Reviewer's report

Title: Identification of a prognostic signature for old-age mortality by integrating genome-wide transcriptomic data with the conventional predictors: the Vitality 90+ Study

Version: 2 Date: 7 July 2014

Reviewer: Glen Jickling

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Survival models of demographic markers were compared to gene expression markers in 151 nonagenarians. RNA was isolated from PBMC by Ficoll-aque stored in RNA later, and processed on Illumina BeadChips. 478 transcripts were identified (p<0.05), of which 378 were associated with mortality after adjusting for BMI, frailty index and cell free DNA.

1. The statistical selection criteria for genes associated with mortality could be more clearly presented. A p<0.05 appears to have been used, which does not adjust for multiple comparisons. The strength of the association of each of the 478 transcripts identified with mortality is unclear. Was a fold change between those who died and did not die applied?

2. Prediction analysis was performed on the derivation cohort using cross-validation. A second validation cohort would be a better method to evaluate the gene predictors of mortality.

3. It would be useful to present table 1 divided by those who died vs those who survived. Currently it is difficulty to determine which factors are different between the compared groups.

4. The number of study subjects that died should be more clearly presented. Cause of death would also be of interest. Might different inflammatory genes be associated with specific causes of death?

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

Quality of written English: Needs some language corrections before being published

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

Declaration of competing interests:

I declare that I have no competing interests