Reviewer's report

Title: Multi-susceptibility genes associated with esophageal squamous cell cancer risk and their potential use to identify subjects at high risk

Version: 1 Date: 22 March 2011

Reviewer: Elias Zintzaras

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For each variant, calculate the unadjusted and adjusted OR for the allele contrast (only unadjusted), dominant, recessive, additive and co-dominant models (See Zintzaras E, Lau J. Synthesis of genetic association studies for pertinent gene-disease associations requires appropriate methodological and statistical approaches. J Clin Epidemiol. 2008 Jul;61(7):634-45).

An additional analysis based on the generalized odds ratio (ORG) should be performed (see Zintzaras E. The generalized odds ratio as a measure of genetic risk effect in the analysis and meta-analysis of association studies. Stat Appl Genet Mol Biol. 2010;9(1):Article21) The ORG utilizes the complete genotype distribution and provides an estimate of the magnitude of the association between disease status (disease vs. healthy or disease progression) and genotype (biallelic or multiallelic). So, apply the ORG for each phenotype, and to investigate disease progression.

Explain how the sample size was calculated, and determine the posterior power of the study.

Omit the discriminant and ROC analysis.

Level of interest: An article of importance in its field

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'