Author’s response to reviews

Title: Genetic variants in FBLIM1 gene do not contribute to SAPHO syndrome and chronic recurrent multifocal osteomyelitis in typical patient groups

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Author’s response to reviews:

Dear Editor,

Thank you for sending out our manuscript for review! We understand the concerns of the assistant editor. We changed the manuscript accordingly and include a point-to-point response to the comments (below). We hope that the manuscript is now acceptable for publication and look forward to hearing from you!

Yours sincerely

Ulrike Hüffmeier

Assistant Editor Comments:

1. Consent to Participate

In your “Ethical approval and consent to participate” section, please clarify whether informed consent to participate, written or verbal, was obtained from all of the participants in the study and clearly state this in your manuscript.
Please note that in the case of minors, which refers to individuals younger than the age of 16, consent to participate must be obtained from their parents or legal guardians. As such, we ask that in your “Ethics approval and consent to participate” section, to clarify whether informed consent to participate, written or verbal, was obtained from the parents or legal guardians of any participant under the age of 16 and clearly state this in your manuscript.

If consent was verbal, please state the reason and whether the ethics committee approved this procedure. If the need for consent was waived by an IRB or is deemed unnecessary according to national regulations, please clearly state this, including the name of the IRB or a reference to the relevant legislation.

We included more details in the declaration section “Ethical approval and consent to participate” that indicates that all individuals gave their written informed consent and that in case of minor patients, legal guardians did the same (p. 10, line 10). We also included this information in the methods section (p. 5, line 16-17).

2. Availability of data and materials

a) Please note that all data must be made public prior to publication and we cannot proceed to publish your manuscript if your data is not deposited and made publicly available.

We are an open access journal and submission of a manuscript to a BMC journal implies that materials described in the manuscript, including all relevant raw data, will be freely available to any scientist wishing to use them for non-commercial purposes. By raw data we mean the minimal dataset that would be necessary to interpret, replicate and build upon the findings reported in the article.

As your data falls under the list of data types which must be deposited (listed below), we ask that you please provide the relevant accession numbers, and the name of the database in which your data is stored, if your data has been deposited into a database or the appropriate web links if the data has been uploaded into a repository. If the data has not yet been deposited, please do so and provide the relevant information needed to access it in the ‘Availability of data and materials’ section in your manuscript. Please ensure all data is already released and that any accession numbers/web links are in the ‘Availability of Data and Materials’ in their final form, and that all web links and accessions allow access to public data.

**Please note that BMC mandates data deposition for the following:

- Protein sequences – can be deposited in Uniprot
- DNA and RNA sequences – can be deposited in Genbank, DNA DataBank of Japan (DDBJ), or EMBL Nucleotide Sequence Database (ENA)
- DNA and RNA sequencing data – can be deposited in NCBI Trace Archive or NCBI Sequence Read Archive (SRA)
- Genetic polymorphisms – can be deposited in NCBI dbSNP, NCBI dbVar, or European Variation Archive (EVA)
- Linked genotype and phenotype data – can be deposited in NCBI dbGAP or The European Genome-phenome Archive (EGA)
- Macromolecular structure – can be deposited in the Worldwide Protein Data Bank (wwPDB) or the Biological Magnetic Resonance Data Bank (BMRB)
- Microarray data (must be MIAME compliant) – can be deposited in Gene Expression Omnibus (GEO) or ArrayExpress
- Crystallographic data for small molecules – can be deposited in Cambridge Structural Database

Your data availability statement can take the following form: “The datasets generated and/or analysed during the current study are available in the [NAME] repository, [PERSISTENT WEB LINK OR ACCESSION NUMBER TO DATASETS]”.

b) Please ensure that you include the accession numbers or direct links and the full names of the data banks/repositories corresponding to any datasets obtained from web-based sources and subsequently analysed in your study in the Availability of Data and Materials section, including any reference datasets. If accession numbers or web links are listed in a table or additional file, please include an in-text reference to the file or table in the Availability of Data and Materials section.

We provided an additional Supplementary Table 3 where we present the details on genetic variants at genotype level. As indicated throughout the manuscript, we performed Sanger sequencing, but did not use next generation sequencing to analyze coding regions of the candidate gene FBLIM1. The databases mentioned above provide formats to upload NGS sequences or results files, but not single electropherograms which are the raw data obtained by Sanger-sequencing.

Within Supplementary Table 3, we indicate individual clinical data; therefore, the summary tables given in Supplementary Tables 2 A and 2B can directly be derived from the detailed data. In “availability of data and materials section” we changed the sentence indicating the main data source.

3. Figure 1D

As per our submission guidelines, we require that all figures, tables and additional files be cited in the text in sequence in a manuscript. Figure 1D is currently not cited in your manuscript. Please ensure that it is appropriately cited within the main body of text in your manuscript.

We included a citation of Figure 1D in the appropriate section, p. 7 line 4.

4. At this stage, please upload your manuscript as a single, final, clean version that does not contain any tracked changes, comments, highlights, strikethroughs or text in different colours. All relevant tables/figures/additional files should also be clean versions. Should you wish to respond to these revision requests, please put your responses to the reviewers'/editors’ comments in the Response to Reviewers box in Editorial Manager. Please do not upload a separate letter.

We provide a single manuscript file without tracked changes and a single clean supplementary data file.