Author’s response to reviews

Title: Screening of exon 11 for BRCA1 using the High Resolution melting for diagnostic in Moroccan breast cancer patients

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To The Editor,
Sub: Re-Submission of Manuscript for publication
Dear Editor,

We would like to resubmit a revised version of the article “Screening of exon 11 for BRCA1 using the High Resolution melting for diagnostic in Moroccan breast cancer patients” (Manuscript ID 2054609999128887) for publication in the journal Research articles.

You will find enclosed a new version of the manuscript, which would now include the modifications that you suggested.

Please do not hesitate would you need further information.

Best Regards
Sellama Nadifi

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Signature
Sellama Nadifi

Editor’s comments:

Page 1 row 4: ?in those genes ? should be ?in BRCA1?
# Yes, thank you for pointing that out. we corrected it with “exon 11 of BRCA1”

Page 5 Result section, rows 2-4. ? In order to accomplish this, we used five negative controls for all the regions except the H part. For this one, we already had two positive controls detected for the first time by Tazzit et al. in 2012 (Tazzit 2010). ? Sentence difficult to understand, why negative controls for regions B, C, D, E, F, I, K and L and only positive controls for region H? Please clarify!

# We used five negative controls for all the regions that we studied. In addition to that, we already had two positive controls for the H region.

# We tried clarified that statement in the manuscript.

Page 7, rows 12-14: ? In our study, we proved that the HRM method is very sensitive, specific, cost-effective and rapid. We can guarantee that all patients who had no difference plots with the wild-type don’t have any mutation or SNP.? I disagree with this conclusion, only 2 positive controls were included, and the patients with normal melting curves were not sequenced to exclude false negatives.

# Yes, we agree. We changed this conclusion now in the manuscript.

Page 7, Conclusion, page 2-4? Thus, this procedure can be performed on the whole sequence of BRCA1 and BRCA2 genes in a way that facilitates the screening of both genes? I disagree on this conclusion also, since only exon 11 of BRCA1 was analysed.

# In this sentence, we meant that the procedure could be used on the whole gene as a suggestion and a perspective. However, sequencing needs to be performed to confirm that statement of course.

The text still contains spelling errors eg positif instead of positive in table 2.

# Thank you for your help. We corrected it.