Reviewer's report

Title: The Roche Cancer Genome Database 2.0

Version: 1 Date: 2 February 2011

Reviewer: Shinsei Minoshima

Reviewer's report:

This manuscript entitled "The Roche Cancer Genome Database 2.0" by Dr. Jan Küntzer and his/her coworkers described their upgraded database for genetic and molecular information for human cancer. This database is obviously excellent, useful and easy to use, and their manuscript is clear. As one of potential users, I had the following impression and feedbacks.

Major Compulsory Revisions
None.

Minor Essential Revisions
None.

Discretionary Revisions
The followings:

1. For manuscript

The previous version of this database was described in Human Mutation and Nucleic Acids Research, 2010. Has the previous version been already abolished? If the previous version is completely included in the new version, it would be better to be mentioned in a text about that. If not, isn't it worth keeping older version on line with the new version? Otherwise, readers of the papers of the previous version might be confused a little.

2. Points to be desired for improvement and further development for database contents and functions:

(1) In spite that the database name has the word "genome", "genomic" functions look not enough. For example, the following data contents and functions are desirable.

a. Graphical genomic view for mutations/polymorphisms in introns, UTRs, promoters and spacer regions.

b. Graphical wide genomic view to show CNVs which affect one or more genes.

(2) Browsing functions for entire contents are desired. Users cannot know if the information of their interests is covered until they actually search it. Especially, number of contents is not available for genes, cell lines and tissues. For these, approximate scale of this database is not clear (e.g. this database includes 100, 500, 1000, or 5000 genes?) .
(3) Currently, domain information is not displayed for any gene as far as I tried. Is that OK? Is the function highly browser-dependent? I used Firefox ver.3.6 and IE ver.6. on WindowsXP.

(4) Search functions using domain information is desired. For example, search for genes/proteins with domain(s) of interest and mutations/polymorphisms within the domain(s) would be very useful.

(5) Regarding the current "Smart search function":

a. If each information in result table has hyper-link, it would be useful.

b. When users wish to add more keywords such as additional genes after some search, it would be better that they can be added in the result view. Currently, it looks no such function. Even, clicking backward button of browser totally abolishes previously typed keywords. It’s very sad.

c. In the Pure Somatic Mutation function in Smart Search, the result with 2 or more genes is displayed without gene names. If it’s within the planned functions, how readers should use this?

**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.