Peer Review File

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Reviewer A

Comment 1: Nevertheless, SMARCA4 (BRG1) as well as RANBP2 seem to be novel findings. SMARCA4 is now in the focus of a set of papers appearing in 2021. These publications should be mentioned and discussed. On the other hand, RANBP2 seems indeed a new interesting gene/protein for tamoxifen resistance.
Reply 1: We have modified our text as you advised (see Page 9-10, line 229-231).
Changes in the text: We have added some discussions about new research in recent years.

Comment 2: Taken together, I expect an evaluation of the new findings using other databases especially concerning patient data, before this manuscript can be published.
Reply 2: The data we use comes from an open database composed of five cell lines: TamR1, TamR4, TamR7, TamR8 and MCF-7/S0.5. There is no prognosis or treatment information on patients. In the next step, we plan to collect more clinical patient information for further research.

Comment 3: Additionally, new literature is available that should be cited.
Reply 3: We have modified our text as you advised (see Page 13, line 313-320; Page 15, line 357-365; Page 16-17, line 395-402).
Changes in the text: We have cited several new literature of recent year.

Reviewer B

Comment 1: Please revise the english
Reply 1: We have polished the language already,and we are going to use the medical writing service if necessary , after the manuscript was modified. All the work will be done before publication.

Comment 2: As ERbeta also exists, the authors have to specify alpha in the text to clarify more.
Reply 2: We have modified our text as you advised (see Page 3, line 46; Page 9, line 214,218).
Changes in the text: We changed the ER into ERα.

Comment 3: The introduction (and discussion) about BC treatment is incomplete: Tam is only used for premenopausal women, and postmenopausal women are treated with aromatase inhibitors.
Reply 3: We have modified our text as you advised (see Page 3, line 49; Page 7, line 163).
Changes in the text: We added sorme directions in the introduction and discussion.

Comment 4: In the method section, please provide more informations about the

patients.
Reply 4: We have modified our text as you advised (see Page 4, line 88-90).
Changes in the text: We added some introduction about original gene samples used in this study.

Comment 5: In the result section, the authors should add the list of gene differentially expressed between the two type of tumors
Reply 5: We have modified our text as advised (see Page 6, line 126).
Changes in the text: We have added a new table to the attachment.

Comment 6: p9: lane 210: and so on is not appropriate.
Reply 6: We have modified our text as advised (see Page 9, line 226).
Changes in the text: We removed this part and made the sentence smooth.

Reviewer C
Comment 1: The bioinformatic analyses employed for such a purpose are quite simple and their description is incomplete and wouldn't allow the reader to replicate the results.
Reply 1: The bioinformatic analyses softwares are simple to use, and many of the database are free to public. But there is a lot of work to do on database selection, data processing, image editing etc,which really consumes a lot of time and energy. We believe the results can be replicated but it needs sufficient preparation and patience.

Comment 2: The results presented in this study are of interest but are insufficient to be relevant. One would have expected to see the response to treatment in different groups with survival curves.
Reply 2: The data we use comes from an open database composed of five cell lines: TamR1, TamR4, TamR7, TamR8 and MCF-7/S0.5. There is no prognosis or treatment information on patients.In the next step, we plan to collect more clinical patient information for further research.

Comment 3: The discussion remains slightly incomplete and lacks of recent references. Recent relevant findings in the field of tamoxifen resistance are not referenced or contrasted.
Reply 3: We have modified our text as advised (see Page 7, line 164-174).
Changes in the text: We have added some discussions about new research in recent years.

Comment 4: More importantly, the results and methodology are not compared to those of the study where the data comes from.
It is unclear why the results of DEGs presented by the authors are different to those presented in the original study
Reply 4: These original data was submitted on Apr 15,2015. All data analyses were performed using Partek Genomic Suite (Partek, Inc., Chesterfield, MO, USA),Ingenuity Pathway Analysis (IPA) 8.6 (Ingenuity Systems, Redwood City, CA,

USA) was used to evaluate whether the genes differentially expressed in association with tamoxifen resistance.And then they updated the data for several times.The latest data was submitted on Mar 25, 2019， and we can not download the data before.The purpose of our research is to find new nodes that may exist by using updated data and new analysis methods. Therefore,the data and analysis tools we used in this study was not exactly the same, and the results of DEGs presented were different to original study.

Comment 5: Also, there are a few language inconsistencies in the manuscript. For example, the terms "resistance" and "resistant" are sometimes crossed and tamoxifen is sometimes referred to by its entire name and sometimes by its acronym (TAM)
Reply 5: We have modified our text as you advised (see Page 4, line 68; Page 6, line 124; Page 7, line 175).
Changes in the text: We changed the words and made sentences smooth.