Reviewer's report

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

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Reviewer: F. David Carmona

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Moon and colleagues have performed a large-scale analysis of CNVs in a Korean cohort of osteoarthritis patients and matched controls. The study aimed to shed light into the genetic background underlying this complex disease.

- Major Compulsory Revisions:

1) The study has important limitations that are acknowledged by the authors. The most relevant one in my opinion is the low statistical power that may rise reasonable doubts about the consistency of the results. The P-values obtained are distant from an acceptable significance threshold in this kind of studies. Therefore, I would recommend the authors to gather additional replication cohorts in order to discard the possibility that the proposed associations are a consequence of type-I errors due to an underpowered analysis.

2) I also have major concerns regarding the structure of the manuscript. The methods and results sections are poor and need a more detailed description. In addition, the discussion is too descriptive and speculative, and lacks continuity in the argumentation. The authors should focus more on developing the main message of their paper rather than just stating the known role of the putative risk loci.

Level of interest: An article of limited interest

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.