Reviewer's report

Title: Association between polymorphisms in XRCC1 gene and clinical outcomes of patients with lung cancer: a meta-analysis

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Reviewer: Qingyi Wei

Reviewer's report:

General comments:
In this meta-analysis, Yin et al. assessed the association of polymorphisms XRCC1 194 C/T and XRCC1 399 G/A with clinical outcomes of patients with lung cancer. They used 22 articles in the final analysis and found that the C/T, T/T and minor variant T allele genotype of XRCC1 194 were statistically significantly associated with objective response in all patients. For XRCC1 399, G/A genotype, A/A genotype and minor variant A allele were associated with objective response in all patients. Both G/A and A/A genotype of XRCC1 399 could influence OS of lung cancer patients. Interaction analysis suggested that patients with genotypes of XRCC1 194C/T and XRCC1 399 G/A or combination of XRCC1 194 T/T and XRCC1 399 G/G showed better objective response compared with the patients carrying XRCC1 194 C/C and XRCC1 399 G/G genotypes. They concluded that genetic polymorphisms in the XRCC1 gene might be associated with prognosis and response to platinum-based chemotherapy in lung cancer patients. Although some of the findings are interesting and potentially significant, most of the studies included in this analysis were in Chinese or Asian populations with a relatively small number in each of the studies. Therefore, it is important that the positive findings should be tested for false positive reporting probability, and the conclusion should be confined to Chinese or Asian populations. Although this is a timely meta-analysis for the association between genotypes and clinical response to treatment in lung cancer, an interesting area for the concept of personalized medicine, the authors need to understand the ethnic difference in genetic background that may have modulate the response differently. Also the sample size issue, even for such meta-analyses, is always a concern in drawing the conclusions.

Minor comments:
1. The gene name should be italicized throughout the text.
2. Please provide the rs# for the SNPs included in the analysis in the abstract.
3. The column label of Table 1 “Biomarker” should be “Outcome”.
4. Table 2 is unnecessary, and the contents can be put into the footnotes of Table 3 and Figure legends instead.
5. Figures 2-4: It is not clear what genetic model was used for each of the 2A, 2B, and 2C figures, such as dominant, recessive, additive or other genetic
models? Please state this in the figure legends.

6. Figure 4: The genotype comparisons were not labeled in each of the figures, nor the events out of the total number of the subjects were given.

7. Some of the forest plots showed one study to be an outlier. In this case, a sensitivity test should be performed by excluding such an outlier to see any improvement in the estimates.

8. Figure 5 should be eliminated because the numbers were too small to test for an interaction.

9. There are numerous typos or grammatical errors throughout the text that need to be corrected. For example, just in the Abstract,
   a) “genetype” should be “genotype”.
   b) “significantly statistically” should be “statistically significantly”.
   c) “%95CI” should be “95% CI”.

**Level of interest:** An article of importance in its field

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

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

**Declaration of competing interests:**

I declare that I have no competing interests'