Reviewer's report

Title: Genomic profiling identifies common HPV-associated chromosomal alterations in squamous cell carcinomas of cervix and head and neck

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Reviewer: Nallasivam Palanisamy

Reviewer's report:

Major compulsory revisions:
Review report for the manuscript entitled “Genomic profiling identifies common HPV-associated chromosomal alterations in squamous cell carcinoma of cervix and head and neck” by Wilting et al.

The authors claim that to the best of their knowledge it is the first study comparing the genomic changes in cervical cancer with head and neck cancer. Although it has been known that human papillomavirus (HPV) is involved in the etiology of both cervical cancer and head and neck cancer, this study was aimed at understanding the existence of common aberrations between the two cancer types.

BAC array data set is not available, through the URL provided, for view until June 2009.

In my opinion, the major weakness in this study is not including a detailed description of the aberrations identified in this study. The CGH aberrations are presented in the same resolution and format as the CGH community used to describe the CGH data obtained using metaphase chromosome based CGH analysis.

Although the resolution limit of BAC array CGH is about 1Mb, copy number changes can be better resolved than conventional chromosome based CGH. Loss of 13q21.1-21.33 and gain of 20p12.1-q13.33 and all common aberrations should be presented in much more details to accurate genomic coordinates and the list of BAC clones and the genes included in these regions should be provided. Although these two cancer types share some common aberrations, do they share the same genomic boundaries; if not a minimal common region (MCR) should be defined. A refined analysis will likely identify a potential target genomic region or genes affected by HPV infection which will be a significant improvement towards understanding the genetic basis of these two cancer types with HPV involvement.

All the aberrations presented in Figure 3 should be presented at its actual genomic resolution and copy number level. I would like to suggest to include an independent validation using FISH to assess the copy number levels for both losses and gains.
Level of interest: An article whose findings are important to those with closely related research interests

Quality of written English: Acceptable

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

Declaration of competing interests:

no financial competing interests