

Review of: "Breast Cancer Subtypes And Prognosis: Answers To Subgroup Classification Questions, Identifying The Worst Subgroup In Our Single-Center Series"

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The novelty and the message of this work should be clarified. The whole point of precision medicine^[1] is to develop treatments patients-specific and authors themselves assert that the survival probability of treated patients is 1.5fold higher. The authors seems surprised that HER2 enriched maintain its worst-prognosis status. Nevertheless the statement that this prevent the identification of patients with a bad prognosis do not seem relevant to me. In fact, efficacy of a treatment should be validated between patients of the same group.

The dataset should be described deeply by the authors or some references should be added. The procedure used to identify subtypes and groups in Table 1 is not very clear. I am not an expert in the field, but I will suggest to show some result (or add references) to justify the parameters used in the Histopathologic Evaluation paragraph.

The authors did not discuss the Normal-like Breast cancer subtype (see^[2] and ^[3]). Is it present in the data or is it missing from the data?

The average DFS could be affected by many covariates, the authors just considered the average. Are there any confounder factors? Moreover I would suggest the authors to discuss how censoring was handled during these analyses.

In order to avoid hidden biases I suggest the authors to validate their results, on an independent dataset. Or are the result robust with a subsampling of the ~2000 samples?

References

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3. ^ Aleix Prat, Charles M. Perou. (2010). *Deconstructing the molecular portraits of breast cancer*. doi:10.1016/j.molonc.2010.11.003.

