Reviewer's report

Title: A genome-wide association study of copy-number variation identifies putative candidate loci associated with osteoarthritis in Koreans

Version: 1 Date: 7 October 2014

Reviewer: James Robinson

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MINOR ESSENTIAL REVISIONS
The authors should describe the cohorts in enough detail to enable meta-analysis of their data in the future, paying particular attention to the guidelines in Kerkhof et al. (Osteoarthritis Cartilage. 2011 19;3:254-64)

The use of CNVtools to analyse the aCGH data should be described in more detail. CNVtools allows for association testing without applying copy number calls. Reporting of the parameter estimates for each of the identified CNVs would enhance the paper.

Figure 1 AND Figure 3 panel A - Axes and labels should be clearly visible. What are the colored lines? Presuming they represent CNVtools posterior probability of copy number there should be a secondary Y axis labelled appropriately.

Figure 3 panel B - the labels are unreadable.

DISCRETIONARY REVISIONS
The authors should indicate what efforts were made to detect batch effects, a common feature of CNV studies.

While discussing limitations of the study the authors could consider estimates of false discovery rates in the discovery phase.

Level of interest: An article of importance in its field

Quality of written English: Acceptable

Statistical review: Yes, but I do not feel adequately qualified to assess the statistics.

Declaration of competing interests:
I declare that I have no competing interests