**Author's response to reviews**

**Title:** Leptin and adiponectin DNA methylation levels in adipose tissues and blood cells are associated with BMI, waist girth and LDL-cholesterol levels in severely obese men and women

**Authors:**

Andrée-Anne Houde (andree-anne.houde@usherbrooke.ca)
Cécilia Légaré (cecilia.legare@usherbrooke.ca)
Simon Biron (simon.biron@chg.ulaval.ca)
Odette Lescelleur (odette.lescelleur@criucpq.ulaval.ca)
Laurent Biertho (laurentbiertho@gmail.com)
Simon Marceau (simon.marceau@ssss.gouv.qc.ca)
André Tchernof (andre.tchernof@criucpq.ulaval.ca)
Marie-Claude Vohl (marie-claude.vohl@usherbrooke.ca)
Marie-France Hivert (marie-france.hivert@usherbrooke.ca)
Luigi Bouchard (luigi.bouchard@usherbrooke.ca)

**Version:** 4  
**Date:** 17 April 2015

**Author's response to reviews:** see over
April 17, 2015

Dr. Matthias Blüher
Associate Editor
BMC Medical Genetics

Re: Manuscript 2663171631567161

Dear Dr Blüher,

We are very pleased that our manuscript entitled "Leptin and adiponectin DNA methylation levels in adipose tissues and blood cells are associated with BMI, waist girth and LDL-cholesterol levels in severely obese men and women " by Houde et al. has been accepted for publication in BMC Medical Genetics.

Please find below our answers to each point of the formatting requirements. The new version of the manuscript has also been modified (in red) according to these points.

**FORMATTING REQUIREMENTS:**

1) Nucleic acid sequences, protein sequences, and atomic coordinates should be deposited in an appropriate database in time for the accession number to be included in the published article. In computational studies where the sequence information is unacceptable for inclusion in databases because of lack of experimental validation, the sequences must be published as an additional file with the article. Where appropriate, authors should adhere to the standards proposed by the Microarray Gene Expression Data Society ([http://www.mged.org](http://www.mged.org)) and must deposit microarray data in MIAME-compliant format in one of the public repositories, such as ArrayExpress ([http://www.ebi.ac.uk/arrayexpress](http://www.ebi.ac.uk/arrayexpress)), Gene Expression Omnibus (GEO; [http://www.ncbi.nlm.nih.gov/projects/geo/](http://www.ncbi.nlm.nih.gov/projects/geo/)) or the Center for Information Biology Gene Expression Database (CIBEX; [http://cibex.nig.ac.jp](http://cibex.nig.ac.jp)).

We have not generated any new nucleic acid sequence in this manuscript. The nucleic acid sequences amplified and analyzed have been numbered according to UCSC Genome Browser (Human Feb 2009) in Additional Files 3 and 4.

2) We encourage authors whose supporting data are available in an open access repository to include an ?Availability of supporting data? section in their manuscript, before the Competing interests and Authors? contributions. The section should state the name of the repository in which your data is deposited and include a link to the dataset.
DOI. If all the supporting data are included as additional files the section should state this. If your manuscript has any supporting sequence data, microarray data, or proteomic data this must be deposited in the appropriate repository and a link to the dataset should be included in the Availability of supporting data section. Deposition of other supporting data is encouraged. Through a special arrangement with LabArchives, LLC (http://www.labarchives.com/), authors submitting manuscripts to BioMed Central journals can obtain a complimentary subscription to LabArchives (http://www.labarchives.com/bmc) with an allotment of 100MB of storage. LabArchives is an Electronic Laboratory Notebook which enables scientists to share and publish data files in situ; you can then link your article to these data using the ?Availability of supporting data? section. Clinical data can be deposited if consent to do so was obtained before the study began, in which case a statement should be in the manuscript, or if the data is deposited in a repository in an anonymized form that complies with data protection/privacy laws. For more information on supporting data please see the following http://www.biomedcentral.com/about/supportingdata.

We have not generated any new sequence data or microarray in this study. Therefore, no data needed to be deposited in an open access repository.

3) Please ensure the headings in the abstract conform to our requirements: http://www.biomedcentral.com/bmcmedgenet/authors/instructions/researcharticle

The format of the abstract has been modified to fulfill your requirements.

4) Please rename Introduction to Background.

The introduction has been renamed Background

5) Clarify ethics approval statement from: Tissue specimens were obtained from the Biobank of the Institut universitaire de cardiologie et de pneumologie de Québec according to institutionally-approved management modalities.

The ethic approval statement has been clarified on page 7

“All participants provided a written informed consent before their inclusion in the study, and all clinical data were denomalized. This project was performed in collaboration with the Tissue bank for the study of obesity and its complications at the Institut Universitaire de Cardiologie et de Pneumologie de Québec. The project was approved by this institution’s and the Université Laval’s ethics committees and was conducted in accordance with the Declaration of Helsinki.”
6) Include an Abbreviations section.

The abbreviation section has been added on page 21.

7) Two authors have the initials LB - please distinguish between them in the Authors’ contributions section.

The complete last name has been added for these two authors in the Authors’ contributions and the Acknowledgments sections

We hope that the format of the manuscript is now appropriate for publication in BMC Medical Genetics

Sincerely yours,

_____________________
Luigi Bouchard, PhD MBA
ECOGENE-21 Laboratory
Assistant professor
Department of biochemistry
Université de Sherbrooke