Reviewer’s report

Title: Molecular prediction for atherogenic risks across different cell types of leukocytes

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Reviewer: HONGJIAN ZHU

Reviewer’s report:

Early detection of atherosclerosis may prevent complications of the disease or slow its progression. However, in practice, it is challenging to diagnose subclinical atherosclerosis since individual are asymptomatic. The authors developed multi-gene biomarker models to predict early-stage atherosclerosis, and also showed the existence of common molecular expression signatures of atherogenic risks across different cell types of WBC. They greatly decrease the number of potentially useful biomarkers from 363 to 56, and the number is even smaller after COXEN algorithm has been applied.

This paper displayed impressive results. However, I am concerned about the following three issues:

1. When COXEN was applied, my understanding is that FH1 and FH2 were used as training data to identify genes that preserved highly concordant gene expression patterns between FH1 and FH2. Subsequently, these biomarkers were used back to analyze FH2. Please explain the validity of this method.

2. FH2 and FH1 share the same sample. Are they still independent?

3. In Figure 3, the authors are trying to show the clusters. But it seems that the results are not good in terms of the sample level. The cluster of sample is messy. Please revise it or explain it.

Overall, this is an interesting paper with novel findings. After a minor revision according to the above points, the paper can be considered to be published in BMC Medical Genomics.

Level of interest: An article whose findings are important to those with closely related research interests

Quality of written English: Acceptable

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

Declaration of competing interests:

I got my Ph.D. degree from the University of Virginia in 2010. I got financial support from U.VA from 2005 to 2010.