Author's response to reviews

Title: Ovarian dysfunction and FMR1 alleles in a large Italian family with POF and FRAXA disorders: Case report

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Version: Date: 1 March 2007

Author's response to reviews:

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Dear Prof. Liz Hoffman
Assistant Editor
BMC-series journals

I wish to thank you for your letter concerning the re-submission of manuscript MS: 5769245361176476 "Ovarian dysfunction and FMR1 alleles in a large Italian family with POF and FRAXA disorders: Case report" by Miano et al.

As requested, I have adjusted the paper according to the Reviewer's 2 comments, and I have submitted the revised version using the online system. The corrections were reported in bold.

Herein, I reported the point-by-point responses.

After the acceptance of the revised paper, I will send the copies of the patient's consent by fax.

I'm looking forward to hearing from you soon,

Yours Sincerely,
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Comments and answers to the Reviewer 2.
Major Compulsory Revisions
The reviewer suggested modifying two sentences in the abstract and in the background in order to clarify better the contribution of this study.

Point1. In the conclusion of the abstract, as suggested by Reviewer, we substituted the sentence "Our case study represents a helpful observation and will provide familial cases with heterogeneous etiology that could be further studied when candidate genes in addition to the FMR1 premutation will be available" with "Our case study represents a helpful observation and will provide familial cases with heterogeneous etiology that could be further studied when candidate genes in addition to the FMR1 premutation will be available".

Point2. We also changed, according to Reviewer's indication, the last sentence of Background section "The aim of this study is to offer new information regarding the complexity of familial POF conditions by
presenting a large pedigree in which two different POF disorders coexist, one FMR1-related and one not FMR1-related" with "Our case study represents a helpful observation and will provide familial cases with heterogeneous etiology that could be further studied when candidate genes in addition to the FMR1 premutation will be available".