

Table S1. Primers' sequences for Electrophoretic mobility shift analyses of the human *MORG1* promoter putative HIF binding sites.

Name	Forward 5'- 3'	Reverse 5'- 3'
<i>HIF A</i>	TACACCCAAG <u>CGT</u> GGGTTTCTAAGGCGCG	CGCGCCTTAGAAACCCACGCTTGGGTGTA
<i>HIF A mut</i>	TACACCCAAGAAAGGGTTTCTAAGGCGCGGA	TCCGCGCCTTAGAAACCCTTTCTTGGGTGTA
<i>HIF B</i>	CAGCTTCCGG <u>CGT</u> GCAAGCTGAGGGCGGAT	ATCCGCCCTCAGCTTGCACGCCGGAAGCTG
<i>HIF B mut</i>	CAGCTTCCGGAAGCAAGCTGAGGGCGGAT	ATCCGCCCTCAGCTTGCTTTCCGGAAGCTG
<i>HIF C</i>	GCCAGATCAGCCTCTTCCGCTGC	GCAGCGGAAGAGGCGTGATCTGGC
<i>HIF C mut</i>	GCCAGATCCTTCTTCCGCTGC	GCAGCGGAAGAGGAAGATCTGGC
<i>HIF D</i>	TACTCTAGATACGTGGTTTCTAGTCCTACT	AGTAGGACTAGAAACCACGTATCTAGAGTA
<i>HIF D mut</i>	TACTCTAGATAAAGGTTTCTAGTCCTACT	AGTAGGACTAGAAACCTTTTATCTAGAGTA
<i>HIF-1α IL8</i>	TCTGTACGTGACCACACTCACCTC	GAGGTGAGTGGTCACGTACAGA
<i>HIF-1α IL8 mut</i>	TCTGTAAAAGACCACACTCACCTC	GAGGTGAGTGGTCTTTTACAGA

* The mutated primer sequences were used as well for generation of the corresponding mutations on the wild type *MORG1* promoter reporter constructs. The HIF binding sites and the mutated HRE binding sites on the sequences are underlined. The HIF-1 α consensus binding sequence is based on the IL-8 promoter.