Author's response to reviews

Title: Adipose Transcript Networks Across Finns and Mexicans Identify Novel Triglyceride-Associated Genes

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Author's response to reviews: see over
Dear Dr Yinglei Lai, Associate Editor,
BioMed Central Editorial Office

November 8, 2012

Dr Yinglei Lai, Associate Editor
BioMed Central Editorial Office

Dear Editor,

Thank you for the opportunity to submit a second revised version of our manuscript (MS:2071192208745599) entitled “Adipose Co-expression Networks Across Finns and Mexicans Identify Novel Triglyceride-Associated Genes” by Blake Haas et al. for publication as an original article in the *BMC Medical Genomics*. We have now carefully addressed the comment of the Reviewer and carried out the revision suggested by the Reviewer. Please find enclosed below our response to the Reviewer’s comment. We sincerely hope that the revised manuscript will be accepted for publication in the *BMC Medical Genomics*.

Thank you for your consideration.

Sincerely yours,

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Responses to Reviewer
We thank the Reviewer for the helpful critique and comment of the manuscript and have addressed the issue that was raised. We hope that the revision satisfactorily responds to the Reviewer's concern.

Reviewer's report (Reviewer Lina Chen)

Point 1.
The authors should discuss genes that were correlated with TG but not in those modules in detail. For example, by comparing the percentage of genes that were no correlated with TG in each module (including the grey one).

Response to Point 1.
As suggested by the Reviewer, we have now compared in the three sets of samples the percentages of genes that were not correlated with TG in each module, including the grey one that in the weighted gene co-expression network analysis (WGCNA) always represents background genes that cannot be clustered into one of the modules. We observed that among all modules the TG-associated network modules in each of the three sets of samples (i.e. the blue module in the Finnish twins, the yellow module in the Mexicans and the brown module in the METSIM TG case/control sample) exhibit the highest percentages of genes correlated with TGs. We have added these comparisons to the Results (page 10, the end of the first paragraph) as well as revised Figure 1 and Additional files 2 and 3 to show the percentages of genes correlated with TGs for each module, including the grey one. Accordingly, now the number of gene expression probes present in each module and the percentage of probes correlated with TGs are listed in parenthesis next to the module color in the revised Figure 1 as well as in revised Additional files 2 and 3. We also added a description into the Methods about how the correlations were calculated (page 23, the last paragraph).