Reviewer’s report

**Title:** Genetic variations in APPL2 are associated with obesity in a Chinese population with normal glucose tolerance

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**Reviewer:** Nabila Bouatia-naji

**Reviewer's report:**

Jiang et al report a well designed and conducted study of APPL2 where they have tested the association of genetic variants located in this gene with obesity related traits. The rationale of the gene, variants selection and analyses are adequate. The paper is succinct and focused. The conclusions driven are appropriate as are the statistical methods.

I only have minor comments:

1. Figure 1 should include more details about the gene structure to locate the variants position on exons and regulatory section. Ideally, this figure should provide all the variants and highlight the tag SNPs, so we can have an idea about the coverage.

2. The authors did not provide any information about the SNPs, if any, that are potentially tagged by rs2272495 (the figure with LD of all SNPs from HapMap would be useful to visualise those that are tagged and not included in the study).  

3. This is the first genetic assessment of APPL2. Reporting association with overweight and BMI and WHR is not a replication, as these traits are highly correlated. Thus these findings need further confirmation in larger studies. This should be stated in the discussion.

4. The authors should provide an in silico assessment of the functionality of this coding variant. There are at least three easily available web tools to perform these assessments: PolyPhen2, SIFT and Panther.

**Level of interest:** An article of importance in its field

**Quality of written English:** Acceptable

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

**Declaration of competing interests:**

NONE