Reviewer’s report

Title: Microarray gene expression profiling of subcutaneous adipose tissue in obesity: Distinct expression of cell-cycle- and differentiation-related genes

Version: 1 Date: 18 October 2010

Reviewer: Birgit Samans

Reviewer’s report:

Major Compulsory Revisions

Image 2B
The number of plotted measurements differs in the captions of the figure (n=155) and the displayed graph (n=169). This should be corrected. Further, the authors need to describe the high number of measurements, because only 15 genes were assayed by RT-PCR.

Sector "Statistical methods"
The description of the statistical methods should be more concrete and mentioned at the point in the publication where they have been used.

Discretionary Revisions

Image 1A has no statistical relevance as it is based on previous calculated differentially expressed genes and should be omitted.

Image 1C does not contribute to the discussion of the data and should be omitted or discussed in detail.

From the statistical point of view the normalisation of the microarrays is not optimal. The loess normalisation is based on the assumption that most of the genes are not differentially expressed and the number of up or down regulated genes are equal. Due to the low number of selected genes on the microarray this assumption might not be fulfilled. I suggest that the authors normalize the data using housekeeping genes or control spots.

Level of interest: An article of importance in its field

Quality of written English: Acceptable

Statistical review: Yes, and I have assessed the statistics in my report.

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