**SUPPLEMENTAL FIGURES**

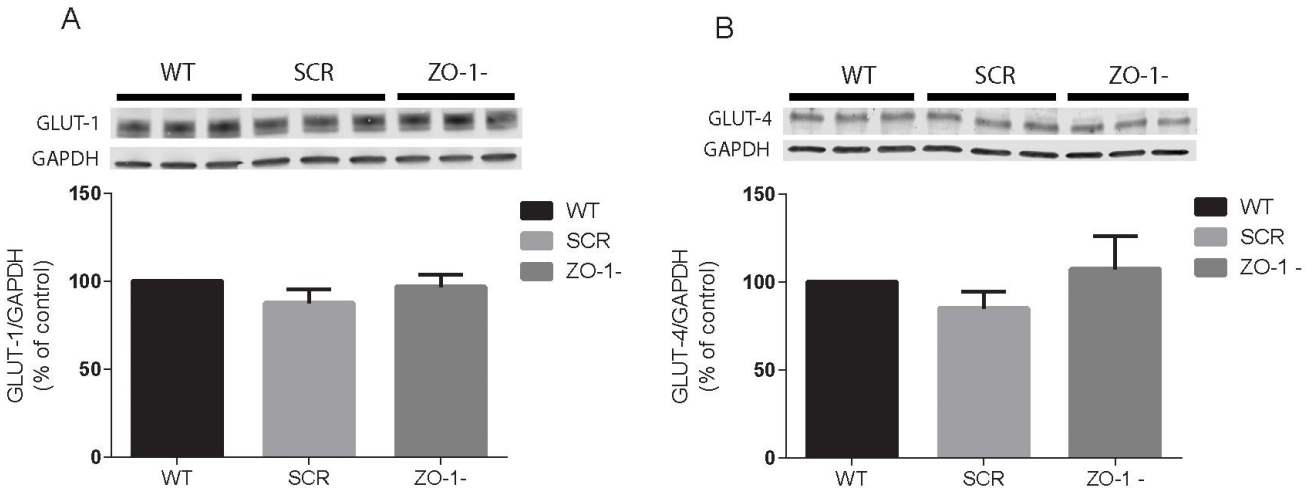


**Figure S1. Related to Figure 1. Expression of GLUT-1 (A) and GLUT-4 (B) in pericytes is not mediated by ZO-1**. Pericytes were left untreated (wild-type, WT), or treated with anti-ZO-1 (ZO-1-) siRNA. Scrambled siRNA (SCR) was used as a negative control. 24h post transfection, expression of GLUT-1 and GLUT-4 was assessed by western blotting (WT). Data are mean ± SD of three independent experiments, each with n = 3, expressed as % of control (WT). The results are not statistically significant.

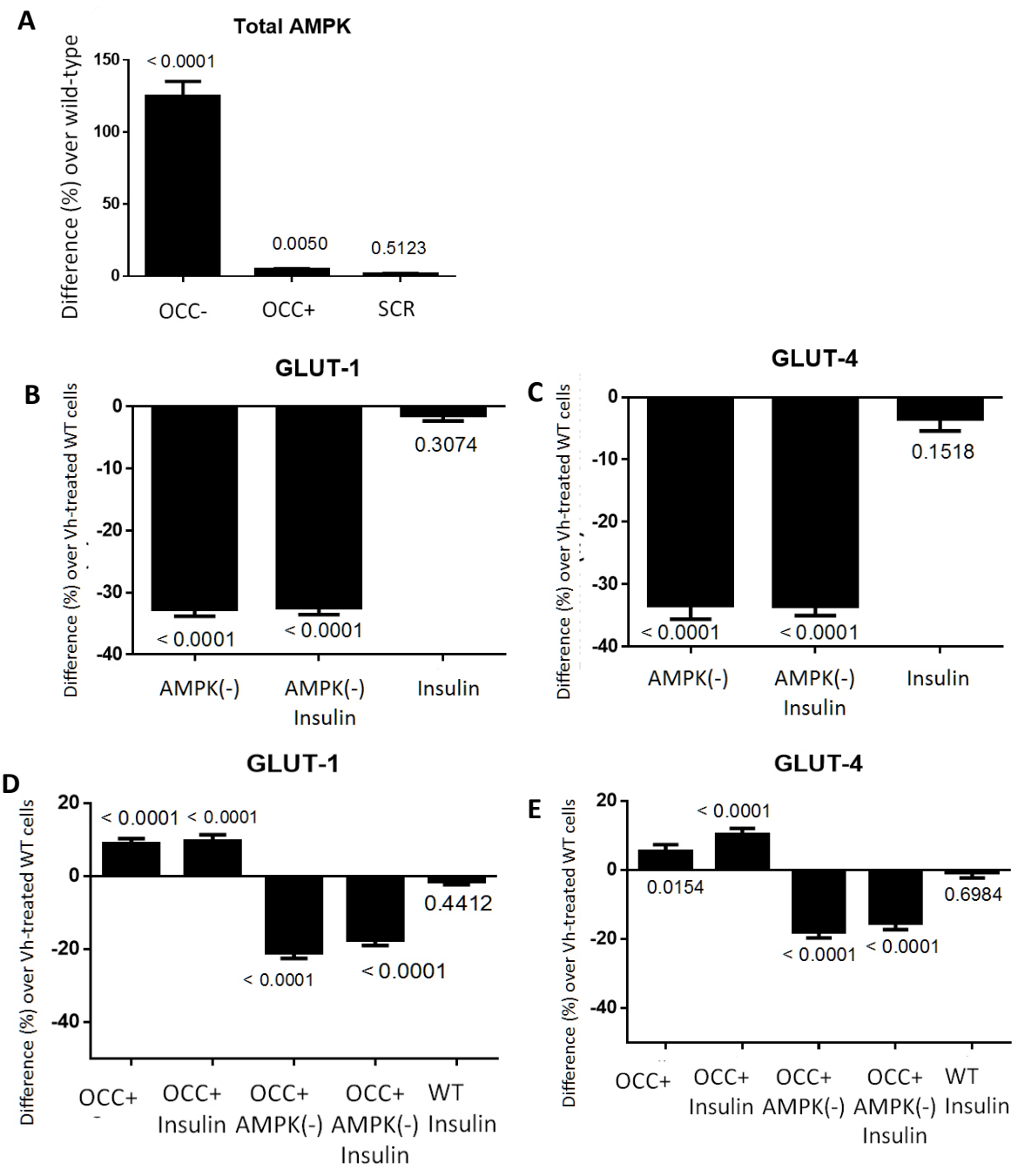


**Figure S2. Related to Figure 2. A)** SPRICE quantitation of total AMPK expression in occludin-deficient (OCC-), occludin overexpressing (OCC+), and control (SCR) pericytes. Values are normalized against DRAQ-5. p vs. wild type (WT) pericytes. **B)** SPRICE quantitation of GLUT-1 and **C)** GLUT-4 in the same cells shown in WT-pericytes treated with dorsomorphin (AMPK-) and/or insulin. **D)** SPRICE quantitation of GLUT-1 and **E)** GLUT-4 in occludin overexpressing (OCC+) pericytes treated with dorsomorphin and/or insulin. Graphs show average percentual difference over WT pericytes treated with PBS (Vh), represented by the horizontal axis at 0. Error bar = SEM. n=6. p vs WT.

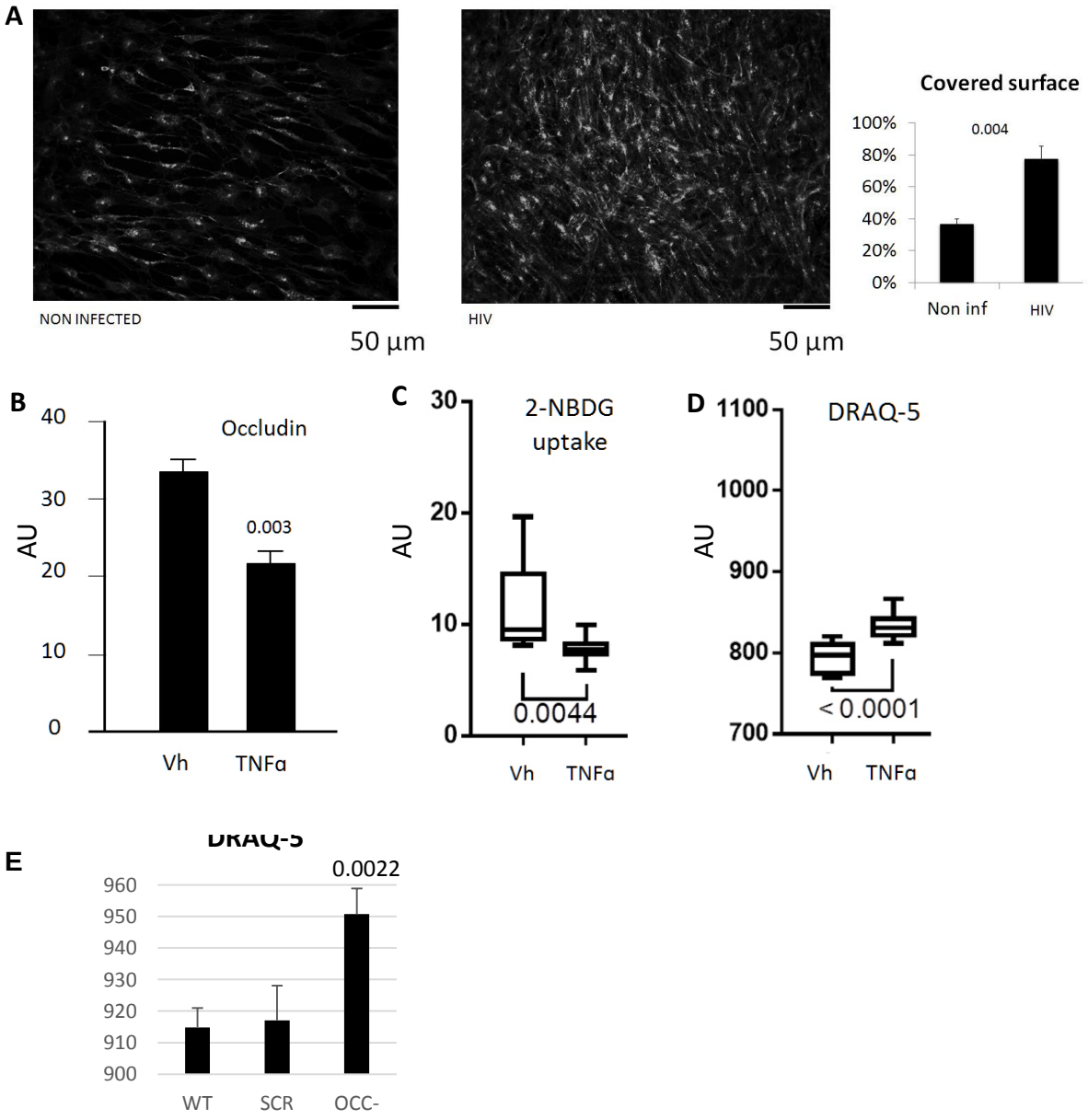


**Figure S3. Related to Figure 3. A)** Fluorescence microscopy image of HIV-infected pericytes after the onset of the occludin depletion phase. Cells were visualized with wheat germ agglutinin. The graph shows the average percentage of substrate covered by non-infected and HIV-infected pericytes, 96h post infection, in 10 fields from 3 separate experiments. Error bar=SEM. **B)** SPRICE quantitation of occludin levels in TNFα-treated pericytes. Vh: Vehicle treated. **C)** 2-NBDG uptake quantitation of pericytes shown in B. **D)** Quantitation of stoichiometric-DRAQ-5 uptake by the same pericytes as shown in B and C, Error bar= SEM, n=6. **E)** Quantitation of stoichiometric-DRAQ-5 uptake by occludin deficient (OCC-), control siRNA treated (SCR), and wild-type (WT) pericytes. n=11

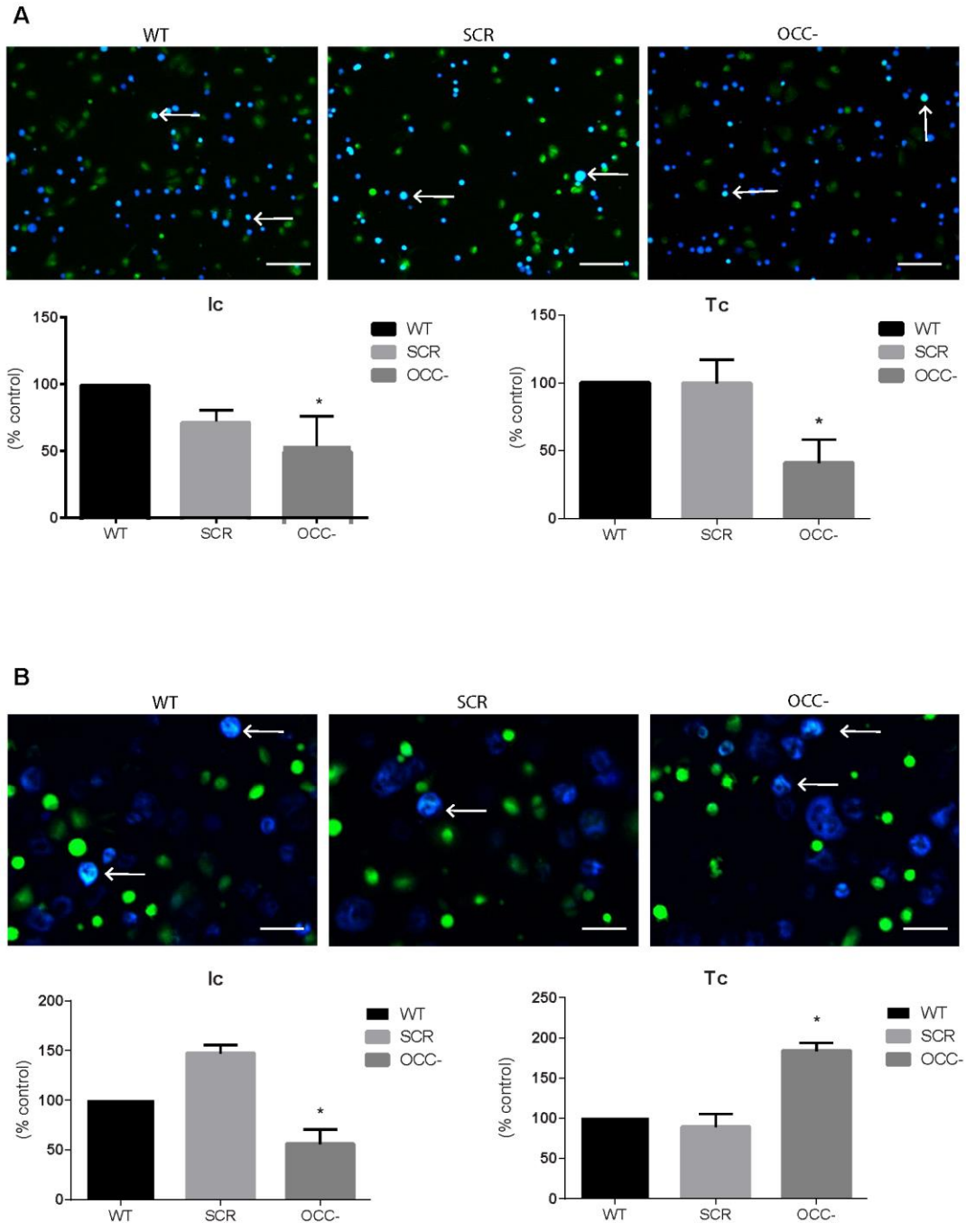


**Figure S4. Related to Figure 4. Glucose sharing between pericytes and endothelial cells (A) and between pericytes and fibroblasts (B).** Pericytes were pre-loaded with glucose analog, 2-NBDG (green) and endothelial cells (hCMEC) **(A)** or fibroblasts **(B)** with violet-BMQC (cell tracker, blue). After 30 minutes of co-culture, transfer of glucose was analyzed. Co-localization of both signals (cyan; arrows) indicate that endothelial cells or fibroblasts received 2-NBDG from pericytes. Results are mean±SD from 4 separate experiments and were expressed as % of control (WT). Ic (Intensity coefficient) and Tc (Transfer coefficient) were calculated as described in the Materials and Methods. *p<0.05 vs WT. Scale bar, (A) 100 µm; (B) 50 µm.

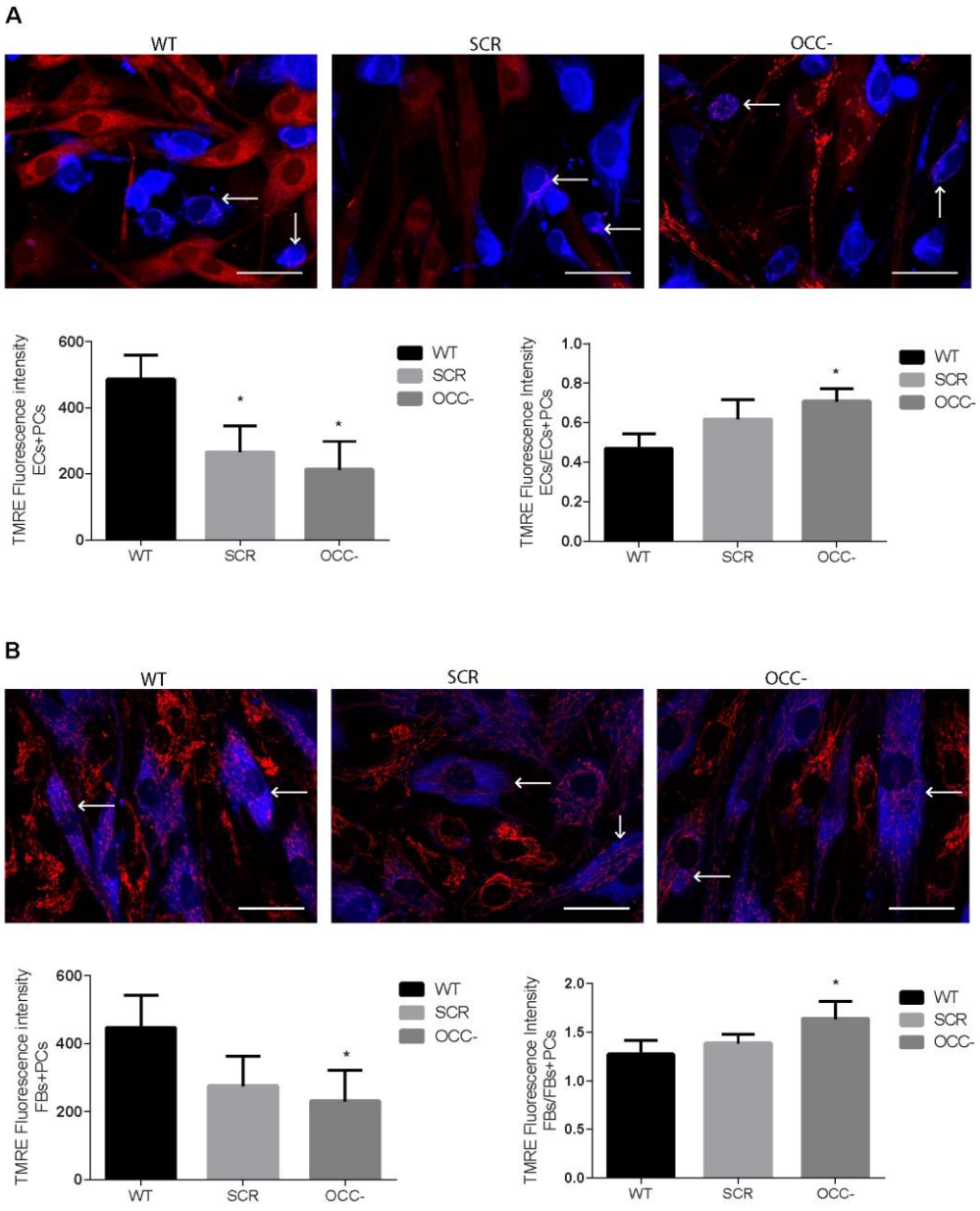


**Figure S5. Related to Figures 5 and 6. Mitochondria sharing between pericytes and endothelial cells (A) and between pericytes and fibroblasts (B).** Pericytes were left untreated (wild-type, WT), or treated with anti-occludin (OCC-) siRNA. Scrambled siRNA (SCR) was used as a negative control. 24h post transfection pericytes were labelled with TMRE (red), simultaneously endothelial cells (hCMEC) (A) or fibroblasts (B) were stained with violet-BMQC (cell tracker, blue). Mitochondria transfer was analyzed after 24h of co-culture. Co-localization of both signals (purple; arrows) indicated that endothelial cells or fibroblasts had received TMRE. Whole TMRE fluorescence reflects mitochondrial membrane potential in the cells. Transfer represents TMRE intensities within endothelial cells or fibroblasts normalized against the entire TMRE fluorescence. Results are mean ± SD from 4 separate experiments, *p<0.05 vs WT.