Author's response to reviews

Title: Elevated MED28 expression predicts poor outcome in women with breast cancer

Authors:

Nam K Yoon (namkeunyoon@gmail.com)
Erin L Maresh (emaresh@mednet.ucla.edu)
Yahya Elshimali (elshimali@gmail.com)
Ai Li (liaipk@gmail.com)
Steve Horvath (shorvath@mednet.ucla.edu)
David B Seligson (dseligson@mednet.ucla.edu)
David Chia (dchia@mednet.ucla.edu)
Lee Goodglick (lgoodglick@mednet.ucla.edu)

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Author's response to reviews: see over
John Kerr  
Assistant Editor  
On behalf of: Sabina Alam, PhD  
Senior Scientific Editor  
BMC series journals  

Re. Manuscript 1891097810305015  

Dear Dr. Kerr:  

Thank you very much for the second review of our manuscript entitled "Elevated MED28 expression predicts poor outcome in women with breast cancer" by Nam K Yoon et al. We appreciate the further comments by Dr. Turashvili. We feel we have addressed all of points and questions (see below).  

If you have any questions or concerns, please don't hesitate to contact me.  

Sincerely,  

Lee Goodglick  
Associate Professor,  
Director, UCLA EDRN  
Department of Pathology and Laboratory Medicine  
UCLA School of Medicine  
Center for the Health Sciences  
10833 Le Conte Ave.  
Los Angeles, CA 90095
Reviewer: Gulisa Turashvili

Abstract Revisions
1. The Reviewer wanted us to commend that a limitations of the study was the "small sample size". We have included a statement about the sample size in the Abstract and Discussion as suggested. However, we respectfully disagree that this is a "limitation" of the study (i.e., this is small compared to some studies and large compared to others).

Methods
1. The 32 patients with more than one surgical procedure are individuals who remained in the UCLA Health Care system and who had recurring tumors. This has now been stated in the Methods.

2. As requested, the histopathology characteristics are now added in more detail in the Methods section.

3. As requested, we have stated in the Methods now that at least 3 cores were arrayed from each case histology.

4. As requested, we specified the antigen retrieval buffer that was used.

5. MED28 was indeed a stronger predictor than stage. In a multivariate Cox model, the P value for Stage was 0.094; the P value for MED28 was 0.030

6. The rationale for separating out nuclear from cytoplasmic expression is that cellular localization supplies a much richer source of information.

Results
1. We have added to Figure legend 2, the number of patients who had some degree of MED28 positivity.

2. Of the total of 2,039 cores, 1,725 were readable. Unreadable spots included those that had fallen off during processing or those that contained only stroma. This is now stated in the Methods section.

3. As the reviewer mentioned, we have at least 3 cores for each histology. The method of pre-pooling and pooling has been detailed in some of our other publications. At this step, we take the average of all cores from a given patient for a given histology.

Figures
1. We have enlarged the images in Figure 1 and presented high quality photographs. All images are labeled correctly in the figure legend.

2. Figure 1G shows MED28 expression levels for each histopathology for all spots on the array. Some cases had more than one histology / histopathology thus leading to the numbers in Figure 1G. This should be clearer now with the revised methods.