Reviewer’s report

Title: MiR-190b, the highest up-regulated miRNA in ERalpha-positive compared to ERalpha-negative breast tumors, a new biomarker in breast cancers?

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Reviewer: Patricia de Cremoux

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The paper aimed to analyse the miRNA expression in large series of ER#-positive and ER#-negative breast cancers, and to determine in this context their functions.

This subject is very interesting regarding the international literature on miRNA in breast cancers. Previous published papers with different aims are heterogenous, and no clear conclusions rose from these data’s. The method used is adapted, and the team has a large expertise in this domain.

This represents an article whose findings are important to those with closely related research interests, which needs some revisions to be published

1/ Major Compulsory Revisions

1-1/ It is difficult to evaluate prognosis factors without the knowledge of the treatment administered. Consequently, the treatment of patients is missing in the paper. As MFS is one of the main objective, the treatment administrated to patient represents a major criteria that will influence the prognosis. In addition the period of patient’s inclusion also will determine the treatment regimen. The samples are well annotated. So the type of chemotherapy and hormone therapy should be very interesting to evaluate.

1-2/ In the context of ER-positive tumors, the response to therapy and the duration of response remains a clear problem. Should the authors also evaluate the RFS or EFS?

1-3 How were selected the first 31 patients and the validation population among the global cohort of patients? Table 1 showed a clear heterogeneity in the characteristics and the events in the screening population and the validation population. This has to be discussed.

1-4 the paper included numerous datas, screening and validation datas, screening of previously published datas and a focus on MiR-190b. In addition descriptive datas and functional datas are presented on human breast cancer cell lines. Perhaps the paper would be more explicit if it was focused only on human breast cancers. The functional datas on human breast cancer cell lines did not clearly improve the paper (supplemental datas?). Presenting the paper with this aim would improve the lecture and understanding
2/ Minor Essential Revisions

2-1/ How was evaluated the normal tissue that represents the reference for the expression of MiRNAs? Reduction mamectomy and adjacent tissue from breast cancer patients do not represent the same tissue. In the methods chapter, 12 normal samples were presented, then, 8 in the screening population and 8 in the validation population. Could you clarify this point?

2-2/ Recent publications that were published during submission might be added

2-3/ The article needs some language corrections before being published