Author's response to reviews

Title: Identification of a robust gene signature that predicts breast cancer outcome in independent data sets

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Dear Sir or Madam:

Please find enclosed a revised version of our manuscript entitled "Identification of a robust gene signature that predicts breast cancer outcome in independent data sets" by James E. Korkola et al., which we are resubmitting for consideration for publication in BMC Cancer (submission # 1345240735108392). We wish to thank the reviewers for their thoughtful and insightful comments. We have made changes to the manuscript based on the comments, as follows.

Reviewer 1 (Friend).

Major Issue

Reviewer Comment: The reviewer feels that the results of the gene set- based classifications are biased because we did not perform feature re-selection during each round of the leave-one-out classification in the training set. He feels the results presented on p.11, 12, Tables 1, 2A, and 2B and Figure 3A are all biased.

Response: We agree that this was classification was biased. We have now performed gene re-sampling in the PAM, correlation, and overlap-based gene sets and have reported the updated results on pages 11-12, Tables 1, 2A, and 2B, and have updated figure 3 accordingly. We have also added a sentence in the methods section (p.8, second line) to indicate that we performed gene re-sampling during the cross validation to better estimate the classification rates, and added an appropriate reference. We have excluded the SAM gene set from the tables, as this is not a classification method.

Reviewer 2 (Hu).

This reviewer had no issues with the revised manuscript.

We hope that these changes will be satisfactory for acceptance of the manuscript for publication. We look forward to hearing your response.

Sincerely,
F.M. Waldman, M.D., Ph.D.