Reviewer’s report

Title: Paternal obesity is associated with IGF2 hypomethylation in newborns: results from a Newborn Epigenetics Study (NEST) cohort.

Version: 2 Date: 2 July 2012

Reviewer: Jeffrey Craig

Reviewer’s report:

The manuscript by Soubry and colleagues describes a study of the effect of paternal and maternal obesity on neonatal methylation in blood leucocytes using bisulfite pyrosequencing. The analysis is well described and the conclusions generally well thought out and convincing. However, there are a small number of details and discussion points missing that should be addressed.

Major compulsory revisions

1. The two IGF2/H19 DMRs used in this study should be better described. The IGF2 DMR they use is a somatic DMR whose methylation is set after conception. This has profound implications for the interpretation of the authors’ findings and must be discussed. The H19 DMR used in this study is presumably part of the imprinting control region (ICR), which is a germline DNA whose methylation levels are set during spermatogenesis. Can the authors please confirm that this is indeed the case? Has anyone else measured DNA methylation within their H19 region?


3. The authors should discuss the weakness of analysing whole blood e.g. cell heterogeneity
No Minor Essential Revisions

Quality of written English: Acceptable

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

Declaration of competing interests:
I declare that I have no competing interests