SUPPLEMENTAL MATERIAL

SUPPLEMENTAL FIGURE LEGENDS

Figure S1. MicroRNAs expression profile in different cell types.

Expression levels of 159 miRNAs were evaluated in endothelial cells (HUVEC, HVMEC, H-END), mesenchimal cells (human primary fibroblasts and smooth muscle cells) and epithelial cells (breast epithelial cells MCF10), by qRT-PCR. Results are shown as ΔCt of the miRNAs, normalized on miR-16 expression level. Colour code represents the 25th percentile subdivision of the data from red (unexpressed miRNAs) to green (highly expressed miRNAs). MiRNAs differentially expressed between endothelial and mesenchymal/epithelial cells are shown as log2 ratio of ΔCt and statistical significance.

Figure S2. Serum deprivation and VEGF stimulation does not change miR-126 expression level

Expression levels of miR-126 were evaluated on ECs maintained in culture medium (CM), serum free medium(SF) or serum free medium with VEGF (VEGF) for 24 hours (left) and 48 hours (right) by qRT-PCR analysis. Results are shown as fold changes relative to EC in culture medium, normalized on miR-16 expression level. Statistical differences were not significant. Two independent experiments were performed in triplicate

Figure S3. miR-126 is expressed in the endocardium

(A) In situ hybridization with specific anti-miR-126 on transverse paraffin section of Zebrafish embryos (5 dpf). The miR-126 is expressed in the atrium of endocardium (black arrow) as well as in the ventricle (black arrowhead) (B) A comparative image of a transverse section of Zebrafish Tg(flk:GFP)s843. The magnification shows the GFP-positive endocardium (white arrowhead) and the myocardium (white arrow).

Figure S4. Over-expression of p85β inhibits endothelial cells survival

EC transduced with empty vector or p85β, stimulated with Ang-1, VEGF or maintained in serum deprived medium (SF), were assayed for apoptosis with Nucleosome-associated DNA fragments detection. Data were shown as mean±s.e.m.