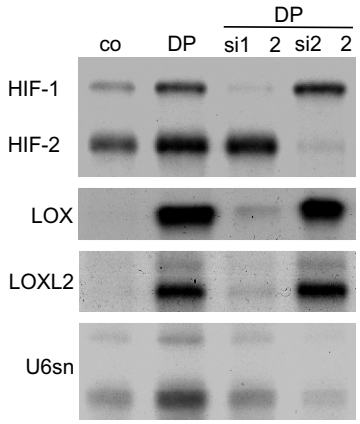
Suppl. Figure 1: LOX and LOXL2 mRNA expression after HIF-1α and HIF-2α knockdown.
HIF dependency of LOX and LOXL2 expression was analysed by knockdown of HIF-1α or HIF-2α with a the independent siRNAs siHIF-1α.2 (si1α.2) and siHIF-2α.2 (si2α.2) under DP treatment in Hep3B cells by RNAse protection.

Suppl. Figure 2: A human LOX reporter is inducible by hypoxia and HIF overexpression.
A. Scheme of the partial genomic structure of the LOX gene (light grey, genomic DNA; black exon (EX); grey intron; arrow, position of putative hypoxia responsive elements)
B. A 568 bp fragment (Accession number NT_034772, nt -294 - +274) containing the three putative HREs located 5' of the translational start site of the LOX gene was amplified from human genomic DNA (forward primer: 5'cggggtaccttcgcctgtctgagtt 3', reverse primer: 5' ccgcacgtgcactcctttgccaga 3'; underlined: generated Mlu I and Bgl II restriction sites) and cloned into the luciferase reporter vector pGL2). Reporter assay was performed in HEK293 cells. Hypoxia (hyp, 1% O_2) and HIF-1 overexpression (expression plasmids bearing cDNA for HIF-1α and HIF-1ß) could induce luciferase expression 2.7-fold and 2.9-fold, respectively. The control was transfected with empty vector pGL2 (pcDNA) and cultured under normoxia. Experimental duration was 16 hours. Results represent mean values of three independent experiments, with the error bars being standard deviation.

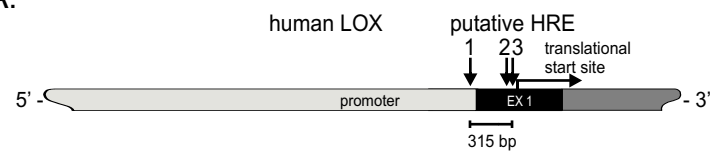
Suppl. Figure 3: siRNA knockdown for the lysyl oxidase LOXL2.
Efficacy and specificity of siRNA knockdown of LOX and LOXL2 was confirmed by RNase protection assay in HKC-8 cells. The siRNAs inhibited LOX and LOXL2 expression in subconfluent cell cultures under hypoxic conditions. For control, siRNA against GFP was added to one sample. All cells were treated with transfection reagent (co, normoxia; hyp, 1% O_2). Functional assays (reporter and invasion assays) were performed with knockdown against LOXL2, where the independent siRNAs siLOXL2 (siLL2), siLOXL2.1 (siLL2.1) and siLOXL2.2 (siLL2.2) were tested (B) and the siRNAs siLOXL2 and siLOXL2.2 were selected for analysis.

Supplementary Figure 1

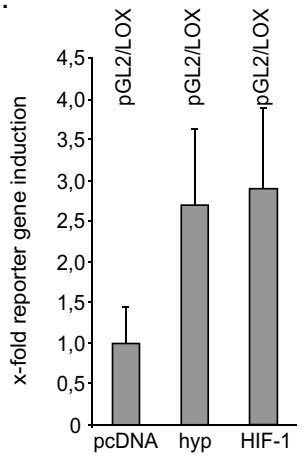


Supplementary Figure 2

A.



B.



Supplementary Figure 3