



Supplementary Table S1. Profile of upregulated genes (< 2.0 and ≥ 1.5-fold change) in pancreatic tumors of mice treated with fucoxanthin (Fx).¹

Gene symbol	Description	Fold change ²	p-value ³
<i>Mlph</i>	Melanophilin	1.99	0.0014
<i>Apln</i>	Apelin	1.98	0.0298
<i>Trim30c</i>	Tripartite motif-containing 30C	1.97	0.0073
<i>Trem1</i>	Triggering receptor expressed on myeloid cells 1	1.94	0.0116
<i>Elf3</i>	E74-like factor 3	1.84	0.0011
<i>Fancg</i>	Fanconi anemia, complementation group G	1.80	0.0023
<i>Fam3b</i>	Family with sequence similarity 3, member B	1.79	0.0333
<i>Gpr84</i>	G protein-coupled receptor 84	1.78	0.043
<i>Cd55b</i>	CD55 molecule, decay accelerating factor for complement B	1.77	0.0023
<i>Arl14epl</i>	ADP-ribosylation factor-like 14 effector protein-like	1.77	0.0145
<i>Dmd</i>	Dystrophin, muscular dystrophy	1.76	0.0328
<i>Tnfrsf21</i>	Tumor necrosis factor receptor superfamily, member 21	1.76	0.0066
<i>Hydin</i>	HYDIN, axonemal central pair apparatus protein	1.76	0.0119
<i>Rorc</i>	RAR-related orphan receptor gamma	1.74	0.0418
<i>Il24</i>	Interleukin 24	1.73	0.007
<i>Per1</i>	Period circadian clock 1	1.73	0.001
<i>Trim13</i>	Tripartite motif-containing 13	1.70	0.0188
<i>Tcaim</i>	T cell activation inhibitor, mitochondrial	1.70	0.027
<i>Olfr6</i>	Olfactory receptor 6	1.69	0.0339
<i>Olfr1277</i>	Olfactory receptor 1277	1.69	0.0381
<i>Leng9</i>	Leukocyte receptor cluster (LRC) member 9	1.68	0.0155
<i>Adam8</i>	A disintegrin and metallopeptidase domain 8	1.68	0.0367
<i>Slc35f1</i>	Solute carrier family 35, member F1	1.68	0.0054
<i>F10</i>	Coagulation factor X	1.66	0.0069
<i>Defb8</i>	Defensin beta 8	1.66	0.0099
<i>Fzd5</i>	Frizzled homolog 5 (Drosophila)	1.66	0.0046
<i>Nlrp10</i>	NLR family, pyrin domain containing 10	1.65	0.0148
<i>Hspa1b; Hspa1a</i>	Heat shock protein 1B; heat shock protein 1A	1.65	0.0234
<i>Cwh43</i>	Cell wall biogenesis 43 C-terminal homolog (S. cerevisiae)	1.64	0.0226
<i>Cxcl5</i>	Chemokine (C-X-C motif) ligand 5	1.64	0.0397
<i>Olfr640</i>	Olfactory receptor 640	1.63	0.0041
<i>Crisp3</i>	Cysteine-rich secretory protein 3	1.63	0.0007
<i>BC100530; Stfa3</i>	cDNA sequence BC100530; stefin A3	1.63	0.0203
<i>Kctd1</i>	Potassium channel tetramerisation domain containing 1	1.63	0.0076
<i>Osm</i>	Oncostatin M	1.62	0.0225
<i>Car2</i>	Carbonic anhydrase 2	1.62	0.004
<i>Ms4a13</i>	Membrane-spanning 4-domains, subfamily A, member 13	1.61	0.0114
<i>Hsph1</i>	Heat shock 105kDa/110kDa protein 1	1.61	0.0254
<i>Igsf9b</i>	Immunoglobulin superfamily, member 9B	1.60	0.0176

<i>Gnrh1</i>	Gonadotropin releasing hormone 1	1.59	0.0081
<i>Aqp7</i>	Aquaporin 7	1.59	0.0114
<i>Spink8</i>	Serine peptidase inhibitor, Kazal type 8	1.58	0.0339
<i>Bhlhe40</i>	Basic helix-loop-helix family, member e40	1.57	0.0248
<i>Bche</i>	Butyrylcholinesterase	1.57	0.0308
<i>Prrg3</i>	Proline rich Gla (G-carboxyglutamic acid) 3 (transmembrane)	1.55	0.005
<i>Banp</i>	BTG3 associated nuclear protein	1.54	0.0383
<i>Cdhr2</i>	Cadherin-related family member 2	1.54	0.0074
<i>Ppp2r4</i>	Protein phosphatase 2A activator, regulatory subunit B	1.54	0.0031
<i>Slc29a2</i>	Solute carrier family 29 (nucleoside transporters), member 2	1.54	0.0046
<i>Tcirg1</i>	T cell, immune regulator 1, ATPase, H ⁺ transporting, lysosomal V0 protein A3	1.54	0.0248
<i>4933417A18Rik</i>	RIKEN cDNA 4933417A18 gene	1.54	0.0478
<i>Zbtb40</i>	Zinc finger and BTB domain containing 40	1.53	0.0154
<i>Zfp945</i>	Zinc finger protein 945	1.53	0.0012
<i>Serpinh5</i>	Serine (or cysteine) peptidase inhibitor, clade B, member 5	1.52	0.0424
<i>Hspa1a</i>	Heat shock protein 1A	1.52	0.0226
<i>Sord</i>	Sorbitol dehydrogenase	1.51	0.049
<i>Slc4a2</i>	Solute carrier family 4 (anion exchanger), member 2	1.51	0.0435
<i>Vmn1r100</i>	Vomerolateral 1 receptor 100	1.51	0.0063
<i>Vmn1r148</i>	Vomerolateral 1 receptor 148	1.51	0.0063
<i>4930549C01Rik</i>	RIKEN cDNA 4930549C01 gene	1.51	0.0157
<i>Olfr191</i>	Olfactory receptor 191	1.50	0.004

¹ Among 86 upregulated genes, 61 upregulated genes with < 2.0 and ≥ 1.5-fold change were showed. ² Fold change in gene expression in pancreatic tumors of mice with Fx administration (group 1) compared to that of control mice (group 2). ³ Significant difference between groups 1 and 2 by an exact test on edge R.

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Supplementary Table S2. Profile of downregulated genes (> -2.0 and < -1.5-fold change) in pancreatic tumors of mice treated with fucoxanthin (Fx).¹9
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Gene symbol	Description	Fold change ²	p-value ³
Trpv6	transient receptor potential cation channel, subfamily V, member 6	-1.98	0.0003
Gpr183	G protein-coupled receptor 183	-1.95	0.0046
Itih5	inter-alpha (globulin) inhibitor H5	-1.94	0.0427
Dock10	dedicator of cytokinesis 10	-1.94	0.0207
Ces2b	carboxyesterase 2B	-1.91	0.0383
Zc3h12d	zinc finger CCCH type containing 12D	-1.86	0.044
Fam205a2; Gm10600	family with sequence similarity 205, member A2; predicted gene 10600	-1.83	0.0098
Slc7a14	solute carrier family 7 (cationic amino acid transporter, y+ system), member 14	-1.82	0.0147
Syt15	synaptotagmin-like 5	-1.77	0.0053
Stra6l	STRA6-like	-1.76	0.0096
Gimap9	GTPase, IMAP family member 9	-1.73	0.0152
Il22ra1	interleukin 22 receptor, alpha 1	-1.71	0.0419
Ackr4	atypical chemokine receptor 4	-1.69	0.0106
Nov	nephroblastoma overexpressed gene	-1.68	0.0371
Fetub	fetuin beta	-1.68	0.005
Gnao1	guanine nucleotide binding protein, alpha O	-1.67	0.0061
Kcnh5	potassium voltage-gated channel, subfamily H (eag-related), member 5	-1.67	0.0424
Vnn3	vanin 3	-1.66	0.0036
St6galnac2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylglactosaminide alpha-2,6-sialyltransferase 2	-1.66	0.0006
Aldh1a7	aldehyde dehydrogenase family 1, subfamily A7	-1.66	0.0136
Far2	fatty acyl CoA reductase 2	-1.66	0.0426
Trmt11	tRNA methyltransferase 11	-1.65	0.0433
Mmp16	matrix metalloproteinase 16	-1.65	0.0055
Gulo	gulonolactone (L-) oxidase	-1.64	0.028
Fmo1	flavin containing monooxygenase 1	-1.63	0.0065
Pkib	protein kinase inhibitor beta, cAMP dependent, testis specific	-1.63	0.0081
Klk9	kallikrein related-peptidase 9	-1.63	0.0035
Cd79a	CD79A antigen (immunoglobulin-associated alpha)	-1.62	0.0231
Olfir1058	olfactory receptor 1058	-1.62	0.0129
Slc7a11	solute carrier family 7 (cationic amino acid transporter, y+ system), member 11	-1.62	0.0307
Ppp4r4	protein phosphatase 4, regulatory subunit 4	-1.61	0.0448
Vmn2r44	vomeroneural 2, receptor 44	-1.61	0.0389
Uts2	urotensin 2	-1.60	0.0252
Cygb	cytoglobin	-1.58	0.026

Sptbn2	spectrin beta, non-erythrocytic 2	-1.58	0.0212
Slc4a8	solute carrier family 4 (anion exchanger), member 8	-1.57	0.0097
Slc35c2	solute carrier family 35, member C2	-1.57	0.0126
Olfr610	olfactory receptor 610	-1.56	0.0178
Crb1	crumbs family member 1, photoreceptor morphogenesis associated	-1.56	0.0013
Gng11	guanine nucleotide binding protein (G protein), gamma 11	-1.56	0.0212
Sema6a	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	-1.55	0.0262
Cyp3a59	cytochrome P450, family 3, subfamily a, polypeptide 59	-1.55	0.0107
Enkur	enkurin, TRPC channel interacting protein	-1.54	0.0421
Hdgfrp3	hepatoma-derived growth factor, related protein 3	-1.54	0.0032
Siglecg	sialic acid binding Ig-like lectin G	-1.53	0.0307
Fam161a	family with sequence similarity 161, member A	-1.52	0.0042
Plk2	polo-like kinase 2	-1.52	0.0394
Olfr44	olfactory receptor 44	-1.51	0.0304
Olfr1247	olfactory receptor 1247	-1.51	0.0023
Abca8a	ATP-binding cassette, sub-family A (ABC1), member 8a	-1.50	0.0307
Setd4	SET domain containing 4	-1.50	0.0348
5031410I06Rik	RIKEN cDNA 5031410I06 gene	-1.50	0.0192

¹ Among all 88 downregulated genes significantly altered, 52 downregulated genes with > -2.0 and < -1.5-fold change were showed. ² Fold change in gene expression in pancreatic tumors of mice with Fx administration (group 1) compared to that of control mice (group 2). ³ Significant difference between groups 1 and 2 by an exact test on edge R.

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