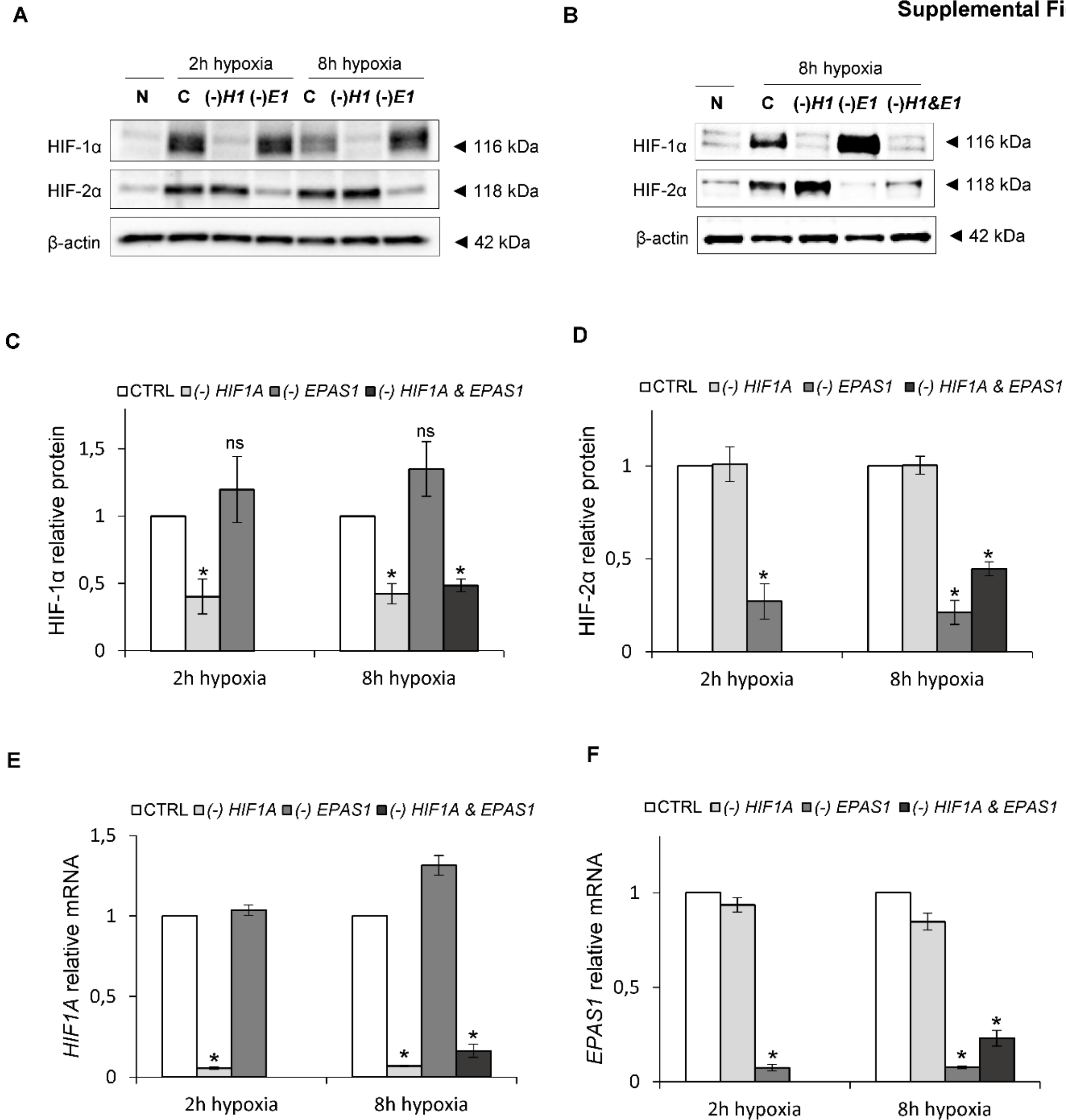

Supplemental Figure 2. *HIF1A and EPAS1 silencing in HUVECs exposed to hypoxia*. (**A** and **B**) HIF-1α and HIF-2α protein levels were evaluated in normoxia and hypoxia, and by Western Blot and normalized to β-actin and total protein levels, and related to the control at the specific time-points of hypoxia. To simultaneously detect without stripping HIF-1α and HIF-2α, which are of similar molecular mass, the same samples were loaded onto two gels and two blots were prepared – each was used to detect each HIFα isoform. The respective densitometry analysis of HIF-1α (**C**) and HIF-2α (**D**) represents three independent experiments (the error bars represent SD, * *P* value < 0.05 was considered significant). N –normoxia; C – hypoxia, negative control siRNA; H1 – hypoxia, *HIF1A* siRNA; E1 – hypoxia, *EPAS1* siRNA. The corresponding *HIF1A* (**E**) and *EPAS1* (**F**) mRNA levels were quantified by quantitative real-time PCR and normalized to *RPLP0* rRNA levels and expressed as a fold change over control at the specific time-point

of hypoxia. Data represent the mean ± SEM of three biological replicates (*$P < 0.05$ was considered significant).; ns – not significant. These sample sets were also used as a material for verification of HRE sequences.