Reviewer’s report

Title: Within-sample co-methylation patterns in normal tissues

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Reviewer: Xiaoke Ma

Reviewer's report:

Epigenetic is critical for many important biological processes, such as gene expression. Thus, it is promising to reveal the methylation patterns since these patterns may shed light on revealing the underlying mechanisms of complex diseases. The authors provide statistical analysis tools to investigate the co-methylation patterns within samples, which is interesting. In all, this is a well conducted study, even though the findings are not surprising. The data analyses are appropriate and uses current standards, which provide clues for further study. I, however, also found some problems in this paper:

1. There are only two datasets are used. Whether these patterns also occur in other datasets? In Fig.2, is the difference of curves significant? i.e. what is the p-value.


In all, the manuscript is well written and well conducted.

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An article of importance in its field

Quality of written English
Please indicate the quality of language in the manuscript:

Acceptable
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