Reviewer's report

Title: Integrative analysis of neuroblastoma and pheochromocytoma genomics data

Version: 1 Date: 26 June 2012

Reviewer: Jianhua Ruan

Reviewer's report:

This manuscript presents an integrated analysis of a large number of microarray datasets to study NB and PCC. Overall, the study is very carefully designed and the results are clearly presented and convincing. My main concerns are that (1) statistical significance was not presented for most of the results; and (2) some analytic methods were not provided in detail, which makes some sections hard to follow.

Major Compulsory Revisions:

1. Figures 1-8 represent the “most significant” pathways identified by IPA from the various gene lists that the authors obtained from the microarray data analysis. However, statistical significance (p-value) was never presented, nor was the statistical test used to determine the significance mentioned in the paper. Furthermore, as IPA is a proprietary software, it is not generally accessible to the public. The authors should consider repeat the pathway analysis with some publicly available tools such as the DAVID functional analysis tools or at least demonstrate that the results are similar on some of the gene lists.

2. The statement that NB and PCC are “more similar to each other than to any other tumor entity” is not true. Looking at the dendrogram, it shows that NB and PCC have a common parent node. But it is hard to determine whether the distance between them is necessarily smaller than the distance between NB or PCC to any of the samples on the left branches of tree. A similarity matrix among all samples is probably a better way to support the authors’ claim. Furthermore, in the dendrogram, it is shown that there is only one node for each type of tumor (including NB and PCC). Are the multiple samples for each tumor averaged before applying hierarchical clustering? This is not described in Methods.

Minor Essential Revisions:

3. Statistical analysis of mRNA profiling studies. Differentially expressed genes were identified using one-way ANOVA, with Benjamini-Hochberg multiple testing correction. What is the significance level (q-value) used for selecting differentially expressed genes?

4. “normalized dCT values”. dCT needs to be spelled out, or simply replaced by “intensity”.

Discretionary Revisions
5. It is a little bit odd to mention NetBeans IDE and codeBlocks.org. It is like saying “this paper is written with Microsoft Word”.

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

**Quality of written English:** Acceptable

**Statistical review:** Yes, and I have assessed the statistics in my report.

**Declaration of competing interests:**

I declare that I have no competing interests.