Reviewer's report

Title: Enhanced genetic maps from family-based disease studies

Version: 1 Date: 22 October 2010

Reviewer: Antonia Flaquer

Reviewer's report:

This work is very well performed and it is extremely useful for linkage analysis and other types of genetic studies. The analysis is expert and uses the appropriate statistical tests. The only thing that worried me was so many genotype inconsistencies. Genotyping errors can lead to an inflation of genetic map lengths (for more information: "Hackett et al. 2003. Effects of genotyping errors, missing values and segregation distortion in molecular marker data on the construction of linkage maps. Heredity 90, 33–38". "Goldstein et al. 1997 The effects of genotyping errors and interference on estimation of genetic distance. Hum. Hered. 47, 86–100". I know it is very difficult to work with raw data, and I consider that the authors used the best techniques to solve those inconsistencies, and due to the large number of informative meiosis those errors should not be a problem.

Minor Essential Revisions:

1. I find the numbers of genetic markers considered (461) quite small. Anyway, it should not be an inconvenient as long as they are well distributed through the genome. It would be helpful to have this information. I nice way to do it is graphically (i.e., x-axis represents the physical location, and y-axis the chromosome number, then each point corresponds to a genetic marker). In this way, one could very quickly identify whether some regions are denser than others. It would also be helpful to have the physical location in the final map (at the website).

2. I would check in more detail the recombinants occurred between D17S1298-D17S974 and between D5S2500-DS1501 (#=0.21). I find the number of recombinants large, unless the markers are very far away from each other.

3. Page 5: the pedigree sized ranged from 3 to 239. Is 239 the real number or a typing error?

Discretionary Revisions:

1. In table 1: I would add a column showing the number of pedigrees considered for each PI.

2. Page 5: the numbers mentioned in the first paragraph refer to the uncleaned data. Some lines later, the text refers to table 2, but in that table the numbers are after cleaning data. Please, specify it in the text.

3. The number of genetic markers used in the construction of the map should
appear in the abstract or in the background when talking about the analysis performed.

4. Figure 2: it would be nice to add a horizontal line to each graph that illustrates the borderline between significant and not significant values.

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

**Quality of written English:** Acceptable

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

**Declaration of competing interests:**

I declare that I have no competing interests