Gu et al. report in this paper approach of characterizing the different expressed autophagy genes and they develop a six autophagy genes-based signature to predict the overall survival of patients with papillary renal cell carcinoma. They also try to investigate the molecular pathway alteration between the patients stratified by the autophagy genes risk scores using gene set enrichment analysis. Following questions/comments were raised during the review of the paper:

1. In the " Materials and methods" section, the second sentence of the second paragraph, the parameters setting should be clarified: The threshold of fold change and P-values were set as LogFC = log2(2) and P-Value <0.001, respectively.
2. Please also clarify the risk score formula description in the method part: mRNA(m) expression × coefficient (n), what is n denoted? This can be written as: the coefficient of each gene was measured by a multivariable Cox regression hazard model with selected autophagy genes. The Sum of mRNA(i) expression × coefficient (i) would be better.
3. The autophagy gene predictor shows a very promising result with pRCC. Could you find other external validation from GEO if possible? That will render this study more reliable!