In the light of the study done by Yang *et. al* and entitled "GPX2 is one of three key genes predicting recurrence-**free survival and regulating proliferation, invasion, and apoptosis based on EMT and Wnt/β-**catenin signaling pathway in prostate cancer". The authors utilize the power tool of bioinformatics and computational analysis to detect a group of genes that are related to prostate cancer (PCa) recurrence.

The study also clearly showed the relationship between Glutathione peroxidase 2 (GPX2) expression and the prognosis of PCa and this can be used in the future as a prognostic tool to improve the health welfare of PCa patients. Also it add more for better understanding this relationship, however, the authors should address the following points to improve their current study to be more sounded

Comments to the authors:

- What are the current rates of survival and death according to the American association of cancer?
- Usually online dataset are updated on a regular basis .Can authors mentioned the time period they visited and downloaded the dataset they used in the study?
- Can authors mention the reference of primers used in this study? Or they designed it?
- What are the PCR conditions used in this study? How many cycles were used?
- How long after transfection authors the LNCap Cells were incubated prior to CCK-8 assay?
- What does the author mean by this sentence? Or they mean 10μl of CCK-8 kit.
- How much protein was loaded by lane? What is the concentration?
- Can authors mention the dilution of antibodies they used ?