Reviewer's report

Title: A streamlined method for analysing genome-wide DNA methylation patterns from low amounts of FFPE DNA

Version: 0 Date: 26 Feb 2017

Reviewer: Dajun Deng

Reviewer's report:

Dr. Ludgate et al. described an optimized method to extract genomic DNA from FFPE samples for analyzing genome-wide DNA methylation. It may be useful for methylation analyses using FFPE samples. However, a proper control method has not been used in their study. It is very difficult to evaluate the exact impact of the optimized method on analyzing genome-wide methylation patterns without a regular method control. Although they compared the performance of the optimized method with those of other methods reported by others, however, the performance of each method maybe laboratory-, personal-, time-dependent. Therefore, a regular control should be added into their study. In addition, as a method manuscript, please consider to use the following concepts, including recovery rate, detection limit, false negative/positive results, and reproducible, to describe the advantage of the optimized method.

Are the methods appropriate and well described?
If not, please specify what is required in your comments to the authors.

Yes

Does the work include the necessary controls?
If not, please specify which controls are required in your comments to the authors.

No

Are the conclusions drawn adequately supported by the data shown?
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