Author's response to reviews

Title: Differential endothelial cell gene expression by African Americans versus Caucasian Americans: A possible contribution to health disparity in vascular disease and cancer

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Author's response to reviews: see over
RE: research article #4758905994073540

Dear Doctors:

Please find enclosed our manuscript, revised in accordance with the Editors’ most recent comments. This revised paper indicates changes with tracking. Most, of course, are in the Methods section. In addition, there are just a few other ‘tweaks’ which I added to enhance readability and/or clarity. IRB approval is still noted at beginning of Methods. The following is the response to the question regarding statistical methods. We hope this satisfies the reviewer’s request; if it does not, the reviewer will have to be more specific as to what he/she wants.

Response: In response to the reviewer’s request, we have provided additional details, as well as new references, on the statistical softwares and statistical methods that were used in our analyses. These are shown in the newly revised manuscript with red tracking highlighting.

Specifically, microarray data preprocessing, including the robust multiarray average (RMA) method [42] and locally weighted scatter-plot smoothing (LOWESS) [43], was implemented in the software Genedata Expressionist Pro3.1PP (Basal, Switzerland). In addition, all analyses of single gene expression, including the Welch t-test [44], FDR-based SAM [45][46] and fold change analysis, were carried out in the statistical software R [47]. We used the R function ‘t.test’ for the Welch t-test and the R package ‘samr’ for the SAM and fold change analyses. Power calculation for analysis of single gene expression was performed using the software Java Applets for Power and Sample Size [48]. Microarray data of 27 BOEC samples from a previous study [37] were used to obtain the levels of expression and variance estimates for power calculation.

To determine whether pre-defined gene sets identified significant biological system differences between AA and CA, we utilized Gene Set Enrichment Analysis (GSEA) [50]. We tested our dataset in GSEA Java desktop software V2.0, which was downloaded from the authors’ website [51]. Since there is no (known) way to perform a power calculation for GSEA analysis, we conducted multiple simulations in the statistical software R [47], based on the effect size and variance estimates from 27 BOEC samples from a previous study [37]. Simulation-based power estimation [52] is a generic approach and suitable for non-standard statistical techniques, such as GSEA.
References:


49. Gene Set Enrichment Analysis. [http://www.broad.mit.edu/gsea/]


Sincerely,

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