Author's response to reviews

Title: Microarray Analysis in Clinical Oncology: Pre-clinical Optimization Using Needle Core Biopsies From Xenograft Tumors

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PDF covering letter
Dear Dr. Christopher Gadd,

We appreciate the comments and suggestions of the reviewers and have enclosed a point-by-point response to each of their comments for our manuscript. I have included the revised version of our paper along with the figures and legends. Thank you in advance for reevaluating our paper for publication in your journal.

Reviewer one Puskas: We appreciate the favorable review from this reviewer.

1) **Major compulsory revisions.**

   None

2) **Minor essential revisions.**

   We agree that the presentation of our conclusion was confusing. We have modified our conclusion to include either direct or indirect labeling.
   The spelling mistakes and the insertion of abnormal “?” throughout has been corrected.

3) **Discretionary revisions.**

   We agree that a dye swap experiment would be useful. There are many other variables that need to be evaluated and we are in process on many of them. In our hands a dye swap experiment leads to a 95% concordance.

Reviewer two Sotiriou: We also appreciate the favorable review from this reviewer.
1) **Major compulsory revisions.**

None

2) **Minor essential revisions.**

None

3) **Discretionary revisions.**

The reviewer makes an excellent observation concerning the “true” outlier number depending on the amount of starting RNA material. As the reviewer knows defining “true” is a moving target. Botstein et al. has presented interesting data comparing microarray data, RT-PCR, RNA protection and Northern hybs and have shown a concordance between any three modalities of less than 50%. In other words, a coin flip is just as good at determining “truth”. We believe that microarray is just another tool in our repertoire to study biological systems and that the truth is born out in well constructed hypothesis testing experiments.

Thank you for your time.

Kevin Camphausen