Reviewer's report

Title: Genotype-Informed Risk of Coronary Heart Disease Based on Genome-Wide Association Data Linked to the Electronic Medical Record

Version: 1 Date: 3 April 2011

Reviewer: Sandosh Padmanabhan

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Ding et show that score from genotypes of 11 SNPs associated with CAD in GWAS did not correlate with Framingham Risk Score but when incorporated resulted in reclassification of 31% of individuals.

Major Compulsory Revisions

The clinical indices used in the calculation of Framingham risk scores are standard measures and it is unclear why the authors have presented this as an advantage of using EMRs. It is likely that the unique advantage of EMRs in genetic studies may be access to longitudinal data rather than cross-sectional data presented here.

There is no mention of family history and perhaps this is not captured in EMRs. In any test of genetic prediction, family history is essential.

The lack of prospective outcomes does not allow any interpretation of the risk scores and the validity of the reclassification. There need to be evidence presented that the reclassification are indeed valid and this requires prospective data.

Level of interest: An article of insufficient interest to warrant publication in a scientific/medical journal

Quality of written English: Acceptable

Statistical review: No, the manuscript does not need to be seen by a statistician.

Declaration of competing interests:

I declare that I have no competing interests