Author's response to reviews

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

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Version: 2 Date: 8 June 2012

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Dear Editor,

Please consider the enclosed manuscript entitled “Adipose Transcript Networks Across Finns and Mexicans Identify Novel Triglyceride Genes” by Blake Haas et al. for publication as an original contribution in the BMC Medical Genomics. Coronary heart disease (CHD) is the major cause of mortality and morbidity worldwide. High serum triglyceride (TG) levels is an independent risk factor for CHD, and adipose tissue is a key regulator of serum TG levels. We hypothesized that searching for biological networks in human adipose tissue associated with serum TG levels and preserved across multiple populations may reveal novel TG genes and gene expression networks involved in TG regulation. We utilized adipose RNA samples from Finnish and Mexican study samples and observed a novel adipose transcript network that was significantly associated with serum TG levels and overlapped (p-value = 1.98x10^{-160}) between the two distinct populations. The novel adipose transcript network shared 34 genes across the populations of which only 11 have prior evidence of involvement in CHD, type 2 diabetes, or obesity. Thus, the new data of our paper identify 23 novel genes for TG regulation in human. This is the first study that identifies a TG network replicated and shared across populations, suggesting that it is a fundamental piece of biology of human. We believe that the novel TG network identifying 23 new genes involved in serum TG regulation consistently across two distinct populations will be of interest to the wide readership of the BMC Medical Genomics. All authors have read and approved the submission of the manuscript. The manuscript is not being considered for publication elsewhere in whole or in part.

Thank you for your consideration.

Sincerely yours,

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