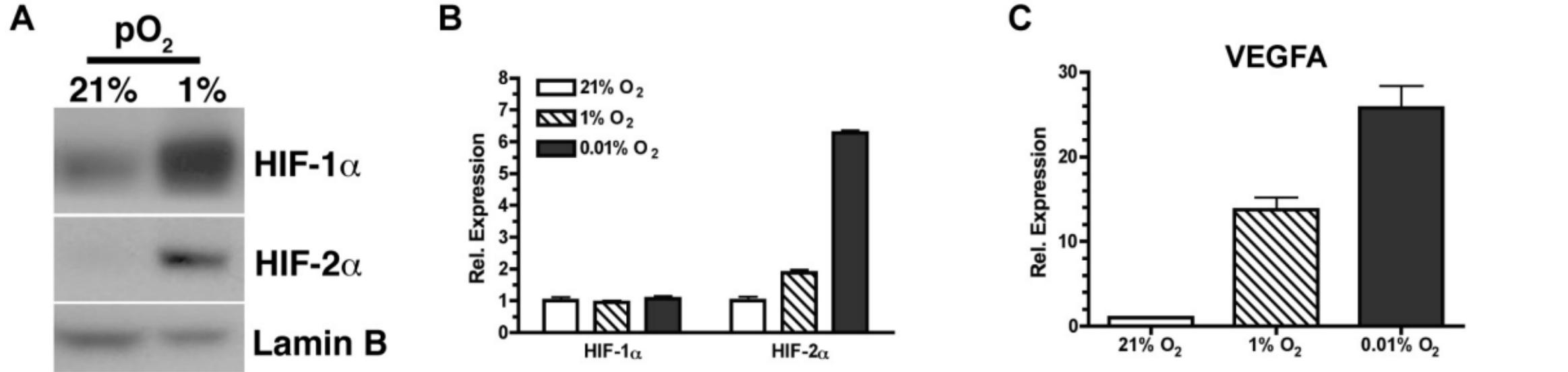


**Table 1. Primers for quantitation of mRNA by qRT-PCR (SYBR Green)**

Gene Symbol	Primer Sequence
HIF-1 $\alpha$	Forward: 5'- CTGCCACCACTGATGAATTA-3' Reverse: 5'- GTATGTGGGTAGGAGATGGA-3' Amplicon = 90 bp
HIF-2 $\alpha$	Forward: 5'- GCGCTAGACTCCGAGAACAT-3' Reverse: 5'- TGGCCACTTACTACCTGACCCTT-3' Amplicon = 71 bp
HIF-1 $\beta$	Forward: 5'- GTGGCAGTAGCTCTGTGGACC-3' Reverse: 5'- AGCCAAGTCCATTCTGTCAT-3' Amplicon = 78 bp
VEGFA	Forward: 5'- GCACCCATGGCAGAAGG-3' Reverse: 5'- CTCGATTGGATGGCAGTAGCT-3' Amplicon = 90 bp
GLUT1	Forward: 5'- GATTGGCTCCTTCTCTGTGG-3' Reverse: 5'- TCAAAGGACTTGCCCAGTTT-3' Amplicon = 129 bp
DEC1/BHLHE40	Forward: 5'- GCAGACAGGAGCGCGCAGTG-3' Reverse: 5' GTGGGCAGGGTACATCCCTGGT-3' Amplicon = 134
18S	Forward: 5'- CGGACAGGATTGACAGATTG-3' Reverse: 5'- CAAATCGCTCCACCACTAA-3' Amplicon = 83 bp

**Table 2. Primers for quantitation of ChIP-isolated genomic DNA by qRT-PCR (SYBR Green)**

Gene Symbol	Primer Sequence
HIF1A-P (proximal)	Forward: 5'-CGCTAAACACAGACGAGCAC-3' Reverse: 5'-GGGTTCTCGAGATCCAATG-3" Amplicon = 142 bp
HIF-1A-D (distal)	Forward: 5'-CCCCTATGTTCCACCTATGC-3' Reverse: 5'-TCCAACCTACAGCGTTCTGG-3' Amplicon = 111 bp
HIF-2A-P (proximal)	Forward: 5'-GAGCTTTACACTCGCGAGCGGA-3' Reverse: 5'-AGGACACTGCCGAGGATTGTAC-3' Amplicon = 98 bp
HIF-2A-D (distal)	Forward: 5'-ACTCCTGGTCACCCCTCAAG-3' Reverse: 5'-TTTCTGGGAGCTCAGAATGG-3' Amplicon = 122
VEGFA	Forward: 5'-AGACTCCACAGTGCATACGTG-3' Reverse: 5'-AGTGTGTCCCTCTGACAATG-3' amplicon = 245 bp
RAD51	Forward: 5'-CCCCCGGCATAAAGTTTGAAT-3' Reverse: 5'-GAAGCGCCGCACTCTCCTTA-3' amplicon = 263 bp



**Supplementary Figure 1. Effects of hypoxia on the expression of *HIF-1α*, *HIF-2α* and *VEGFA* in human glioblastoma U373 cells.** Cells were exposed to hypoxic conditions (1% or 0.01% O<sub>2</sub>) for 24 hr or maintained under normoxic culture condition (21% O<sub>2</sub>). (A) Whole-cell extracts were used for detection of HIF-1α and HIF-2α, respectively, using Western blots with lamin B as a loading control. (B, C) Total RNA was isolated for quantitative analysis of gene expression by qRT-PCR (mean ± sd).