Reviewer's report

Title: Network analysis of an in vitro model of androgen-resistance in prostate cancer

Version: 2 Date: 5 May 2015

Reviewer: Bairong Shen

Reviewer's report:

The work's aim is to understand biological network profiles of transcriptomic changes occurring during the transition to androgen-resistance and to validate these changes between our in vitro model and clinical datasets. The work is interesting and have interesting results for the future prostate cancer study, a few points need to be considered and discussed as follows,

1) a related work need to be mentioned and cited, the following work apply protin network and machine learning to the analyses of prostate cancer at the network level.


2) for study of transcription factor in prostate cancer, the previous work can be seen from, Jiang J, et.al. Key regulators in prostate cancer identified by co-expression module analysis. BMC Genomics. 2014 Nov 24;15:1015.

3#the consensus for cancer mechanism is often found at the pathway level, as you state, "...found that differential expression in both datasets converged at the pathway level (full results Supplementary Tables 1 & 2)" The following work should be used to support the findings. Their works just proposaled that pathway level analysis is more consensus for cancer study.


4) the heterogenous of prostate cancer is not discussed, and the following works should be referenced, such as the following work reported the prostate cancer from different populations is not the same for their molecular mechanisms.


Level of interest: An article whose findings are important to those with closely
related research interests

**Quality of written English:** Acceptable

**Statistical review:** No, the manuscript does not need to be seen by a statistician.

**Declaration of competing interests:**

'I declare that I have no competing interests'