Author’s response to reviews

Title: Genetic Variation in Fcgamma Receptor IIa and Risk of Coronary Heart Disease: Negative Results From Two Large Independent Populations.

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Version: 3 Date: 26 April 2009

Author’s response to reviews: see over
Dear Dr Edmunds,

Thank you very much for your kind letter of February 26th, 2009 giving us the opportunity to revise the above mentioned manuscript.

We would like to thank the editors and the reviewers for their constructive criticisms and especially for their insightful recommendations concerning changes of several aspects of the content of this manuscript.

We have considerably revised the design of the tables. Furthermore we also provide a detailed point-by-point response to each comment of the reviewers.

We hope that the revised version will now be acceptable for publication in *BMC Medical Genetics*.

Looking forward to hearing from you.

Sincerely,

Wolfgang Koenig, MD, FRCP, FACC, FESC, FAHA
Professor of Medicine/Cardiology
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Point-by-point response

First, we would like to thank the reviewers for their constructive criticisms and we are grateful for the opportunity to improve this paper.

**Reviewer #1:**
No additional comments.

**Response to Reviewer Reviewer #2:**

**Point 1:** Add (again I ask this) the allele frequencies in Table 3.

→ The allelic frequencies are added in table 3.

**Point 2:** Add in Table 3 the total number of cases and controls in top row of your Table: sp example add in the line just under cases (for main header Men): (n=466) and so on.

→ We considerably revised the design of the tables and added the total number of cases and controls in top row in table 3.

**Point 3:** Power calculations need to be described in Materials and presented in Results section.

→ We added a descriptive sentence to the materials section. Finally, we calculated a power assessment: A two group Chi-square test based on a two-sided α of 0.050 and a power of 80% was used to estimate which statistically significant excess risk (Odds ratio) between cases and control of each study could be detected at minimum based on the proportions of the genotype HH131 versus the other two genotypes combined.

See page 9, lines 8-12 (materials section);
See page 15, lines 3-6 (results section).