

# Peer Review File

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## Reviewer Comments

Yang and Wang confirmed ESCRT-III gene expression patterns in endometrial cancer samples from public omics databases. This paper is suitable to the scope of TCR journal, and provides interesting topics for endometrial cancer studies. The logical streams of this study are good. Thus, after minor revision, this paper should be published in the TCR journal.

### Comment 1:

This paper contains nine figures and two tables. Because many figures were listed in one manuscript, I suggest that some figures should move to supplementary figures.

### Reply 1:

We have modified our text as advised. Since we analyzed the data in the original Figure 1,3,4,6,8,9 from TCGA dataset depend on UALCAN, TISIDB, GEPIA online tool. We moved Figure 1 to Supplementary Figure 2, Figure 3 to Supplementary Figure 3, Figure 4 to Supplementary Figure 4, Figure 6 to Supplementary Figure 5, Figure 8 to Supplementary Figure 6, Figure 9 to Supplementary Figure 7. We renamed Supplementary Figure S1 as Supplementary Figure 1

While we analyzed the data in the original Figure 2,5,7 by GraphPad Prism 8.0 tool ourselves, so we reserved these figures, and renamed Figure 2 as Figure 1, Figure 5 as Figure 2, Figure 7 as Figure 3,

### Changes in the text:

Figure 1: see Page 11, line 15; Page 12, line 6; Page 14, line 18;

Figure 2: see Page 13, line 4-5, 7-11;

Figure 3: see Page 15, line 17, 22; Page 16, line 1;

Supplementary Figure 2: see Page 10, line 1-2, 6-7, 12-13;

Supplementary Figure 3: see Page 12, line 13;

Supplementary Figure 4: see Page 13, line 2;

Supplementary Figure 5: see Page 15, line 2;

Supplementary Figure 6: see Page 16, line 4-5, 15; Page 16, line 2;

Supplementary Figure 7: see Page 16, line 20;

Figure Legend: see Page 32, line 2-22; Page 33-34, line 1-21;

### Comment 2:

In figure 3A, there is no “C5” in the x-axis.

### Reply 2:

We have checked the data on TISIDB (<http://cis.hku.hk/TISIDB/index.phpon>). Since there were no cases in C5 (immunologically quiet) type in UCEC Tumors on TCGA database, so there is no “C5” in the x-axis on Figure 3A. UCEC tumors on TCGA database were classified into 6 immune subtypes based on immunogenicity analysis. C1 (wound healing) (n = 247); C2 (IFN-gamma dominant) (n = 212); C3 (inflammatory) (n = 52); C4 (lymphocyte depleted) (n = 16); C5

(immunologically quiet) (n=0); C6 (TGF-b dominant) (n = 1).

We added C5 (immunologically quiet) “(n=0)” on Legend of Supplementary Figure 3A

Changes in the text:

see Page 34, line 8;

Comment 3:

If possible, regression lines should be provided in each figure.

Reply 3:

We have modified our text as advised: we added multiple liner regression to analysis relationship between TILs (rho value) and ESCRT genes, and data was listed in table 3.

Changes in the text:

see Page 15, line 17-20;

see Page 11, line 1-2 in Table file;

Comment 4:

In the method section, there is no description of the visualization of each figure. I think the figure 2 and 7 were visualized as Python. Please provide visualization platforms or packages.

Reply 4:

We have modified our text as advised: We have saved all the Figures and Supplementary Figures as JPEG format. We designed the original Figure 2, 5 and 7, which is renamed Figure 1, 2 and 3 by GraphPad Prism 8.0 tool. We attached original data in Figure 1,2 and 3 in Supplementary file 2. Pzfx.

Changes in the text:

See Figure 1, 2 and 3; See supplementary file 2. Pzfx.

Comment 5:

Page 3, line 27: “microarray RNA-Seq” → Microarray and RNA-Seq are different tools.

Reply 5:

We have modified our text as advised: by Transcriptome RNA sequence (RNA-Seq)

Changes in the text

see Page 5, line 18;

Comment 6:

Page 4, line 10, and page 5, line 29: Maybe  $-\log_{10}(\text{p-value})$ ?

Reply 6:

We have modified our text as advised:  $-\log_{10}(\text{p-value})$ ;

Changes in the text:

See Page 6, line 18; and page 34, line 5;

Comment 7:

Page 4, lines 20-31: Many parameters were listed. I suggest that these parameters should be summarized as a table.

Reply 7:

We have modified our text as advised: the parameters of mutation types were summarized in

Supplementary Table 3. And we changed the order of the originally Supplementary Table 3 and 4.

Changes in the text:

See Page 7, line 9; page 10, line 2, 7, 13; page 11, line 15; page 12, line 6, 17; page 13, line 11;

See Supplementary file 1 Page 4-12;

Comment 8:

Page 5, line 3: GEPIA202 → Maybe GEPIA2021?

Reply 8:

We have modified our text as advised: GEPIA2021

Changes in the text:

See Page 7, line 20;

Comment 9:

Page 14, line 14: “nd” → Maybe “and”?

Reply 9: We have modified our text as advised: and;

Changes in the text:

See Page 19, line 8;