Author's response to reviews

Title: Association of adipocyte genes with ASP expression: a microarray analysis of subcutaneous and omental adipose tissue in morbidly obese subjects

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Author's response to reviews: see over
Dear Dr Edmunds

We would like to resubmit our paper entitled: Association of adipocyte genes with ASP expression: a microarray analysis of subcutaneous and omental adipose tissue in morbidly obese subjects (MS: 1211627805229324) by authors Robin MacLaren, Wei Cui, HuiLing Lu, Serge Simard and Katherine Cianflone.

We have revised the manuscript in response to the minor comments suggested by the reviewer’s report of 30 November 2009 (reviewer Johanna Hardin). Specifically as requested we have added the three clarifications requested (as detailed in the response to reviewers below).

We appreciate the opportunity to submit to BMC Genomics, and look forward to the response.

Sincerely
Katherine Cianflone PhD
Response to reviewer:

We appreciate the positive comments of the reviewer: “It seems as though the authors have done substantial work to address the previous concerns addressing the statistical analysis…..An article of importance in its field”. Further, we appreciate the helpful comments and we have completed the modifications as suggested. We feel that this has further improved the manuscript.

* At the top of page 5 the q-values are listed as percentages. It would be more appropriate to list them as raw numbers (from 0.000 to 0.02103).

As suggested, we have listed the q values (page 5) as raw numbers.

* I appreciate the explicit description of how the 88 genes were arrived at. However, I still think the 2.3% comparison is slightly misleading. As you say, a microarray has a lot of housekeeping and other genes, and the more of those genes you put on a chip, the lower that percentage of enrichment will be. That is, 464/20,000 = 2.3% and if you add another 10000 housekeeping genes, your results will look even better compared to 464/30,000 = 1.5% (which isn't really the point). I would change those last few sentences to: "A number of these genes had also been identified using the SAM analysis (such as genes involved in lipid synthesis); this is a substantial pathway enrichment." (middle of page 5)

This statement has been modified as suggested.

* This may be somewhat repetitive, but I would add the following parenthetical comment as the very last thing on page 12 "... whether significantly different or not (according to a 2-sided t-test)."

The clarification on the statistics is now clearly indicated, as suggested.