Reviewer’s report

**Title:** DNA methylation changes in ovarian cancer are cumulative with disease progression and identify tumor stage.

**Version:** 4  **Date:** 7 August 2008

**Reviewer:** Robert Brown

**Reviewer’s report:**

The authors have addressed all of the concerns raised in my original report satisfactorily, with the exception of confirming the discriminatory power of the 3 class predictors of Stage III versus benign/LMP samples loci using an independent method of methylation analysis. I do accept that there is substantial information that many sequences identified on these types of arrays do validate. However, there can be issues of false-positives and it would have been reassuring to have seen these data. Nevertheless given the consistency of methylation change observed for multiple samples in present study and the previous published literature, I am prepared not to insist on this.

**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:**

Work in our laboratory is also conducting genome-wide analysis of methylation patterns in ovarian cancer. This work has been funded by Cancer Research UK, Ovarian Cancer Action and Orion Genomics (St Louis, USA).