript showed five genes may be associated with the development of DLBCL, there are many issues should be addressed. My comments are in the following 1. The author first used the GSE60 dataset to evaluate different gene expressions in DLBCL and normal tissue. Do the differentially expressed genes in DLBCL could further be divided into germinal center (GC) B-like or activated B-like DLBCL? I think this is important because the gene expressions in these two groups are different. 2. The author used the STRING to identify five hub overexpressed genes in DLBCL. The legends of Figure 2B-F are needed to describe the data validation from TCGA dataset. 3. The author studied the five hub genes that were higher expressed in late stages than in early stages. The FN1 gene expression had a stage-dependent increase. Are there any significant differences (P value) when comparing stage 2, 3 or 4 to stage 4? In addition, is FN1 gene expression also associated with high IPI scores in DLBCL? 4. In figure 5-8, the overexpression of 5 genes had different Spearman's relationship to stromal score or CAF. It is better to describe high, moderate, or low correlations of every genes, respectively. In addition, it is better to arrange other experiments to validate these correlations.