

## 1 Supplemental materials

2 **Table 1.** Proteins significantly differentially regulated ( $p < 0.05$ , expression  $> \pm 1.5$ ) 12 h postprandial in the liver of Mongolian Gerbils after  
3 receiving either a single dose of carotenoids lycopene (LYC), lutein (LUT), all-*trans*  $\beta$ -carotene (ATBC), retinol (ROL) or control (Cremophor  
4 EL solution). Protein functionality (biological process involvement and protein type) according to UniProt ([www.uniprot.org](http://www.uniprot.org)). As isoforms  
5 were determined also, proteins could also be in part up-and down-regulated at the same time.

comparison against vehicle

LUT	ATBC	LYC	ROL	Protein name	abbreviation	gene abbreviation*	protein abbreviation*	biological process	protein category	Mascot confidence score**	alternative proteins
↑↑	↑↑	↑↑		3-ketoacyl-CoA thiolase A, peroxisomal	ACAA1A	ACAA1A	THIKA	fatty acid metabolism	lipid metabolism	377	Fructose-bisphosphate aldolase B
↑↑				3-ketoacyl-CoA thiolase B, peroxisomal	ACAA1B	ACAA1B	THIKB	fatty acid metabolism	lipid metabolism	296	Aspartate aminotransferase, mitochondrial
		↓	↓	Actin, cytoplasmic 1	ACTB	ACTB	ACTB	cytoskeleton filament	structure	358, 370, 607, 976,	
		↓↓	↓↓	Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2	ALDH2	oxidoreductase	detoxification	638, 126,	Argininosuccinate lyase
		↓↓		Aldo-keto reductase type L16	AKR	AKR-L16	Q05KR4	oxidoreductase	detoxification	371	Ornithine carbamoyltransferase, mitochondrial
↑↑				Alpha-enolase	ENO1	ENO1	ENOA	glycolytic process	energy metabolism	413	Aldehyde dehydrogenase, mitochondrial
		↑↑	↑↑	Apolipoprotein A-I	APOA1	APOA1	APOA1	lipid metabolism	lipid metabolism	167, 139,	
↓↓		↓↓	↓↓	Argininosuccinate lyase	ASL	ASL	ARYL	amino acid biosynthesis	protein metabolism	514, 79	
↑↑	↑↑			Aspartate aminotransferase, mitochondrial	ASP1	GOT2	AATM	amino acid binding	protein metabolism	496, 248,	3-ketoacyl-CoA thiolase B, peroxisomal
		↓↓	↓↓	ATP synthase subunit beta, mitochondrial	ATPB	ATPB	ATP5B	ATP hydrolysis	energy metabolism	882, 1070	
		↓↓		Bile salt sulfotransferase-like	SULT2A1	LOC106157106	A0A1S3HPU2	bile acid metabolism	other metabolism	114	
		↓↓		Carbonyl reductase (Nadph) 1	CRBR1	CBR1	CBR1	nucleotide binding	nucleotide metabolism	158, 160,	Omega-amidase NIT2 isoform X1, bile salt sulfotransferase-like
↓	↓	↓	↓	Carbonyl reductase (Nadph) 3	CRBR3	CBR3	CBR3	nucleotide binding	nucleotide metabolism	288, 73, 231	Omega-amidase NIT2 , Purine nucleoside phosphorylase
			↓	Cytochrome b5	CYB5A	CYB5A	CYB5A	electron	energy	415, 803, 1020	Eukaryotic translation

								transport	metabolism		initiation factor 5A-1
		↓↓		Cytoplasmic aconitate hydratase	ACO1	ACO1	ACOC	cellular iron homeostasis	transport	107, 344	
	↑↑	↑↑		D-beta-hydroxybutyrate dehydrogenase, mitochondrial	BDH1	BDH1	BDH	oxidoreductase	lipid metabolism	225	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial
		↓	↓	Elongation factor 2	EEF2	EEF2	EF2	protein biosynthesis	protein metabolism	256, 236	Cytoplasmic aconitate hydratase
↑	↑	↓		Fructose-bisphosphate aldolase B	ALDOB	ALDOB	ALDOB	glycolytic process	energy metabolism	430, 549, 499, 597,	3-ketoacyl-CoA thiolase A, peroxisomal, Alcohol dehydrogenase 1
		↓↓	↓↓	Glutathione S-transferase Mu 7	GSTM7	GSTM7	GSTM7	acetylation	detoxification	448	
		↑↓	↓	Glutathione-S-transferase Yb-3	GSTM3	GSTM3	GSTM4	acetylation	detoxification	62, 201, 366, 476, 578, 512, 564, 411,	
	↓	↓	↓	Hemoglobin, subunit alpha	HBA	HBA1	HBA	oxygen transport	transport	92, 278, 247, 510, 120,	
		↑↑		Keratin, type II cytoskeletal 8	KRT8	KRT8	K2C8	Intermediate filament	structure	158, 409	
↑			↓	Ornithine carbamoyltransferase, mitochondrial	OTC	OTC	OTC	amino acid binding	protein metabolism	133, 119	Eukaryotic translation initiation factor 3 subunit I , Glutathione S-transferase Yb-3
↓↓	↓↓			Peroxiredoxin-1	PER1	PRDX1	PRDX1	redox homeostasis	detoxification	248, 120	
			↑↑	Protein disulfide-isomerase	PDI	P4HB	PDIA1	redox homeostasis	protein metabolism	485	60 kDa heat shock protein, mitochondrial (Fragments)
↑	↑	↑		selenium-binding protein 1	SBP1	SELENBP1	SBP1	Se-binding	transport	420	
		↑		Serum albumin	ALB	ALB	ALBU	transport - metal binding	transport	1080, 962, 1270, 1190, 851	
↓↓	↓↓			Translationally-controlled tumor protein	TPT1	TPT1	TCTP	calcium binding	structure	242	Peroxiredoxin-1
		↓↓		UDP-glucose 6-dehydrogenase	UGDH	UGDH	UGDH	NAD binding	other metabolism	74	Glutamate dehydrogenase 1, mitochondrial

- 6 ↑↑ up-regulated compared to control (vehicle); all isoforms significantly up-regulated  
7 ↑ partly up-regulated compared to control (vehicle), some isoforms significantly up-regulated  
8 ↓↓ down-regulated compared to control (vehicle); all isoforms significantly down-regulated  
9 ↓ partly down-regulated compared to control (vehicle), some isoforms significantly down-regulated  
10 ↑↓ up- and down-regulated compared to control (vehicle)  
11 \*according to UniProt ([www.uniprot.org](http://www.uniprot.org)); \*\*values in 1 cell indicating the different isoforms  
12

13 **Table 2.** Proteins significantly differentially regulated ( $p < 0.05$ , expression  $> \pm 1.5$ ) 12 h postprandial in the white adipose tissue of Mongolian Gerbils  
 14 after receiving either a single dose of carotenoids lycopene (LYC), lutein (LUT), all-*trans*  $\beta$ -carotene (ATBC), retinol (ROL) or control (Cremophor EL  
 15 solution). Protein functionality (biological process involvement and protein type) according to UniProt ([www.uniprot.org](http://www.uniprot.org)).

comparison against. vehicle				protein name	abbreviation	gene abbreviation*	protein abbreviation*	biological process	protein category	Mascot confidence score**	alternative protein
LUT	ATBC	LYC	ROL								
			↓↓	14-3-3 protein beta/alpha	YWHAB	YWHAB	1433B	signalling cascade	other metabolism	134	
			↑	Actin, aortic smooth muscle	ACTA2	ACTA2	ACTA	cell motility	structure	190, 155, 536, 182, 833, 287, 1030, 500,	
			↑↑	Adenylate kinase isoenzyme 1	AK1	AK1	KAD1	ATP regeneration	energy metabolism	380	
		↓	↓↓	Adiponectin	ADIPO	ADIPOQ	ADIPO	hormone, lipid differentiation	lipid metabolism	292, 255, 152	Prohibitin (Fragments)
		↓	↓	Cytochrome b5	CYB5A	CYB5A	CYB5A	electron transport	energy metabolism	112, 581	
↓↓				Cytoplasmic dynein 1 intermediate chain 2	CD1IC	Dync1i2	DC1I2	microtubule motor activity	structure	87	
	↓↓		↓↓	D-dopachrome decarboxylase	DDT	DDT	DOPD	immune system	immune system, inflammation	309	
↑↑	↑			Desmin	DES	DES	DESM	cytoskeletal protein binding	structure	1050, 189, 309	
↓↓			↓↓	Endoplasmic reticulum resident protein 29	ERP29	ERP29	ERP29	chaperone binding	protein metabolism	208	
			↓↓	Eukaryotic translation initiation factor 4H	EIF4H	EIF4H	IF4H	nucleotide binding	nucleotide metabolism	159	
			↑	Ezrin	EZR	EZR	EZRI	actin binding	structure	179, 355	
↑↑				Heat shock protein beta-1	HSPB1	HSPB1	HSPB1	actin organization	structure	403	
	↑↑			L-lactate dehydrogenase B chain	LDHB	LDHB	LDHB	carbohydrate metabolism	energy metabolism	165	
↑↑			↑↑	Myosin-11	MYH11	MYH11	MYH11	muscle contraction	structure	118	
↑↑	↑↑		↑↑	Retinal dehydrogenase 2	ALDH1A2	ALDHA2	AL1H2	retinol metabolism	lipid metabolism	126	Desmin
			↓↓	Rho GDP-dissociation inhibitor 1	GDIR1	ARHGDI A	GDIR1	fatty acid binding	lipid metabolism	147	
	↑↑			Serine/threonine-protein phosphatase PP1-beta catalytic subunit	PP1CB	PP1CB	PP1B	phosphorylation processes	protein metabolism	102, 76	
		↑		Serum albumin	ALB	ALB	ALBU	metal binding, transport	transport	259, 294, 548, 243, 151, 936, 824,	

	↑			Vimentin	VIM	VIM	VIME	cytoskeleton component	structure	274, 564, 1120
16	↑↑	up-regulated compared to control (vehicle); all isoforms significantly up-regulated								
17	↑	partly up-regulated compared to control (vehicle), some isoforms significantly up-regulated								
18	↓↓	down-regulated compared to control (vehicle); all isoforms significantly down-regulated								
19	↓	partly down-regulated compared to control (vehicle), some isoforms significantly down-regulated								
20	*according to UniProt ( <a href="http://www.uniprot.org">www.uniprot.org</a> ); **values in 1 cell indicating the different isoforms									

21 **Table 3.** Proteins significantly differentially regulated ( $p < 0.05$ , expression  $> \pm 1.5$ ) 12 h postprandial in the blood plasma of Mongolian  
 22 Gerbils after receiving either a single dose of carotenoids lycopene (LYC), lutein (LUT), all-*trans*  $\beta$ -carotene (ATBC), retinol (ROL) or control  
 23 (Cremophor EL solution). Protein functionality (biological process involvement and protein type) according to UniProt ([www.uniprot.org](http://www.uniprot.org)). As  
 24 isoforms were determined also, proteins could also be in part up-and down-regulated at the same time.  
 25

comparison against vehicle

LUT	ATBC	LYC	ROL	protein name	abbreviation	gene abbreviation*	protein abbreviation*	biological process	protein category	Mascot confidence score**
↓↓				Actin, cytoplasmic 1	ACTB	ACTB	ACTB	cytoskeleton	structure	93-524
↑↑		↑↑	↑↑	Adiponectin	ADIPO	ADIPO	ADIPOQ	hormone, lipid differentiation	lipid metabolism	58-714
	↑			Alpha-1-antitrypsin	A1AT	SERPINA1	A1AT	acute phase response	blood coagulation	748-3216, 106-242
		↑↑	↑↑	Alpha-1-macroglobulin	AMBPG	A1M	A1M	neurotrophic factor binding	protein metabolism	1273-4862
	↑↑			Alpha-2-HS-glycoprotein	AHSG	AHSG	FETUA	acute phase response	immune system, inflammation	153-1721
↓	↓		↓	Alpha-2-macroglobulin	A2M	A2M	A2MG	calcium binding, blood coagulation	protein metabolism	2367-5542, 291-1594, 118-197
		↑↑	↑↑	Antithrombin-III	ANT3	SERPINC1	ANT3	blood coagulation	blood coagulation	267-1084
↑↑				AP-1 complex subunit gamma-1	AP1G1	AP1G1	AP1G1	protein transport	protein metabolism	32-55
		↓↓	↓↓	Apolipoprotein E	APOE	APOE	APOE	cholesterol transport	lipid metabolism	101-219
	↑↑			Axin-2	AXIN2	AXIN2	AXIN2	enzyme binding and phosphorylation	other metabolism	39-96
	↓↓			Carboxylesterase 1C	CES1C	CES1C	EST1C	hydrolase, ester bonds	detoxification	134-688
		↑↑	↑↑	Carboxypeptidase B2	CPB2	CPB2	CPB2	fibrinolysis	blood coagulation	52-167
	↓	↓	↓	Ceruloplasmin	CP	CP	CERU	iron transport	transport	1441-8353, 1537-9288
↑↑	↑↑			Citron Rho-interacting kinase	CIT	CIT	CTRO	cytokinesis and nervous system	other metabolism	33-53
↑↑		↑↑	↑↑	Clusterin	CLU	CLU	CLUS	stress response, chaperone	structure	38-335
↑↑		↑↑	↑↑	Complement C1q subcomponent subunit B	C1QB	C1QB	C1QB	immune system	immune system, inflammation	54-54
			↑↑	Complement C1s subcomponent	C1S	C1S	C1S	immune system	immune system, inflammation	40-179
		↑↑	↑↑	Complement C3	C3	C3	CO3	immune system	immune system, inflammation	2103-6223, 1751-6927, 2335-8014
		↑↑		Complement C4	C4	C4	CO4	immune system	immune system, inflammation	1326-3750
	↓↓	↓↓	↓↓	Complement component C6	C6	C6	CO6	immune system	immune system, inflammation	27-76

	↓↓	↓↓		Complement component C9	C9	C9	CO9	immune system	immune system, inflammation	32-211
		↑↑	↑↑	Complement factor B	CFB	CFB	CFAB	immune system	immune system, inflammation	66-662
		↑↑		Fetuin-B	FETUB	FETUB	FETUB	protease inhibitor	protein metabolism	52-258
			↓	Fibronectin	FN1	FN1	FINC	heparin binding	structure	515-5582, 402-5747
		↑↑	↑↑	Gelsolin	GSN	GSN	GELS	calcium binding	structure	847-2303
	↓↓	↓↓	↓↓	Glutathione peroxidase 3	GPX3	GPX3	GPX3	cell protection	detoxification	36-91
			↑↑	Haptoglobin	HP	HP	HPT	heme iron recycling	detoxification	45-646, 114-776
↓	↑↑	↑↓	↓	Hemoglobin subunit alpha	HBA1	HBA1	HBA	oxygen transport	transport	113-3254, 298-3321, 325-1261, 223-1301,332-1193, 72-4314
↓			↓↓	Hemoglobin subunit beta	HBB	HBB	HBB	oxygen transport	transport	265-3283
		↑	↑	Hemopexin	HPX	HPX	HEMO	oxygen transport	transport	584-2936, 366-2722
		↑↑	↑↑	Ig gamma-2A chain C region secreted form	GCAB	na	AGCAB	antigen binding	immune system, inflammation	485-1849
↓↓	↓↓			Ig heavy chain V region 441	HVM36	na	HVM36	antigen binding	immune system, inflammation	82-682
↓↓	↓↓		↓↓	Ig kappa chain V19-17	IGK19-17	IGK19-17	KV5A1	antigen binding	immune system, inflammation	74-124
↑↑		↑↑	↑↑	Ig kappa chain V-I region S107A	IGKS170AKV1A1	IGKV-33	KV1A1	antigen binding	immune system, inflammation	36-127
↑			↑	Ig kappa chain V-V regions	IGKVKV5AG	na	KV5AG	antigen binding	immune system, inflammation	30-60, 33-111
	↓↓			Inter-alpha-trypsin inhibitor, heavy chain 4	ITIH4	ITIH4	ITIH4	acute phase response	immune system, inflammation	51-227
		↓	↓	Inter-alpha-trypsin inhibitor heavy chain H1	ITIH1	ITIH1	ITIH1	acute phase response	immune system, inflammation	227-917, 134-657
		↑↑	↑↑	Inter-alpha-trypsin inhibitor heavy chain H2	ITIH2	ITIH2	ITIH2	acute phase response	immune system, inflammation	582-3410, 1182-2855
		↑	↑	Inter-alpha-trypsin inhibitor heavy chain H3	ITIH3	ITIH3	ITIH3	acute phase response	immune system, inflammation	150-1100, 171-850, 170-1026
	↓			Keratin, type I cytoskeletal 10	KRT10	KRT10	K1C10	cytoskeleton protein binding	structure	71-1655, 57-783
	↓↓	↓↓		Keratin, type I cytoskeletal 15	KRT15	KRT15	K1C15	cytoskeleton protein binding	structure	89-256
			↑↑	Keratin, type II cytoskeletal 1	KRT1	KRT1	K2C1	cytoskeleton protein binding	structure	62-3834
			↑↑	Keratin, type II cytoskeletal 2 oral	KRT76	K22O	KRT76	cytoskeleton protein binding	structure	136-502
		↑	↑	Keratin, type II cytoskeletal 6A	KRT6A	KRT6A	K2C6A	cytoskeleton protein binding	structure	421-2251, 256-893
			↑↑	Keratin, type II cytoskeletal 79	KRT79	KRT79	K2C79	cytoskeleton protein binding	structure	234-1524
	↓↓	↓↓	↑↑	Keratin, type II cytoskeletal 8	KRT8	KRT8	K2C8	cytoskeleton protein binding	structure	67-945

↑↑				Lumican	LUM	LUM	LUM	collagen binding	structure	80-80
↑	↑	↑	↑	Murinoglobulin-2	MUG2	MUG2	MUG2	protease inhibitor	protein metabolism	471-1709, 1505-4710
		↑↑	↑↑	Pecanex-like protein 2	PCNX2	PCNX2	PCX	tumorigenesis	transport	31-61
↓↓	↓↓	↓↓	↓↓	Peroxiredoxin-2	PRDX2	PRDX2	PRDX2	antioxidant response	detoxification	65-73
	↓↓			Phosphatidylinositol-glycan-specific phospholipase D	GPLD1	GPLD1	PHLD	cell migration	protein metabolism	104-504
	↑↓	↑↓	↑↓	Plasma protease C1 inhibitor	SERPING1	SERPING1	IC1	aging	protein metabolism	209-1020, 282-634
		↑		Plasminogen	PLG	PLG	PLMN	blood coagulation	blood coagulation	259-2401, 278-2285
		↑↑		Protein AMBP	AMBP	AMBP	AMBP	cell adhesion	protein metabolism	1353-4311
↓↓	↓↓	↓↓	↓↓	Protein VPRBP	VPRBP	DCAF1	DCAF1	protein ubiquitination	protein metabolism	75-105
↑	↓			Protein Z-dependent protease inhibitor	SERPINA10	SERPINA10	ZPI	blood coagulation	blood coagulation	54-808, 67-193
↑↓	↑	↑	↑↓	Prothrombin	F2	F2	THRB	acute phase response	blood coagulation	135-820, 46-424
↑↑	↑↑	↑↑	↑↑	Serine protease inhibitor A3N	SERPINA3N	SERPINA3N	SPA3N	protease inhibitor	protein metabolism	324-3672
		↑↑	↑↑	Serotransferrin	TF	TF	TRFE	iron transport	transport	3171-8148, 2415-6337
		↓	↓	Serum albumin	ALB	ALB	ALBU	various metabolism	transport	112184-303439, 19049-40637, 12996-63725, 21692-79508
			↑	Serum paraoxonase/arylesterase 1	PON1	PON1	PON1	hydrolase	detoxification	123-830, 270-1731
		↓↓	↓↓	Terminal uridylyltransferase 7	ZCCHC6	ZCCHC6	TUT7	RNA binding	other metabolism	35-60
			↓↓	Thrombospondin-1	THBS1	THBS1	TSP1	collagen binding	immune system, inflammation	66-351
↓↓	↓↓	↓↓	↓↓	Titin	TTN	TTN	TITIN	actin filament binding	structure	24-36
		↑↑	↑↑	Transthyretin	TTR	TTR	TTHY	retinol binding	transport	95-515
		↓		Vitamin D-binding protein	GC	GC	VTDB	vitamin D metabolims	lipid metabolism	436-1014, 219-555

26 ↑↑ up-regulated compared to control (vehicle); all isoforms significantly up-regulated

27 ↑ partly up-regulated compared to control (vehicle), some isoforms significantly up-regulated

28 ↓↓ down-regulated compared to control (vehicle); all isoforms significantly down-regulated

29 ↓ partly down-regulated compared to control (vehicle), some isoforms significantly down-regulated

30 ↑↓ up- and down-regulated compared to control (vehicle)

31 \*according to UniProt ([www.uniprot.org](http://www.uniprot.org))

32 \*\*range given for protein determination in the different plasma samples of individual animals, comma-separators indicate ranges for different isoforms

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