

Table S1 Relationship between GLS1 and GLS2 expression in tissue microarrays which contain a serial set of colorectal tissues

Variables	Total	Number of patients					
		GLS1 expression (%)		χ^2 (P)	GLS2 expression (%)		χ^2 (P)
		Low	High		Low	High	
Normal colorectal tissue	15	15 (100.0)	0 (0.0)	<0.0001	7 (46.7)	8 (53.3)	<0.0001
Inflammatory hyperplasia	17	16 (94.1)	1 (5.9)		6 (35.2)	11 (64.7)	
Colorectal adenoma	9	9 (100.0)	0 (0.0)		9 (100.0)	0 (0.0)	
Colorectal adenocarcinoma	39	13 (33.3)	26 (66.7)		39 (100.0)	0 (0.0)	

Table S2 Relationship between clinicopathological parameters of colon cancer cases and expression of GLS1

Variables	Total	Number of patients (%)		Chi-square test
		GLS1 low expression	GLS1 high expression	P value
Age (year)				
<60	38	13 (34.2)	25 (65.8)	0.052 ^a
≥60	47	26 (55.3)	21 (44.7)	
Gender				
Male	50	21 (42.0)	29 (58.0)	0.391 ^a
Female	35	18 (51.4)	17 (48.6)	
Lymph node metastasis				
Present	24	4 (16.7)	20 (83.3)	0.001 ^b
Absent	61	35 (57.4)	26 (42.6)	
Grade				
well and moderately differentiated	60	31 (51.7)	29 (48.3)	0.097 ^a
poorly and non-differentiated	25	8 (32.0)	17 (68.0)	
Clinical stage				
early stage	51	34 (66.7)	17 (33.3)	<0.001 ^b
advanced stage	34	5 (17.4)	29 (85.3)	

Median values were used as cut-off points for definition of age subgroups

a, Pearson Chi-Square Test; b, Fisher's Exact Test

Table S3 *GLS1* gene expression is correlated with the expression of known HIF target genes in colorectal carcinomas

<i>Category</i>	<i>HIF targets</i>										<i>Non-HIF target</i>
<i>GENE</i>	<i>VEGFA</i>	<i>PDGFB</i>	<i>LOX</i>	<i>CXCR3</i>	<i>ANGPTL4</i>	<i>LICAM</i>	<i>SLC2A1</i>	<i>P4HA1</i>	<i>P4HA2</i>	<i>MET</i>	<i>RPL4</i>
<i>GLS1</i>	***	**	*	**	***	***	**	<i>n.s.</i>	***	***	<i>n.s.</i>
<i>PDGFB</i>	**	—	***	**	***	***	***	***	*	<i>n.s.</i>	<i>n.s.</i>
<i>LOX</i>	<i>n.s.</i>	***	—	**	***	***	***	***	***	<i>n.s.</i>	<i>n.s.</i>
<i>MET</i>	***	<i>n.s.</i>	<i>n.s.</i>	<i>n.s.</i>	**	***	***	**	<i>n.s.</i>	—	<i>n.s.</i>

* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, *n.s.*, not significant, Pearson's correlation test of microarray data from The Cancer Genome Atlas (TCGA) dataset of 433 colorectal carcinomas.

Table S4. Sequences of Oligonucleotide Primers Used for RT-qPCR and ChIP, Related to Methods.

Primers used in qRT-PCR assays	Sequence
Human-GLS1-FWD	tctacaggattgccaacgtct
Human-GLS1-REV	ctttgtctagcatgacacccatct
Human-GLS2-FWD	atcagaaagtggcatgctgt
Human-GLS2-REV	gcctttagtgcagtggtgaa
Human-HK2-FWD	ccagttcattcacatcatcag
Human-HK2-REV	cttacacgaggtcacatagc
Human and Mouse-18S-FWD	cggcgacgaccattcgaac
Human and Mouse-18S-REV	gaatcgaaccctgattccccgctc
Human-18S-FWD	gaggatgaggtggaacgtgt
Human-18S-REV	agaagtgacgcagccctcta
Primers used in ChIP assays	Sequence
PDK1-HRE-FWD	cgcgtttgattccgtg
PDK1-HRE-REV	ccagttataatctgccttcctattatc
GLS1-HRE-FWD	tgcacctgacatacacccctt
GLS1-HRE-REV	ctggtttcgagggatctgca