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The author has no potential conflicts of interest to disclose.

The Author's Response: Bioinformatics Analysis in Downstream Genes of the mTOR Pathway to Predict Recurrence and Progression of Bladder Cancer

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► See the letter "Letter to the Editor: Bioinformatics Analysis in Downstream Genes of the mTOR Pathway to Predict Recurrence and Progression of Bladder Cancer" in volume 33 on page e103.

Dear editor,

Thank you for your interest to our recent report. Also, I really appreciate you and your reasonable comments for our paper.

Due to the high false positive caused by the characteristics of microarray, it is right that gene selection is performed by rational statistical method, based on analysis of variance model and so on. However, in practice, changes in expression of at least 2-fold have been considered significant, although only rarely has any statistical or biological justification been offered for the selection of this threshold.^{1,2} Of course, the data must be normalized to eliminate systematic variations, which are not related to changes in relative RNA abundance for individual genes.

I agree with you that choosing the proper statistical method and obtaining more accurate and convincing results of differentially expressed genes (DEGs) analysis is the basis for further analysis. As you know, over the past years, numerous tools have emerged for microarray data analysis. Nonetheless, depending on what statistical method researcher use, the results of microarray data are slightly different.^{3,4} Although we did not use the proper statistical method, we selected highly expression level-changes genes of at least 2-fold and confirmed the expression level of genes considered as key genes using reverse transcription-polymerase chain reaction or western blot.⁵ I think our results show the unprecedented insight of gene regulation in recurrence and progression of bladder cancer.

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