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Supplemental Information

UCP2 Deficiency Increases Colon Tumorigenesis

by Promoting Lipid Synthesis and Depleting

NADPH for Antioxidant Defenses

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Figure S1, related to Figure 1. UCP2 detection by immunohistochemistry, immunofluorescence and western blot analysis.

(A) UCP2 detection by immunohistochemistry analysis using colon tissue from $Ucp2^{+/+}$ and $Ucp2^{-/-}$ AOM/DSS-treated mice. Our homemade UCP2-605 antibody and the commercial UCP2 antibody ab203244 were tested. For each antibody: low magnification (left), scale bar 100 μ m, and high magnification (right), scale bar 50 μ m.

(B) UCP2 detection by immunofluorescence (green) using colon samples. Our homemade UCP2-605 antibody and the commercial UCP2 antibody sc6526 were tested. Nuclei were stained with Hoechst 3342 (blue). Scale bar = 100 μ m.

(C) Western blot analysis of UCP2 protein levels using mitochondria protein lysates from colon and lung samples from $Ucp2^{+/+}$ and $Ucp2^{-/-}$ mice. Our homemade UCP2-605 antibody and the commercial UCP2 antibodies sc6525, sc6526 and ab203244 were used. Porin was used as a loading control.



Figure S2, related to Figure 2. UCP2 invalidation does not affect the rate of cell proliferation and cell death. (A) Lgr5 mRNA levels relative to $Ucp2^{+/+}$ samples. Data represent mean \pm SEM for duodenum (Duo, n = 6), jejunum (n = 3), ileum (Ile, n = 7) and colon (n = 7).

(B) Ki-67 mRNA levels relative to $Ucp2^{+/+}$ samples. Data represent mean ± SEM for duodenum (Duo, n = 7), jejunum (n = 3), ileum (Ile, n = 7) and colon (n = 7).

(C) Representative duodenum sections stained with Ki-67. Data represent mean \pm SEM (n = 3-4). Scale bar = 100 μ m.

(D) Representative colonic sections, showing tumoral and non-tumoral regions, stained with Ki-67. Data represent mean \pm SEM (n = 4). Scale bar = 200 μ m.

(E) Immunoblot of caspase-3 and its cleaved form. Data represent mean \pm SEM (n = 6).

Α



Figure S3, related to Figure 5. Complex IV activity is reduced in Ucp2^{-/-} tumors.

(A) Representative immunoblot analysis of OXPHOS complexes (CI to CV) using whole cell extracts ($Ucp2^{+/+}$ T n = 10, $Ucp2^{-/-}$ T n = 7). Data indicate mean ± SEM.

(B) Enzyme activities of OXPHOS complexes CI, CII and CIV normalized to protein content. Data indicate mean \pm SEM.

(C) PDH activity measured as ¹⁴CO₂ release from [1-¹⁴C]-pyruvate ($Ucp2^{+/+}$ T n = 7, $Ucp2^{-/-}$ T n = 9). Data indicate mean ± SEM.



Figure S4, related to Figure 5. Effect of UCP2 invalidation on the expression of enzymes from glycolysis. Representative immunoblot of GLUT1, p-PFK2, PFK, p-PKM2 and PKM2 using whole cell extracts from tumors (T) with β -Actin as a loading control for quantification. Data indicate mean ± SEM (n = 7-10).

 Table S1, related to Figure 1. UCP2 expression in multiple microarray colorectal cancer data sets available from

 Oncomine (<u>http://www.oncomine.com</u>).

Data set	Normal type	Colorectal cancer subtype	Samples (N)	p value	Changes
GAEDKE	Rectum	Rectal adenocarcinoma	65 vs. 65	0.0817	=
GASPAR	Intestinal mucosa	Colorectal adenoma	22 vs. 47	0.0012	^
GRAUDENS	Colon	Colorectal carcinoma	12 vs. 18	0.3038	=
HONG	Colon	Colorectal carcinoma	12 vs. 70	0.0662	=
KAISER	Colon	Colon adenocarcinoma	5 vs. 41	0.1171	=
	Colon	Colon mucinous adenocarcinoma	5 vs. 13	0.2508	=
	Colon	Rectal adenocarcinoma	5 vs. 8	0.3692	H
	Colon	Rectal mucinous adenocarcinoma	5 vs. 4	0.7165	=
	Colon	Rectosigmoid adenocarcinoma	5 vs. 10	0.0010	1
KI	Colorectal mucosa	Colorectal	28 vs. 53	0.6584	=
SABATES-BELLVER	Colon mucosa	Colorectal adenoma	32 vs. 32	0.0007	1
	Colon mucosa	Rectal adenoma	32 vs. 7	0.1769	=
SKRZPCZAK	Colon	Colorectal adenocarcinoma	24 vs. 45	0.0112	^
	Colon	Colorectal carcinoma	24 vs. 36	0.7489	=
SKRZPCZAK 2	Colon	Colon adenoma	10 vs. 5	0.0011	1
	Colon	Colon carcinoma	10 vs. 5	0.7276	=
TCGA	Colon	Colon adenocarcinoma	19 vs. 102	0.0023	→
	Colon	Colon mucinous adenocarcinoma	19 vs. 20	0.4327	=
	Colon	Rectal adenocarcinoma	19 vs. 60	0.0010	. ↓
	Colon	Rectal mucinous adenocarcinoma	19 vs. 6	0.0565	=
ZOU	Colon	Colon carcinoma	8 vs. 9	0.3845	=

Table S3, related to STAR Methods. Sequences of primers used in this study.

Gene		Sequence (5'-3')			
mouso Ki 67	forward	AGGATGGAAGCAAGCCAACA			
mouse Ni-07	reverse	GGCCCTTGGCATACACAAAA			
mouso Lar5	forward	CGAGCCTTACAGAGCCTGATACC			
mouse Lyis	reverse	TTGCCGTCGTCTTTATTCCATTGG			
	forward	TCGAAGCCTACAAGACCATTGCAC			
	reverse	ACCAGCTCAGCACAGTTGACAATG			
human LICD2	forward	CTACAGCCAGCGCCCAGTA			
	reverse	TCAGTACGCACCATGGTCAGA			
mouso avalanhilin	forward	ATGGCACTGGCGGCAGGTCC			
mouse cyclophillin	reverse	TTGCCATTCCTGGACCCAAA			
	forward	GTCAACCCCACCGTGTTCTT			
питтап сустортши	reverse	CTGCTGTCTTTGGGACCTTGT			