Reviewer’s report

Title: The database of chromosome imbalance regions and genes resided in lung cancer from Asian and Caucasian identified by array-comparative genomic hybridization

Version: 1 Date: 23 February 2012

Reviewer: Giovanni Blandino

Reviewer’s report:

Nice work about the identification of relevant chromosome imbalance regions in Asian and Caucasian lung cancer, showing ethnic variations but also common regions that might play a role in lung tumorigenesis.

Minor Essential Revisions:

1) Abbreviation of DAVID: Database for Annotation, Visualization and Integrated Discovery
2) Figure numbers are within the figure (Figure 2, Figure 3)
3) Page 7 on top: dH2O instead of DH2O
4) Page 17: (Fig.2) should be (Fig.3)
5) Page 7 and page 10, one time Cy5 was described to be used for the tumor samples, one time for the reference (Methods vs Results section).
6) Figure legend 2: MetaCre should be MetaCore?

Major Compulsory Revisions:

1) Page 8 “cutoff value for amplification was the mean of normal lung tissue expression”: The authors should state that the GAPDH primers for normalization are located within the promoter of GAPDH. So the normalization was probably not done against the normal lung tissue EXPRESSION. They should try to explain their calculation/normalization method in a different way.
2) Also for the “cutoff value for overexpression…” in the RT-qPCR section I prefer the explanation within Figure 3.
3) Page 11: “seven common chromosomal imbalance regions harboring 117 genes”: the authors should explain why there are only 117 genes; looking at the table 1 one could think that more genes are included in the common chromosomal imbalance regions.
4) Page 13: The authors should make a little comment on the fact that the DNA copy number validation for ZNF322A is a bit lower compared to the CGH result.
5) Figure legend 4A: The authors could add: “Representative” in front of the CISH images…and add the patient number(s).
6) Page 15, Discussion: “identified THE causal chromosomic regions whose
structural alteration is critical for lung tumorigenesis”. Considering the fact that the CGH array and also the initial analysis for LOH that determined the construction of their CGH array [reference 13 in the text] contained always a kind of section and not a whole genome analysis the authors should be more careful in their statement.

7) The authors should include the publication “Genomic Profiles Specific to Patient Ethnicity in Lung Adenocarcinoma” by Philippe Broët et al. in the Discussion.

8) The English should be improved in some parts of the manuscript.

Level of interest: An article of importance in its field

Quality of written English: Needs some language corrections before being published

Statistical review: Yes, but I do not feel adequately qualified to assess the statistics.

Declaration of competing interests:

I declare that I have no competing interests