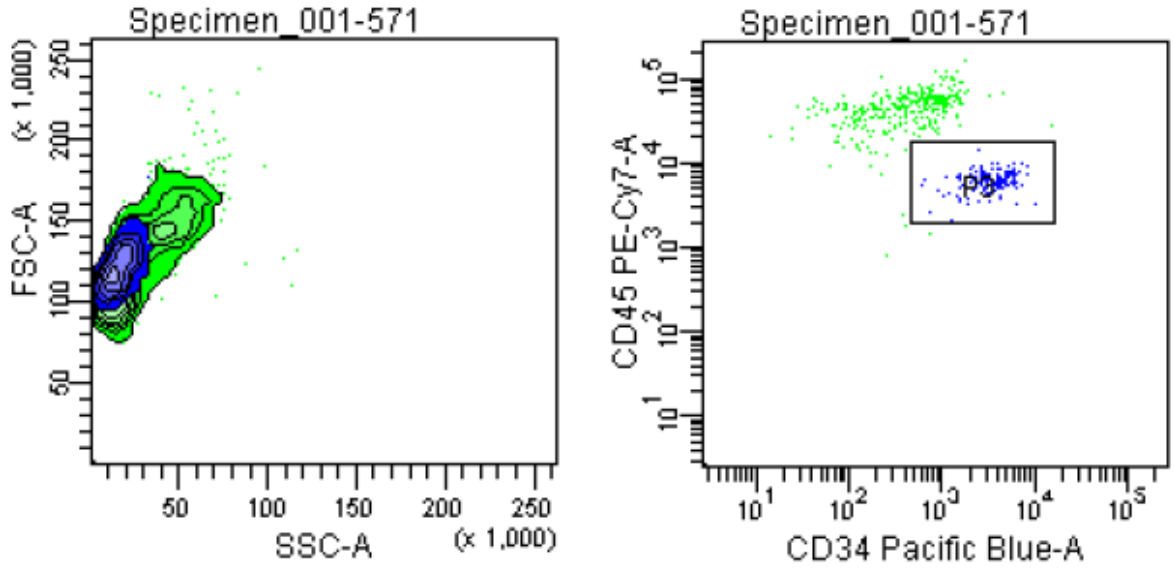
SUPPLEMENTARY DATA

The IPA software was used to analyze the complex data set obtained from the gene array study. The genomic data was integrated from a variety of experimental platforms and the bar graph provides insight into the 6 main areas (of a multitude of molecular and chemical interactions, cellular phenotypes, and disease processes examined by the IPA software) that were identified to be highly affected in the cohort of individuals studied. IPA provides insight into the causes of observed gene expression changes and into the predicted downstream biological effects of those changes. The top 6 signaling pathways mapped by transcripts identified in microarray analysis are shown and the data is displayed as a bar chart. The bar chart represents a ratio of numbers of genes in the current study that directly overlaps with the ingenuity database for the respective canonical pathway. Within each of the 6 areas there are both up-regulated and down-regulated genes. The percentage of up-regulated (red) and down-regulated (green) molecules are showed by the bars, while –log p value is displayed in the line graph.

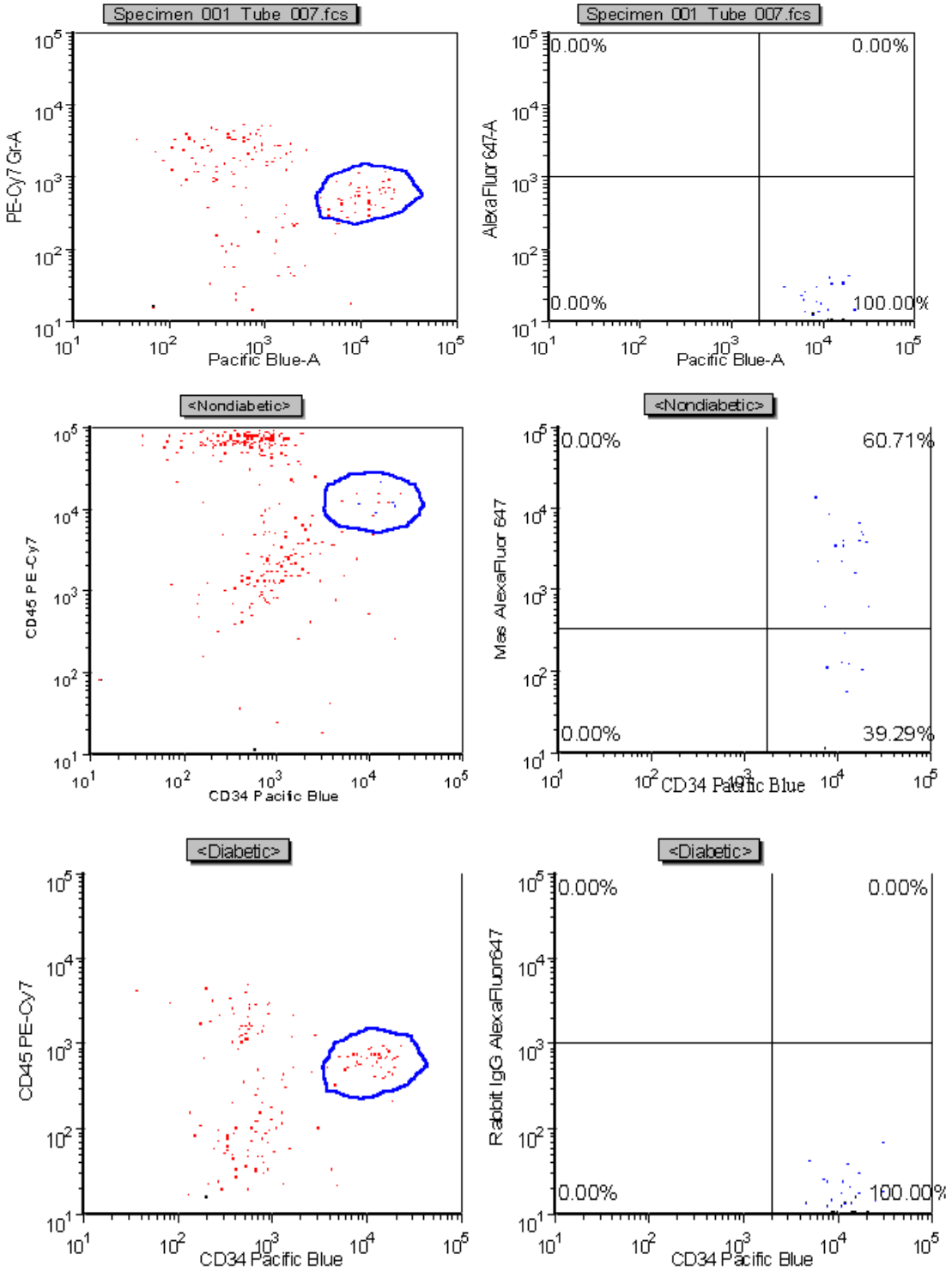
The Ang-(1-7)-fusion transgene construct used in our study was described by Santos et al (Physiol Genomics. 2004;17:292-299). Briefly, the human prorenin signal peptide and the immunoglobulin fragment from mouse IgG2b were linked to a portion of the human prorenin prosegment, and the *Bgl*II site after the prorenin segment was used to insert a furin cleavage site and the coding sequence for Ang-(1-7). This construct was cloned into the PCR-Blunt TOPO vector (Invitrogen, Carlsbad, CA) and then subcloned from this vector into pTY-EF1α to set it under the control of human elongation factor1α. The control gene construct has a similar sequence except the coding sequence for Ang-(1-7). Vesicular stomatitis virus G protein (VSV-G) pseudotyped lentiviral particles were prepared, as previously described (Coleman et al. Physiol Genomics 2003;12:221-228). $CD34^+$ cells were transduced at a concentration of 100 MOI, as described by Sengupta et al (Mol Ther .2009;17:1594-1604).

Supplementary Figure 1. Representative contour plot of the $Lin^-CD45^{mid}CD34^+$ selection from peripheral blood Lin^- cells used in the study.



SUPPLEMENTARY DATA

Supplementary Figure 2. Representative dot plots of $CD45^{mid}CD34^{+}$ Mas^{+} cells identified in the peripheral blood Lin^{-} cells by flow cytometry. Fluorophores: PE-Cy5.5 CD45, pacific blue-CD34, and AlexaFluor 647 conjugated isotype control (mouse IgG1) or Mas receptor. A. Nondiabetic Lin^{-} cells: i) isotype control, ii) Mas receptor (ii), and diabetic Lin^{-} cells: iii) isotype control and iv) Mas receptor.



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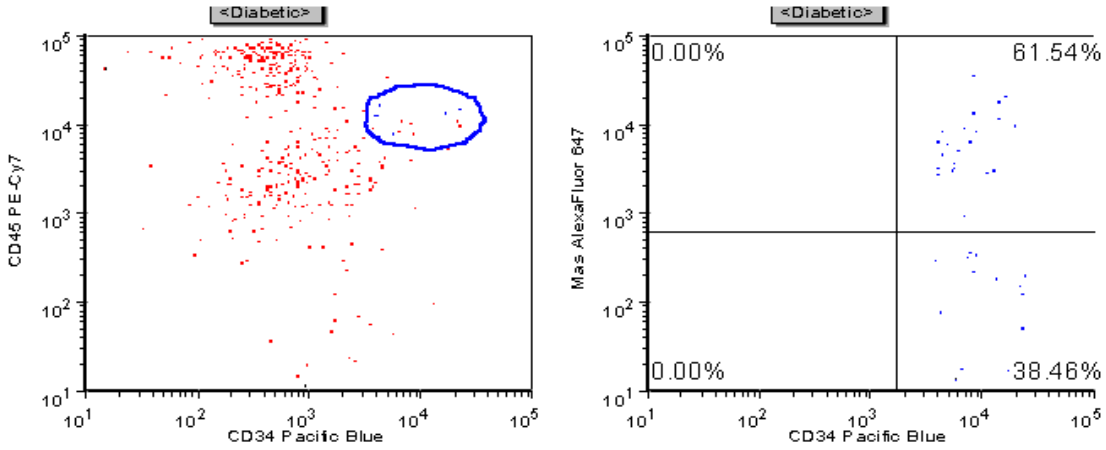
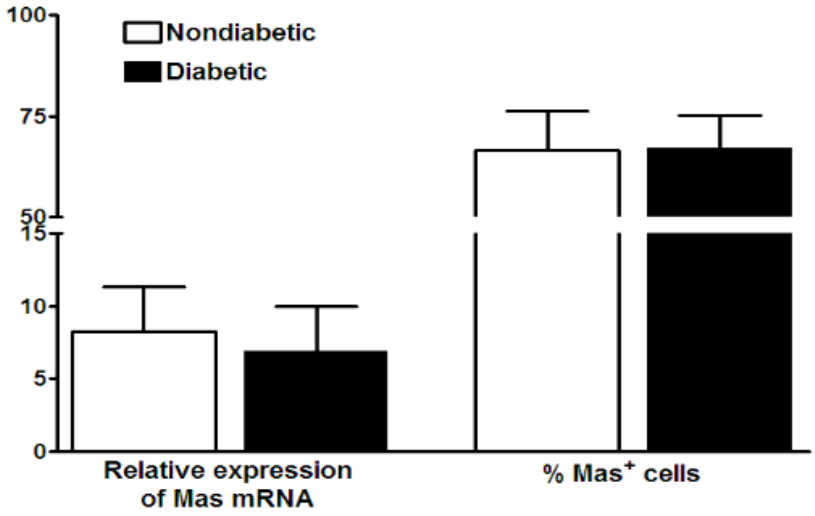
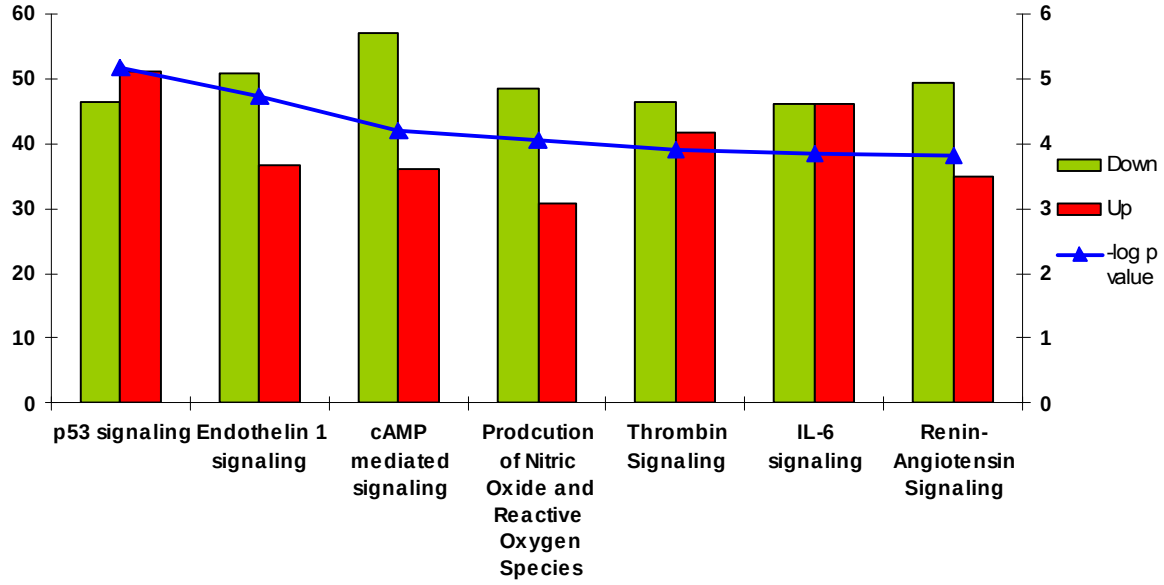




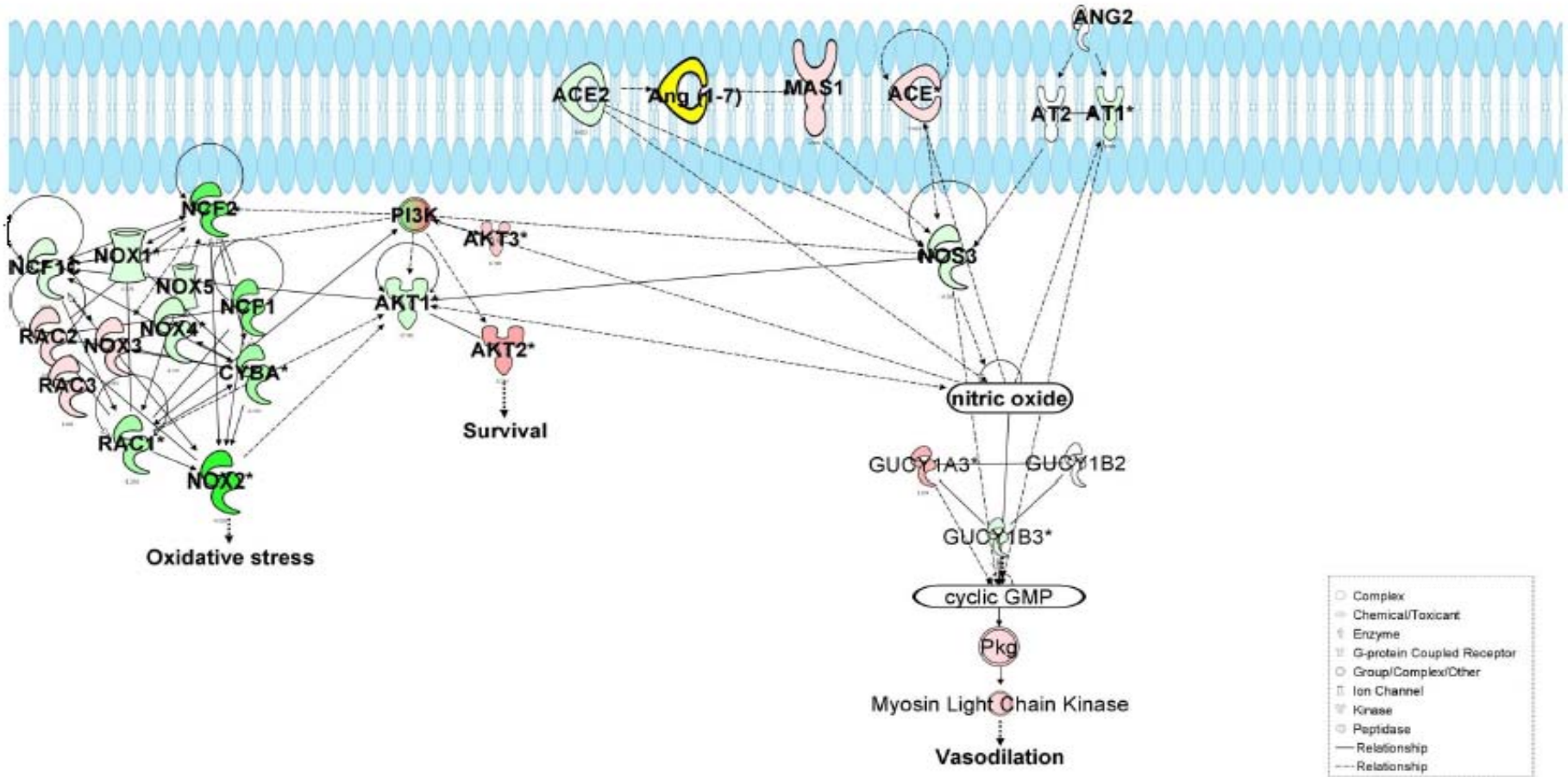
SUPPLEMENTARY DATA

Supplementary Figure 3. Signaling pathways mapped by transcripts identified in microarray analysis: Bar chart displaying significant pathways identified by Ingenuity pathway analysis software (IPA) in relation to EPC function. Percentage of upregulated (red) and downregulated (green) molecules are showed in bars, while –log p value is displayed in the line graph.



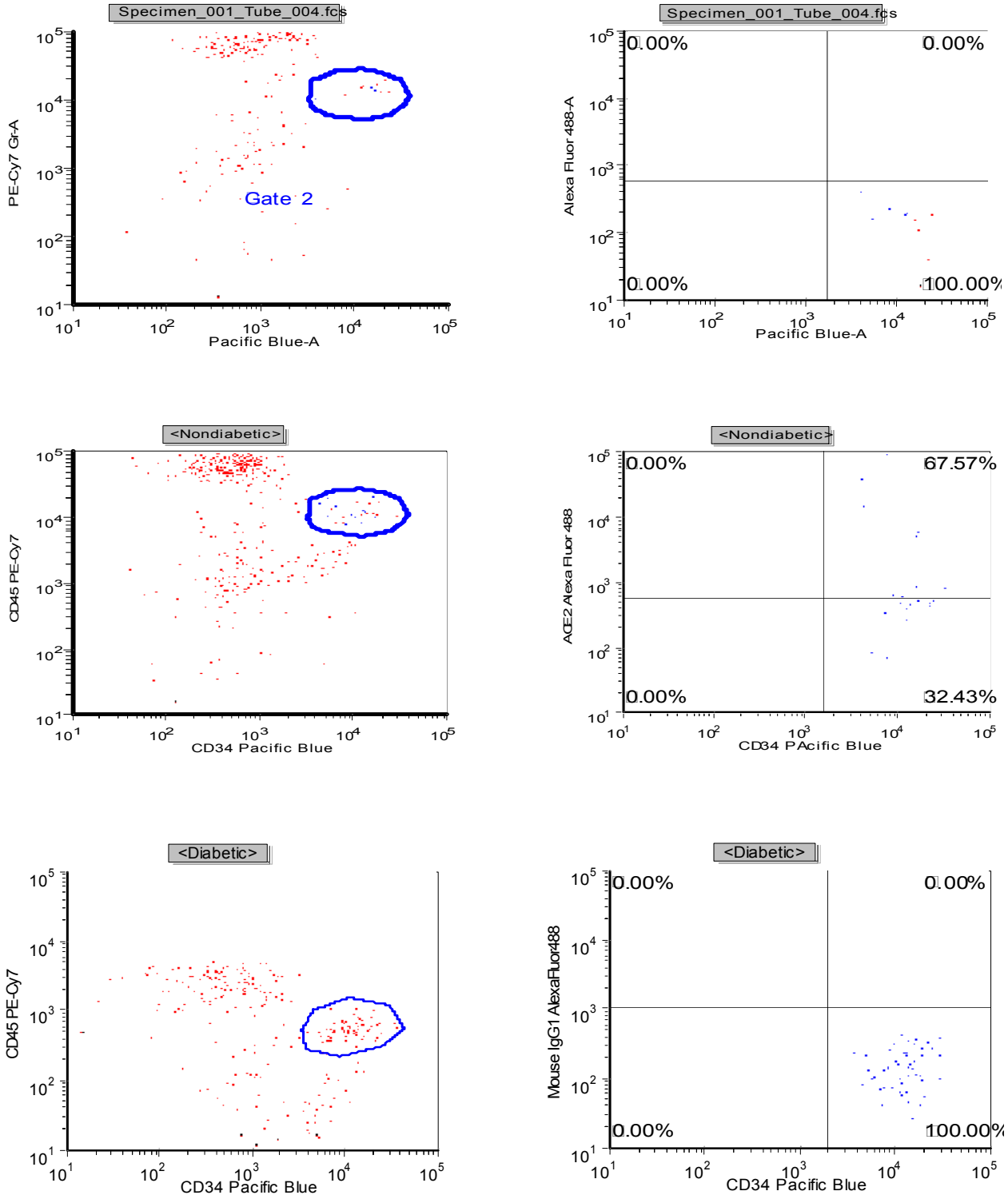
SUPPLEMENTARY DATA

Supplementary Figure 4. Transcripts identified by microarray analysis were mapped in the pathway of the RAS. Patients protected from the development of microvascular complications showed optimum bioavailability of NO resulting in an increase in migratory potential of EPCs; concurrently, there was an increase in survival and a reduction in oxidative stress, as indicated by an increase in Akt expression and an overall reduction in NADPH oxidase activity.



SUPPLEMENTARY DATA

Supplementary Figure 5. Representative dot plots of $CD45^{mid}CD34^{+}$ $ACE2^{+}$ cells identified in the peripheral blood Lin^{-} cells by flow cytometry. Fluorophores: PE-Cy5.5 CD45, pacific blue-CD34, and AlexaFluor 488 conjugated isotype control (rabbit IgG) or ACE2. A. Nondiabetic Lin^{-} cells: i) isotype control, ii) ACE2 (ii), and diabetic Lin^{-} cells: iii) isotype control and iv) ACE2.



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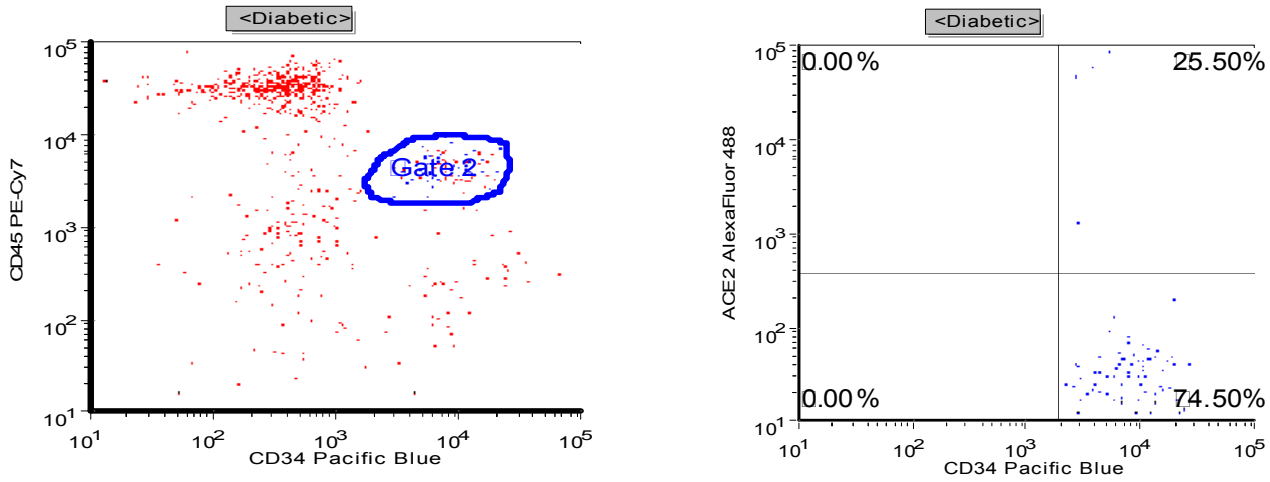
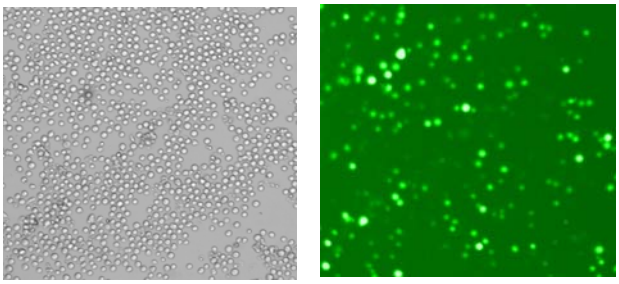
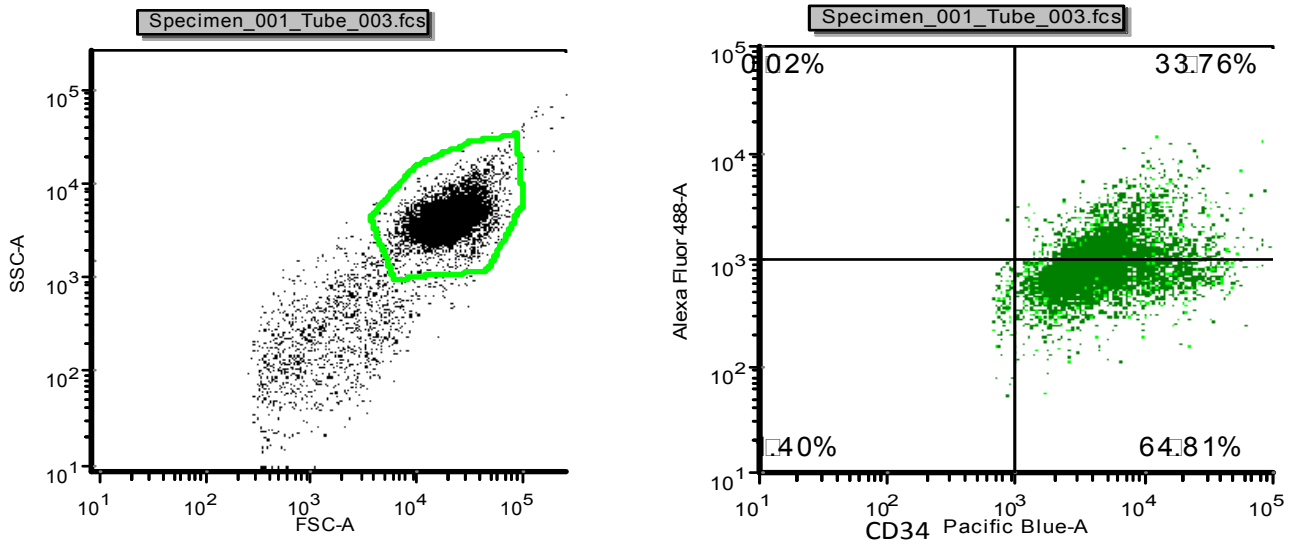


Supplementary Figure 6. A. Representative brightfield (left) and fluorescence (right) images of diabetic CD34$^+$ cells expressing eGFP 72 hours after lentiviral transduction. B. Representative FACS profile of enriched CD34$^+$ cells expressing eGFP. Expression was evaluated 72 hours after lentiviral eGFP gene modification of cells.



A



B

SUPPLEMENTARY DATA

Supplementary Figure 7. A. Nondiabetic CD34^{+} cells: i) control, ii) transduced with lenti-control, or iii) transduced with lenti-Ang-(1-7) clearly incorporated into the degenerated vasculature of ischemia-reperfusion injured mouse retina. B. Quantification of vascular engraftment of cells showed no differences in the function of cells with various treatments.