Author's response to reviews

Title: Whole genome assessment of the retinal response to diabetes reveals a progressive neurovascular inflammatory response.

Authors:

   Robert M Brucklacher (rbrucklacher@psu.edu)
   Kruti M Patel (krutims@gmail.com)
   Heather D VanGuilder (hdv108@psu.edu)
   Georgina V Bixler (gbixler2@psu.edu)
   Alistair J Barber (abarber@psu.edu)
   David A Antonetti (dantonetti@psu.edu)
   Cheng-Mao Lin (clin@psu.edu)
   Kathryn F LaNoue (kfl1@psu.edu)
   Thomas W Gardner (tgardner@psu.edu)
   Sarah K Bronson (sbronson@psu.edu)
   Willard M Freeman (wfreeman@psu.edu)

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The authors would like to thank the reviewers and journal staff for their review of the manuscript. We have made minor changes in the manuscript, as detailed below. A redline manuscript of the changes has been included.

Reviewer #1: As the review suggested acceptance without revision, we have no changes for Reviewer #1.

Reviewer #2:

1) Title - This is the sole point on which the authors respectfully disagree with the reviewer. The data describes significant changes in a number of genes related to microvascular and neuronal dysfunction, and inflammation. These changes are confirmed in multiple independent sets of animals in conjunction with functional assessment of vascular permeability and caspase activity. While these data do not determine the exact, causal outcome of each gene expression change the study is best described by the current title. Naturally, we will defer to the editor's decision on this point.

2) Figure 8 - We have moved the last figure into the supplemental figures for those readers who are interested in the network analysis.

3) Discussion length - We have endeavored to make the discussion more concise and reduced the length by 277 words. However, we have retained many points of the gene descriptions. The authors believe that with qPCR confirmation of the mRNA changes in multiple sets of animals some discussion is warranted.

4) Fold changes - Two sentences in the Results have been added on the relative fold changes in the microarray and qPCR experiments.
5) Protein levels - A couple of sentences have been added to the Discussion describing the need for future proteomic studies and the relationship of mRNA to protein levels.

6) Open symbols- This has been changed.

7) Fold change – The standard deviation has been added.

8) Figure Numbers- We have deleted the Figure number from our illustration files.