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Letter to the Editor: Bioinformatics Analysis in Downstream Genes of the mTOR Pathway to Predict Recurrence and Progression of Bladder Cancer

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▸ See the article "Identification of Downstream Genes of the mTOR Pathway that Predict Recurrence and Progression in Non-Muscle Invasive High-Grade Urothelial Carcinoma of the Bladder" in volume 32 on page 1327.

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The authors have no potential conflicts of interest to disclose.

Dear editor,

We read with great interest the recent report by Jin et al.,[1] "Identification of Downstream Genes of the mTOR Pathway that Predict Recurrence and Progression in Non-Muscle Invasive High-Grade Urothelial Carcinoma of the Bladder," which appeared on 7 June 2017 in *Journal of Korean Medical Science*. The results of the report are very helpful for us, however, from our perspective, the author's methods in bioinformatics analysis are inappropriate.

We are noticed that the authors only consider gene expression values for detecting differentially expressed genes (DEGs) after small interfering RNA (siRNA) or rapamycin treatment. Actually, due to the high false positive caused by a huge number of probes and multiple comparisons, it is fundamental to analyze microarray data properly to reach a reliable result by a rational statistical method. Obviously, only selecting genes with 2-fold change in expression is not reliable and suitable for high-level microarray analysis. From our perspective, we recommend using specialized high-level microarray analysis, Linear Models for Microarray Analysis,[2] a commonly used statistical test to analysis differential expression package by using linear models, and choosing more than 1.5-fold expression change and false discovery rate < 0.05 as the cutoff is an appropriate and conservative approach to obtain DEGs. Moreover, Significant Analysis of Microarray (SAM)[3] is also a considerable non-parametric statistical algorithm, and 2-fold expression change and q < 0.1 is a rational cutoff to obtain DEGs.

Above all, although the authors performed extra analysis for a portion of DEGs in order to verify the results of the microarray, it is impractical using reverse transcription-polymerase chain reaction or other technology to verify all DEGs. Choosing the proper statistical method[4] and obtaining more accurate and convincing results of DEGs analysis is the basis for further analysis such as gene ontology enrichment analysis and Kyoto Encyclopedia of Genes and Genomes pathway analysis.

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