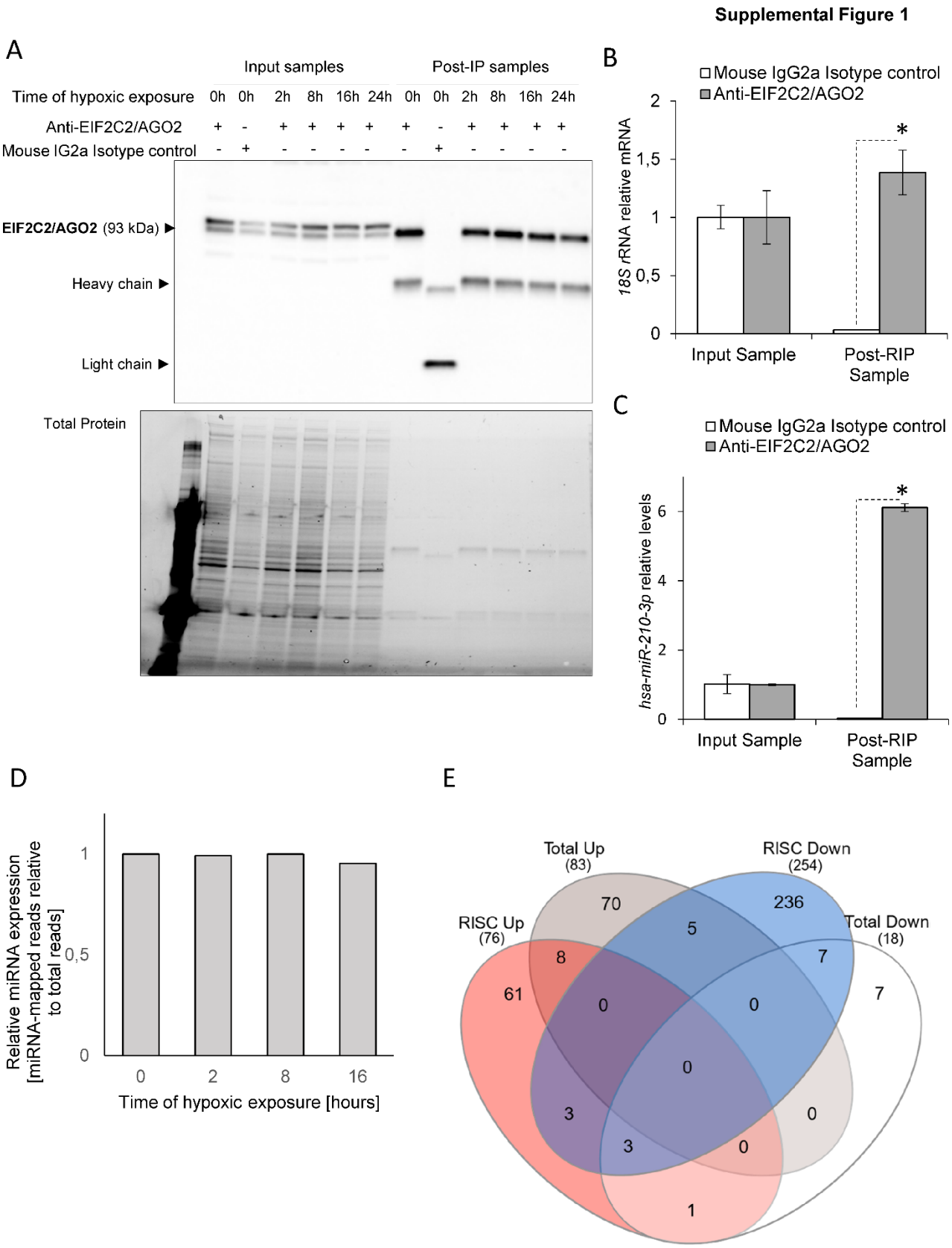

Supplemental Figure 1. (**A**) *Post-RIP and Input samples quality verification were shown in a Western blot.* For immunoprecipitation, 15 µg of anti-EIF2C2/AGO2 or mouse IgG2a (isotype control) was used, and a clear AGO2 enrichment was observed in Post-IP samples.

Furthermore, the Post-RIP samples were enriched in both (**B**) mRNA and (**C**) miRNA when compared to both input samples and the isotype control samples. The data represent mean of 3 replicates (± SEM of three ,**P*< 0.05 was considered significant). (**D**) Hypoxia does not affect miRNA global content in RISC components isolated from HUVECs. The mapped miRNA reads in the NGS analysis were normalized to total mapped RNA reads and expressed as fold change over the normoxia control. (**E**) The Venn diagram represents the differences between in NGS-based general distribution of unique miRNAs levels that changed by at least a log fold in HUVECs exposed to hypoxia in the RISC components as well as in the total global miRNA levels.