Dear Editors:

In this work, we firstly constructed a risk model using 4 IRGs (IL13RA2, CCL19, BIRC5, and INHBE) for the prognostic prediction of patients with PRCC from the TCGA database. The risk score generated by this model can as an independent prognostic predictor to distinguish patients with different survival outcomes for PRCC. Moreover, this prognostic model may also serve as predictor for increased immune cells infiltration (B cells and CD4+ T) and can stratify patients with different mutation burdens in PRCC patients. Our study develops the knowledge of IRGs in PRCC and provides new potential prognostic and therapeutic biomarkers. I hope this paper is suitable for “Algorithms for Molecular Biology”.  
 We deeply appreciate your consideration of our manuscript. If you have any queries, please don’t hesitate to contact me at the address below.

Thank you and best regards.  
Yours sincerely,

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