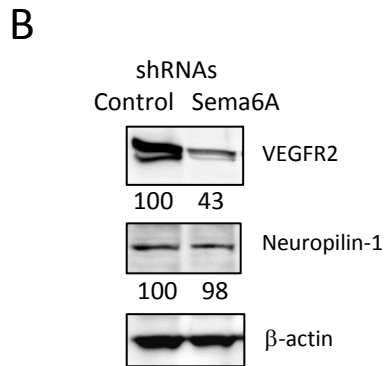
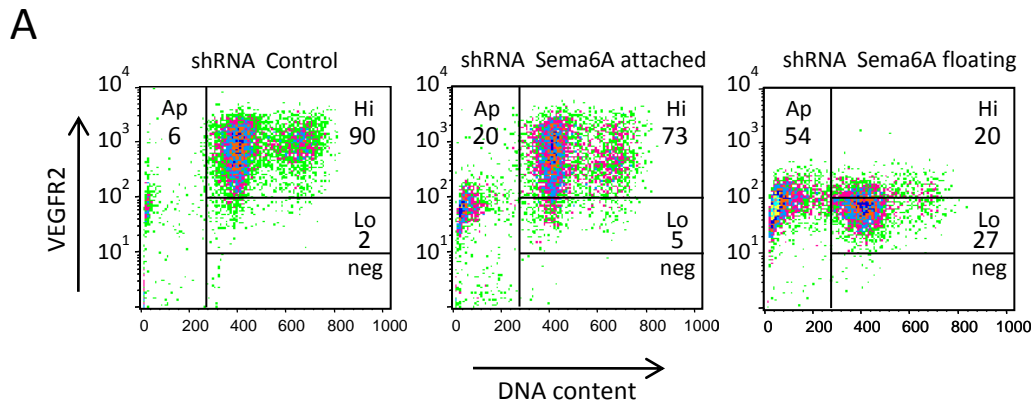
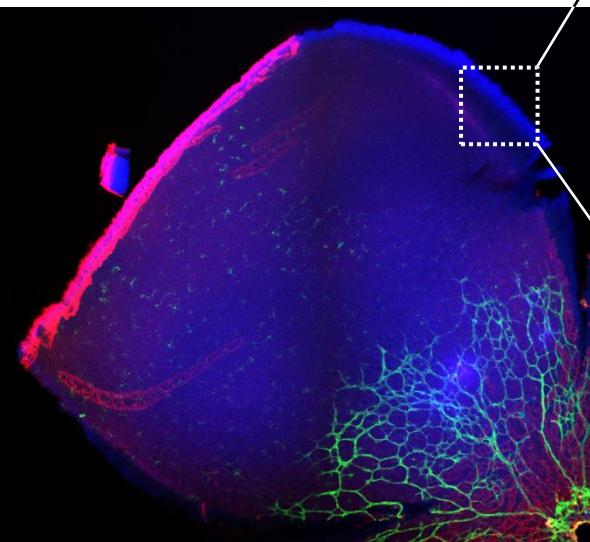


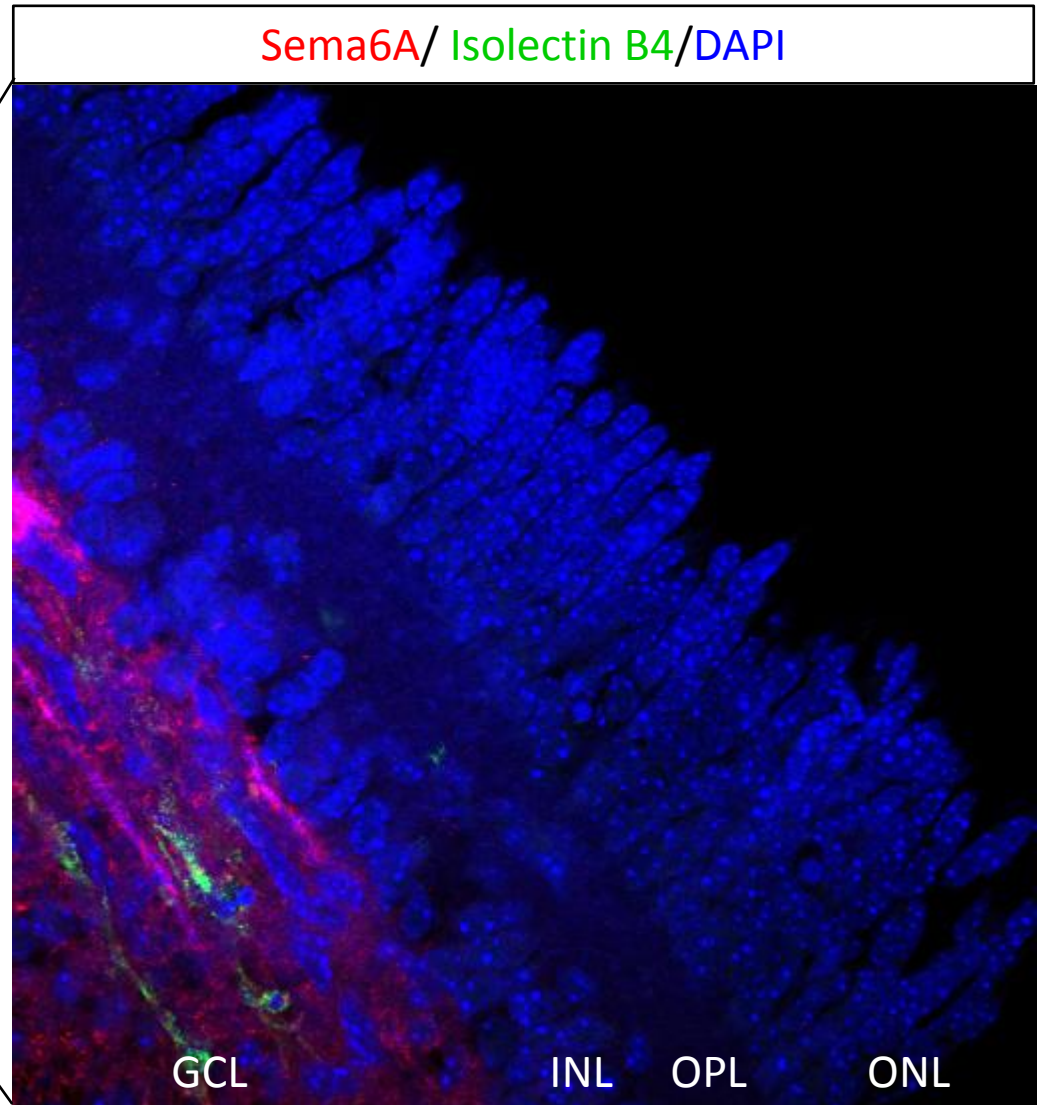
Supplemental Figure 1. HUVEC were infected with a control shRNA or with two different Sema6A shRNAs (TRCN0000061112, abbreviated 112 and TRCN0000061111, abbreviated 111); 96 hours post infection the cells were **A)** evaluated for Sema6A expression by quantitative PCR; **B)** stained with Propidium iodide and Hoechst 33342, and the distribution of viable, apoptotic and necrotic cells was measured by flow cytometry; and **C)** evaluated for VEGFR2 and FGFR1 expression by quantitative PCR. The results of quantitative PCR are expressed as relative levels and reflect the means \pm SD of 4 determinations. * $p < 0.001$.



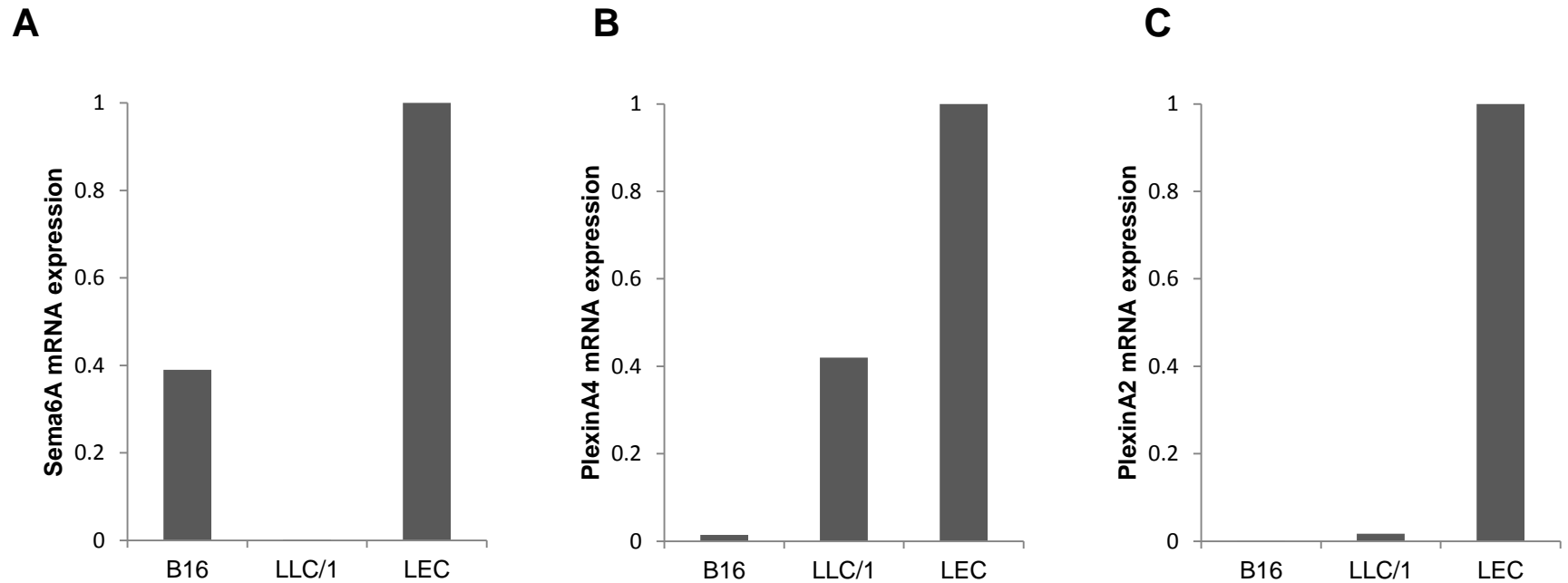
Supplemental Figure 2. A. HUVEC were infected with a control shRNA or Sema6A shRNA; 72 hours post infection a proportion of cells infected with Sema6A shRNA detached from the plate whereas cells infected with control shRNA remained mostly attached. Using flow cytometry, we measured VEGFR2 expression separately in control cells and in cells infected with Sema6A shRNA that were attached or floating. Ap:apoptotic cells. Representative flow cytometry profiles are displayed. **B.** VEGFR2 and Neuropilin-1 protein levels in cell lysates of HUVEC 72 hr post infection with control or Sema6A shRNAs; β -actin was used as a loading control. Normalized values of VEGFR2/ β -actin and Neuropilin-1/ β -actin band intensities are displayed.



GCL: Ganglion cell layer
INL: Inner nuclear layer
OPL: outer plexiform layer
ONL: outer nuclear layer



Supplemental Figure 3. Sema6A is expressed in the retinal ganglion cell layer. Retinal whole mount (p4) was stained with Sema6A antibody, IsolectinB 4 and DAPI. The images from different magnifications of the retina show the selective distribution of Sema6A immunostaining. GCL: ganglion cell layer; OPL: outer plexiform layer; INL inner nuclear layer; and ONL outer nuclear layer.



Supplemental Figure 4. A) Sema6A, B) PlexinA4 and C) PlexinA2 gene expression levels in B16 and LLC1/1 tumor cells measured by quantitative PCR. The results are expressed as mRNA levels relative to those detected in primary wild type murine lung endothelial cells (LEC).