Supplementary Table 1. Inversely regulated (differentially expressed) genes at the initiation and progression stages: Fish vs olive oil comparison. Fold change (relative expression) at 12 h and 10 wk represents fish oil divided by olive oil expression level. All genes have a p-value less than 0.05, indicating that genes were differentially expressed by diet. Only Entrez annotated genes are shown.

Gene symbol	fold change (12 h)	fold change (10 wk)	Description
Tnc	0.4	1.4	Tenascin C
Sec24a	0.7	1.2	SEC24 family, member A (S. cerevisiae)
Lpgat1	0.7	1.2	Similar to lysophosphatidylglycerol acyltransferase 1
Gja1	0.7	1.4	Gap junction protein, alpha 1
Efnb3	1.3	0.8	Ephrin B3
Arhgef19	0.7	1.8	Rho guanine nucleotide exchange factor (GEF) 19
Ube2g2	0.9	1.1	Ubiquitin-conjugating enzyme E2G 2
Gpx7	0.7	1.6	Glutathione peroxidase 7
Upf3b	0.7	1.4	UPF3 regulator of nonsense transcripts homolog B (yeast)
Hnrnpa1	0.5	1.4	Heterogeneous nuclear ribonucleoprotein A1
Fktn	0.7	1.2	Fukutin
Klhdc8a	0.6	1.7	Kelch domain containing 8A
Klc2	0.6	1.3	Kinesin light chain 2
Abca1	0.7	1.4	ATP-binding cassette, sub-family A (ABC1), member 1
Rtf1	0.7	1.3	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)
Pitpnm1	0.8	1.2	Phosphatidylinositol transfer protein, membrane-associated 1
Ccdc22	0.8	1.5	Coiled-coil domain containing 22
Dis3l2	1.2	0.8	DIS3 mitotic control homolog (S. cerevisiae)-like 2
Morc3	0.7	1.3	Microrchidia 3
Polr3a	0.7	1.2	Polymerase (RNA) III (DNA directed) polypeptide A, 155kDa
Doc2g	0.5	1.7	Double C2, gamma
Aldh18a1	0.6	1.3	Pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase)
Bnip2	0.7	1.5	BCL2/adenovirus E1B interacting protein 2
Prkci	0.7	1.2	Protein kinase C, iota
Aurkc	0.6	1.4	Aurora kinase C
Sppl2b	0.9	1.2	Signal peptide peptidase-like 2B
Sgsm2	0.7	1.4	Small G protein signaling modulator 2
Pias2	0.8	1.3	Protein inhibitor of activated STAT, 2
Rnf14	0.6	1.4	Ring finger protein 14
Ewsr1	0.7	1.3	Ewing sarcoma breakpoint region 1
Adra2a	0.7	1.4	Adrenergic, alpha-2A-, receptor

Mmp11	0.7	1.3	Matrix metallopeptidase 11
Cpt1b	0.5	2.0	Carnitine palmitoyltransferase 1b, muscle
Alox5ap	0.7	1.2	Arachidonate 5-lipoxygenase activating protein
Pla2g2c	0.7	1.4	Phospholipase A2, group IIC
Zfp386	0.6	1.4	Zinc finger protein 386 (Kruppel-like)
Sfrs12	0.6	1.3	Splicing factor, arginine/serine-rich 12
Adam15	0.8	1.7	A disintegrin and metallopeptidase domain 15 (metargidin)
Shank3	1.2	0.8	SH3 and multiple ankyrin repeat domains 3
Tcf4	1.3	0.5	Transcription factor 4
Fxc1	0.7	1.3	Fractured callus expressed transcript 1
socs3	0.7	1.3	Suppressor of cytokine signaling 3
nelf	0.7	1.6	Nasal embryonic LHRH factor
Pank4	0.9	1.2	Pantothenate kinase 4
Mxd3	0.7	1.4	Max dimerization protein 3

Represents the complete list of inversely regulated differentially expressed genes (annotated genes plus other GenBank accession ID numbers).

Fish vs olive oil comparison. Fold change (relative expression) at 12 h and 10 wk represents fish oil divided by olive oil expression level. All genes have a p-value less than 0.05, indicating that genes were differentially expressed by diet.

(*Represents an Entrez annotated gene).

Gene identifier	Fold change (12 h)	Fold change (10 wk)	Description
AA801116	0.605386	1.372712976	EST190613 Rattus norvegicus cDNA, 5 end
AA849738	0.733118	1.307226378	EST192505 Normalized rat muscle, Bento Soares Rattus sp. cDNA clone RMUAI31 3 end, mRNA sequence.
AA892824	0.447732	1.421612232	Tenascin C*
AA894084	0.794113	1.191405893	Transcribed locus
AA963874	0.613438	1.518926436	Similar to RIKEN cDNA 2700081O15
AI010342	0.742964	1.440043108	Transcribed locus
AI012573	0.769069	1.562725084	EST207024 Normalized rat placenta, Bento Soares Rattus sp. cDNA clone RPLAZ10 3 end, mRNA sequence.
AI102744	0.712772	1.322451671	Transcribed locus
AI170671	0.69375	1.549158759	Transcribed locus
AI171975	0.738909	1.237994581	SEC24 family, member A (S. cerevisiae)*
AI235950	0.527667	1.436432301	EST232512 Normalized rat

			ovary, Bento Soares Rattus sp. cDNA clone ROVCZ23 3 end, mRNA sequence.
AI406322	0.696364	1.248114248	Similar to lysophosphatidylglycerol acyltransferase 1 *
AI407147	0.908604	1.284850052	Similar to hypothetical protein FLJ13045
AI411352	0.672011	1.376677849	Gap junction protein, alpha 1*
AI412662	1.280684	0.845270497	Ephrin B3*
AI556408	0.721782	1.767323326	Rho guanine nucleotide exchange factor (GEF) 19*
AI599349	0.717325	1.376241831	Transcribed locus, strongly similar to NP_001028289.1 SLIT-ROBO Rho GTPase activating protein 3 isoform b [Homo sapiens]
AI713324	0.874607	1.130363668	Ubiquitin-conjugating enzyme E2G 2*
AW142311	0.749108	1.552232859	Glutathione peroxidase 7*
AW251339	0.874952	1.159338611	Transcribed locus
AW525099	0.664462	1.446207938	UPF3 regulator of nonsense transcripts homolog B (yeast)*
AW532652	1.348466	0.530294981	Transcription factor 4*
AW915082	0.493959	1.372558843	Heterogeneous nuclear ribonucleoprotein A1*
AW915268	0.712479	1.221960796	Fukutin*
AW915437	0.597325	1.745735512	Kelch domain containing 8A*
AW915609	0.717386	1.367953319	Transcribed locus
AW915749	0.646363	1.297826923	Kinesin light chain 2*
AW916344	0.850456	1.089424336	Similar to RIKEN cDNA 2310033P09
AW916925	0.694628	1.351174494	Transcribed locus
AW918387	0.714192	1.364878945	ATP-binding cassette, sub-family A (ABC1), member 1*
AW918816	1.227974	0.832933949	Similar to paired immunoglobin-like type 2 receptor beta
AW920557	0.597873	1.592106671	Transcribed locus, strongly similar to XP_001077488.1 PREDICTED: similar to ankyrin repeat domain 25 [Rattus norvegicus]
BE096995	0.673887	1.330740254	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)*
BE100607	0.777573	1.205236274	Phosphatidylinositol transfer protein, membrane-associated 1*
BE106191	0.756113	1.466657494	Coiled-coil domain containing 22*
BE109616	0.620803	1.252914528	Transcribed locus
BE111729	1.182556	0.849525407	DIS3 mitotic control homolog (S. cerevisiae)-like 2*

BE111888	0.677617	1.281199375	Microrchidia 3*
BE113380	0.716689	1.227665053	Polymerase (RNA) III (DNA directed) polypeptide A, 155kDa*
BE113655	0.47818	1.745718572	Double C2, gamma*
BF281787	0.561814	1.290358549	Pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase)*
BF282292	0.700446	1.517825565	BCL2/adenovirus E1B interacting protein 2*
BF282349	0.736624	1.255131045	Similar to RIKEN cDNA 5830404H04
BF284303	0.655769	1.60139477	EST448894 Rat Gene Index, normalized rat, Rattus norvegicus cDNA Rattus norvegicus cDNA clone RGIEO12 3 sequence, mRNA sequence.
BF284699	0.736779	1.208711552	Protein kinase C, iota*
BF400684	0.827014	1.258132616	Transcribed locus
BF404590	0.652851	1.345592902	Similar to GC-rich sequence DNA-binding factor homolog
BF410389	0.628179	1.39121655	Aurora kinase C*
BF411134	0.877252	1.189972307	Signal peptide peptidase-like 2B*
BF418673	0.743461	1.252880659	Similar to PRO1853 homolog
BF419044	0.706455	1.352377576	Small G protein signaling modulator 2*
BF523622	0.688812	1.434329019	Transcribed locus
BF544602	0.732666	1.339168966	Transcribed locus
BF549878	0.783693	1.254725695	Protein inhibitor of activated STAT, 2*
BF558112	0.623839	1.380686713	Ring finger protein 14*
BF563670	0.744943	1.256384457	Transcribed locus
BG153269	0.705378	1.292188016	Ewing sarcoma breakpoint region 1*
NM_012739	0.739523	1.437114489	Adrenergic, alpha-2A-, receptor*
NM_012980	0.717302	1.324009983	Matrix metallopeptidase 11*
NM_013200	0.476639	1.993146839	Carnitine palmitoyltransferase 1b, muscle*
NM_017260	0.733665	1.229620395	Arachidonate 5-lipoxygenase activating protein*
NM_019202	0.704905	1.39266764	Phospholipase A2, group IIC*
NM_019620	0.560647	1.396392003	Zinc finger protein 386 (Kruppel-like)*
NM_020092	0.563368	1.303205863	Splicing factor, arginine/serine-rich 12*
NM_020308	0.785159	1.703600431	A disintegrin and metallopeptidase domain 15 (metargidin)*
NM_021676	1.184099	0.755029019	SH3 and multiple ankyrin repeat domains 3*

NM_053369	1.297591	0.546649496	Transcription factor 4
NM_053371	0.709766	1.275738821	Fractured callus expressed transcript 1*
NM_053565	0.660999	1.259556641	Suppressor of cytokine signaling 3*
NM_057190	0.747128	1.587699629	Nasal embryonic LHRH factor*
NM_133531	0.875447	1.183066361	Pantothenate kinase 4*
U43563	0.768518	1.414039087	Similar to hypothetical protein FLJ20154
U45986	0.696892	1.411170199	Max dimerization protein 3*

Supplementary Table 2. Inversely regulated genes at the initiation and progression stages: Fish vs corn oil comparison. Fold change (relative expression) at 12 h and 10 wk represents fish oil divided by corn oil expression level. All genes have a p-value less than 0.05, indicating that genes were differentially expressed by diet. Only Entrez annotated genes are shown.

Gene	Fold change (12 h)	Fold change (10 wk)	Description
Gfpt2	1.5	0.6	Glutamine-fructose-6-phosphate transaminase 2
Chd7	0.7	1.9	Chromodomain helicase DNA binding protein 7
Pole3	1.2	0.8	Polymerase (DNA directed), epsilon 3 (p17 subunit)
Nf1	0.8	1.4	Neurofibromin 1
Cpt1b	0.6	1.8	Carnitine palmitoyltransferase 1b, muscle
Slc10a1	0.4	2.6	Solute carrier family 10 (sodium/bile acid cotransporter family), member 1
Kcnh3	1.3	0.7	Potassium voltage-gated channel, subfamily H (eag-related), member 3
Sult1b1	1.3	0.7	Sulfotransferase family, cytosolic, 1B, member 1
Gpr12	1.2	0.8	G-protein coupled receptor 12
Serpina3n	1.6	0.7	Serine (or cysteine) peptidase inhibitor, clade A, member 3N
Slc15a2	1.3	0.8	Solute carrier family 15 (H+/peptide transporter), member 2
Gda	0.6	1.4	Guanine deaminase
Nox1	1.2	0.8	NADPH oxidase 1
Abcc5	1.2	0.7	ATP-binding cassette, sub-family C (CFTR/MRP), member 5
Dnase2a	1.3	0.8	Deoxyribonuclease II alpha

Represents the complete list of inversely regulated differentially expressed genes (annotated genes plus other GenBank accession ID numbers).

Fish vs corn oil comparison. Fold change (relative expression) at 12 h and 10 wk represents fish oil divided by corn oil expression level. All genes have a p-value less than 0.05, indicating that genes were differentially expressed by diet.
(*Represents an Entrez annotated gene).

Gene identifier	Fold change (12 h)	Fold change (10 wk)	Description

AA850319	0.658971	1.242944	Cleavage and polyadenylation specific factor 6
AA850576	0.620998	1.203828	Transcribed locus
AA963874	0.668279	1.280113	Similar to RIKEN cDNA 2700081O15
AI012250	0.527642	1.397689	EST206701 Normalized rat placenta, Bento Soares Rattus sp. cDNA clone RPLAU45 3 end, mRNA sequence.
AI045026	1.50976	0.648048	Glutamine-fructose-6-phosphate transaminase 2*
AI111803	1.301519	0.787702	Transcribed locus
AI178257	0.64883	1.205677	Transcribed locus
AI179372	0.73247	1.750917	Transcribed locus
AI599104	0.663896	1.892686	Chromodomain helicase DNA binding protein 7*
AW142350	1.167202	0.801924	Polymerase (DNA directed), epsilon 3 (p17 subunit)*
AW143273	1.111811	0.818204	Transcribed locus
AW253043	0.764801	1.996296	Hypothetical protein LOC685233
AW532214	0.559165	1.244409	Transcribed locus
AW916860	1.919957	0.548431	Transcribed locus
AW920624	0.603507	1.292021	Transcribed locus
BE103430	1.219238	0.853299	Transcribed locus
BE104322	0.569178	1.631607	Transcribed locus
BE110624	1.277904	0.808098	Transmembrane protein 218
BE113655	0.478169	1.350479	Double C2, gamma
BF290953	0.625117	1.325599	Transcribed locus
NM_012609	0.801702	1.429319	Neurofibromin 1*
NM_013200	0.563929	1.824308	Carnitine palmitoyltransferase 1b, muscle*
NM_017047	0.426692	2.645147	Solute carrier family 10 (sodium/bile acid cotransporter family), member 1*
NM_017108	1.303705	0.747027	Potassium voltage-gated channel, subfamily H (eag-related), member 3*
NM_022513	1.316997	0.679511	Sulfotransferase family, cytosolic, 1B, member 1*
NM_030831	1.246035	0.786807	G-protein coupled receptor 12*
NM_031531	1.596907	0.696108	Serine (or cysteine) peptidase inhibitor, clade A, member 3N*
NM_031531	1.596907	0.696108	Serine (or cysteine) peptidase inhibitor, clade A, member 3N
NM_031672	1.281305	0.834343	Solute carrier family 15 (H+/peptide transporter), member 2*
NM_031776	0.620538	1.442399	Guanine deaminase*
NM_053683	1.215974	0.812313	NADPH oxidase 1*
NM_053924	1.255434	0.680262	ATP-binding cassette, sub-family C (CFTR/MRP), member 5*

NM_138539	1.336824	0.773456	Deoxyribonuclease II alpha*

Supplementary Table 3. Inversely regulated genes at the initiation and progression stages: Olive vs corn oil comparison. Fold change (relative expression) at 12 h and 10 wk represents olive oil divided by corn oil expression level. All genes have a p-value less than 0.05, indicating that genes were differentially expressed by diet. Only Entrez annotated genes are shown.

Gene Symbol	fold change (12 h)	fold change (10 wk)	Description
aqp1	1.7	0.7	aquaporin 1
B3galt4	1.2	0.8	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4
Brca2	1.3	0.8	breast cancer 2
C3	1.3	0.7	complement component 3
C4bpa	1.3	0.7	complement component 4 binding protein, alpha
Cyp1b1	1.3	0.8	cytochrome P450, family 1, subfamily b, polypeptide 1
ddx20	1.1	0.8	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20
Edn1	1.4	0.7	endothelin 1
Fosl1	1.4	0.7	fos-like antigen 1
Foxa2	1.3	0.8	forkhead box A2
gas7	1.4	0.7	growth arrest specific 7
htr2c	1.3	0.7	5-hydroxytryptamine (serotonin) receptor 2C
Ighmbp2	1.2	0.8	immunoglobulin mu binding protein 2
Kcnh3	1.3	0.7	similar to Potassium voltage-gated channel subfamily H member 3
Kcnj6	1.3	0.7	potassium inwardly-rectifying channel, subfamily J, member 6
Kif2c	1.5	0.7	kinesin family member 2C
Lrpap1	1.3	0.7	low density lipoprotein receptor-related protein associated protein 1
Magi2	1.4	0.7	membrane associated guanylate kinase, WW and PDZ domain containing 2
Mkln1	1.2	0.8	muskelin 1, intracellular mediator containing kelch motifs
Mybpc1	1.4	0.8	myosin binding protein C,

			slow type
Nup88	1.1	0.8	nucleoporin 88kDa
Psmd1	1.2	0.7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1
Ptgs1	1.2	0.8	prostaglandin-endoperoxide synthase 1
Sfrs12	1.4	0.7	splicing factor, arginine/serine-rich 12
Slc10a1	0.5	1.5	solute carrier family 10 (sodium/bile acid cotransporter family), member 1
Slc27a1	1.2	0.8	solute carrier family 27 (fatty acid transporter), member 1
Slc37a4	1.4	0.7	solute carrier family 37 (glucose-6-phosphate transporter), member 4
Slc6a7	1.3	0.7	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7
socs3	1.4	0.7	suppressor of cytokine signaling 3
sqlE	1.3	0.7	squalene epoxidase
Sult1b1	1.4	0.6	sulfotransferase family, cytosolic, 1B, member 1
Tnfrsf1a	1.2	0.7	tumor necrosis factor receptor superfamily, member 1a
Tnfrsf1b	1.2	0.7	tumor necrosis factor receptor superfamily, member 1b
Trhr	1.2	0.7	thyrotropin releasing hormone receptor
usf1	1.2	0.7	upstream transcription factor 1

Represents the complete list of inversely regulated differentially expressed genes (annotated genes plus other GenBank accession ID numbers).

Olive vs corn oil comparison. Fold change (relative expression) at 12 h and 10 wk represents olive oil divided by corn oil expression level. All genes have a p-value less than 0.05, indicating that genes were differentially expressed by diet.

(*Represents an Entrez annotated gene).

Gene identifier	Fold change (12 h)	Fold change (10 wk)	Description
AA801116	1.643196	0.740393	EST190613 Rattus norvegicus cDNA, 5 end

AA818018	1.242889	0.795805	Melanocyte proliferating gene 1
AA819481	1.568884	0.639055	Transcribed locus
AA850319	0.598481	1.18838	Cleavage and polyadenylation specific factor 6
AA891790	1.226878	0.756218	CDNA clone IMAGE:7368410
AA900983	1.332997	0.754234	Solute carrier family 17 (anion/sugar transporter), member 5
AF142499	1.230564	0.698577	Tumor necrosis factor receptor superfamily, member 1b*
AF220455	1.109473	0.811358	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20*
AI009946	1.325001	0.768638	Carboxypeptidase M
AI010234	1.499175	0.648638	EH domain binding protein 1
AI170285	1.30156	0.799892	Similar to RIKEN cDNA 0610037L13
AI176734	1.208226	0.756801	Similar to RIKEN cDNA 0610037L13
AI177590	1.201856	0.825655	Component of oligomeric golgi complex 4
AI227843	1.342011	0.791381	Transcribed locus
AI227985	1.174883	0.786918	Rhomboid domain containing 3
AI231716	1.53119	0.662588	Transcribed locus
AI232494	1.113878	0.792809	Coenzyme Q9 homolog (S. cerevisiae)
AI233903	0.353281	1.400709	Similar to RIKEN cDNA 2410146L05
AI235950	1.512678	0.751599	EST232512 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone ROVCZ23 3 end, mRNA sequence.
AI407755	1.19616	0.741369	Mesoderm development candidate 1
AI411222	1.165743	0.815323	Tissue inhibitor of metalloproteinase 4
AI547421	1.253469	0.802468	Dipeptidyl peptidase 9
AI556408	1.398341	0.598355	Rho guanine nucleotide exchange factor (GEF) 19
AJ131902	1.369616	0.670395	Growth arrest specific 7*
AW141259	1.326165	0.759728	Dynein, axonemal, light chain 4
AW141867	1.272456	0.742333	Transcribed locus, strongly similar to NP_032909.2 plexin A3 [Mus musculus]
AW143273	1.104915	0.783984	Transcribed locus
AW143362	1.384833	0.769621	Putative homeodomain transcription factor 1
AW143568	1.100982	0.781078	Vacuolar protein sorting 18 homolog (S. cerevisiae)
AW915437	1.573266	0.682941	Kelch domain containing 8A
AW915749	1.31586	0.704766	Kinesin light chain 2
AW916344	1.364831	0.823593	Similar to RIKEN cDNA 2310033P09
AW916911	1.377017	0.722611	Transcribed locus, strongly similar to NP_056493.3 neurobeachin [Homo sapiens]
AW916925	2.155937	0.694751	Transcribed locus
AW917562	1.216576	0.814602	Transcribed locus
AW920501	1.381473	0.771476	Transcribed locus
AW920557	1.627141	0.607488	Transcribed locus, strongly similar to XP_001077488.1 PREDICTED:

			similar to ankyrin repeat domain 25 [Rattus norvegicus]
BE096995	1.377631	0.710732	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)
BE103430	1.205045	0.794914	Transcribed locus
BE108837	1.389721	0.58472	Centromere protein E
BE109075	1.244244	0.715188	Zinc finger, FYVE domain containing 21
BE113321	1.365684	0.688609	Transcribed locus
BF281787	1.304783	0.657823	Pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase)
BF282349	1.250483	0.76502	Similar to RIKEN cDNA 5830404H04
BF284303	1.546268	0.770892	EST448894 Rat Gene Index, normalized rat, Rattus norvegicus cDNA Rattus norvegicus cDNA clone RGIEO12 3 sequence, mRNA sequence.
BF284803	1.407228	0.656037	Interferon regulatory factor 7
BF393126	1.500294	0.708604	Transcribed locus
BF396218	1.222925	0.736783	Similar to RIKEN cDNA 0610039J04
BF397523	1.251917	0.790097	Family with sequence similarity 32, member A
BF400684	1.204369	0.812748	Transcribed locus
BF400697	1.257016	0.791018	Similar to zinc finger, RAN-binding domain containing 3
BF401710	1.312767	0.713884	T-complex 11 (mouse) like 2
BF414998	1.678112	0.708815	Similar to RIKEN cDNA 2610318G18
BF419044	1.47497	0.666977	Small G protein signaling modulator 2
BF547233	1.484874	0.714484	Transcribed locus
BF548454	1.214463	0.786379	Transcribed locus
BF558112	1.309284	0.725678	Ring finger protein 14
BG671895	1.129634	0.7941	Transcribed locus, strongly similar to NP_057131.1 splicing factor 3B, 14 kDa subunit [Homo sapiens]
NM_012516	1.304904	0.738308	Complement component 4 binding protein, alpha*
NM_012548	1.373679	0.688031	Endothelin 1*
NM_012743	1.277293	0.777989	Forkhead box A2*
NM_012765	1.260934	0.742829	5-hydroxytryptamine (serotonin) receptor 2C*
NM_012778	1.749838	0.68442	Aquaporin 1*
NM_012940	1.262793	0.781185	Cytochrome P450, family 1, subfamily b, polypeptide 1*
NM_012953	1.406039	0.726107	Fos-like antigen 1*
NM_013047	1.182974	0.741419	Thyrotropin releasing hormone receptor*
NM_013091	1.238357	0.718651	Tumor necrosis factor receptor superfamily, member 1a*
NM_013192	1.278628	0.745767	Potassium inwardly-rectifying channel, subfamily J, member 6*

NM_016994	1.323341	0.748975	Complement component 3*
NM_017043	1.25072	0.758844	Prostaglandin-endoperoxide synthase 1*
NM_017047	0.472064	1.52303	Solute carrier family 10 (sodium/bile acid cotransporter family), member 1*
NM_017047	0.472064	1.52303	Solute carrier family 10 (sodium/bile acid cotransporter family), member 1
NM_017108	1.277403	0.696651	Potassium voltage-gated channel, subfamily H (eag-related), member 3*
NM_017136	1.331414	0.677935	Squalene epoxidase*
NM_019376	1.263714	0.632482	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide
NM_020092	1.393965	0.749656	Splicing factor, arginine/serine-rich 12*
NM_022513	1.378612	0.600983	Sulfotransferase family, cytosolic, 1B, member 1*
NM_031359	1.237554	0.842521	Muskelin 1, intracellular mediator containing kelch motifs*
NM_031542	1.280391	0.786489	Breast cancer 2*
NM_031586	1.175927	0.835505	Immunoglobulin mu binding protein 2*
NM_031589	1.403112	0.718249	Solute carrier family 37 (glucose-6-phosphate transporter), member 4*
NM_031777	1.171772	0.680362	Upstream transcription factor 1*
NM_031978	1.179079	0.7332	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 1*
NM_053565	1.411427	0.747492	Suppressor of cytokine signaling 3*
NM_053580	1.178213	0.79833	Solute carrier family 27 (fatty acid transporter), member 1*
NM_053616	1.107625	0.766923	Nucleoporin 88kDa*
NM_053621	1.366427	0.721561	Membrane associated guanylate kinase, WW and PDZ domain containing 2*
NM_053996	1.306778	0.701811	Solute carrier family 6 (neurotransmitter transporter, L-proline), member 7*
NM_133553	1.16782	0.801158	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4*
U44979	1.474103	0.691397	kinesin family member 2C*
U46958	1.253258	0.775536	Rattus norvegicus hyaluronan-binding protein CD44i mRNA, partial cds.
X90475	1.367227	0.753309	Myosin binding protein C, slow type*
Z11994	1.332941	0.708551	Low density lipoprotein receptor-related protein associated protein 1*

Supplementary Table 4. Classification of fish versus olive oil colonic expression values at the initiation stage (12 h). The top 10 single, pair-wise, and triplet-wise gene LDA classifiers are shown. $\varepsilon_{\text{bolstered}}$ denotes bolstered resubstitution error for the respective classifier; the classifiers are ranked according to that error measurement. $\Delta\varepsilon_{\text{bolstered}}$ denotes the decrease in error for each feature set relative to its highest ranked subset of features.

1 feature	2 feature	3 feature	$\varepsilon_{\text{bolstered}}$	$\Delta\varepsilon_{\text{bolstered}}$
Sfrp2			0.0726	
Plcg1			0.1268	
Notch1			0.1298	
Bdkrb2			0.1407	
Tcf4			0.1495	
Tat			0.156	
Efnb1			0.161	
Gsr			0.1633	
Lamr1			0.1692	
Pla2g2c			0.1748	
Sfrp2	Nppa		0.0108	0.0618
Bdkrb2	Pde4d		0.0126	0.1281
Bdkrb2	Ceacam3		0.0166	0.1241
Sfrp2	Tnf		0.0227	0.0499
Bdkrb2	Bmp4		0.0243	0.1164
Bdkrb2	Gja1		0.0303	0.1104
Sfrp2	Men1		0.0305	0.0421
Tcf4	Sfrp2		0.0308	0.0418
Sfrp2	Tat		0.0315	0.0411
Col18a1	Bdkrb2		0.034	0.1067
Sfrp2	Nppa	Ltbp1	0.0032	0.0076
Ncam1	Sfrp2	Nppa	0.0034	0.0193
Sfrp2	Nppa	Pi3ka	0.0039	0.0069
Sfrp2	Nppa	Syp	0.004	0.0068
Sfrp2	Nppa	hoxa1	0.004	0.0068
Sfrp2	Nppa	Skr6r	0.0041	0.0067
Sfrp2	Nppa	Nes	0.0042	0.0066
Sfrp2	Nppa	Sycp3	0.0045	0.0063

Supplementary Table 5. Classification of fish versus corn oil colonic expression values at the initiation stage (12 h). The top 10 single, pair-wise, and triplet-wise gene LDA classifiers are shown. $\varepsilon_{\text{bolstered}}$ denotes bolstered resubstitution error for the respective classifier; the classifiers are ranked according to that error measurement. $\Delta\varepsilon_{\text{bolstered}}$ denotes the decrease in error for each feature set relative to its highest ranked subset of features.

1 feature	2 feature	3 feature	$\varepsilon_{\text{bolstered}}$	$\Delta\varepsilon_{\text{bolstered}}$
Efnb1			0.0002	
Nras			0.1031	
Bmp4			0.1579	
Serpinh2			0.1734	
Tgfb1			0.1747	
Pkcb			0.1866	
Hnf3g			0.1883	
Gja1			0.1884	
Rbbp9			0.2005	
Esr	Efnb1		0	0.0002
Ucp3	Efnb1		0	0.0002
Efnb1	Ltbp1		0	0.0002
Gpx4	Efnb1		0.0001	0.0001
Prkm7	Efnb1		0.0001	0.0001
Kras2	Efnb1		0.0001	0.0001
Bmpr2	Efnb1	Bcl2l2	0	0.0002
Itgb7	Mapk7	Efnb1	0	0.0002
Gpx4	Mapk7	Efnb1	0	0.0001
Gpx4	Bdkrb2	Efnb1	0	0.0001
Gpx4	Ucp3	Efnb1	0	0
Mapk7	Cacnb4	Efnb1	0	0.0001

Supplementary Table 6. Classification of olive versus corn oil colonic expression values at the initiation stage (12 h). The top 10 single, pair-wise, and triplet-wise gene LDA classifiers are shown. $\varepsilon_{\text{bolstered}}$ denotes bolstered resubstitution error for the respective classifier; the classifiers are ranked according to that error measurement. $\Delta\varepsilon_{\text{bolstered}}$ denotes the decrease in error for each feature set relative to its highest ranked subset of features.

1 feature	2 feature	3 feature	$\varepsilon_{\text{bolstered}}$	$\Delta\varepsilon_{\text{bolstered}}$
Lamr1			0.1023	
Ywhag			0.1041	
Id3			0.1109	
Rb1			0.1252	
Nras			0.1381	
Serpinh2			0.1554	
Alcam			0.1619	
Sparc			0.1739	
Colia1			0.1829	
anx5	Serpinh2		0.0465	0.1089
Id1	Lamr1		0.0466	0.0557
Pparg	Lamr1		0.0493	0.053
Prkm7	Ywhag		0.0523	0.0518
Sparc	anx5		0.0575	0.1164
Erbb2	Ywhag		0.0583	0.0458
Mfap4	Ywhag		0.0608	0.0433
Sell	Ywhag		0.0621	0.042
Bmp4	anx5		0.0638	0.1228
Hnf3b	Id1	Lamr1	0.0261	0.0205
Ncam1	anx5	Serpinh2	0.0269	0.0196
Id1	Id3	Lamr1	0.0277	0.0189
Rep3a	anx5	Serpinh2	0.0281	0.0184
Id1	Erbb2	Lamr1	0.0291	0.0175
anx5	Pde4d	Serpinh2	0.0293	0.0172
Gpx4	anx5	Serpinh2	0.0297	0.0168
Id3	Pparg	Lamr1	0.0309	0.0184
Lyz2	Id1	Lamr1	0.0311	0.0155

Supplementary Table 7. Classification of fish versus olive oil colonic expression values at the progression stage (10 wk). The top 10 single, pair-wise, and triplet-wise gene LDA classifiers are shown. $\varepsilon_{\text{bolstered}}$ denotes bolstered resubstitution error for the respective classifier; the classifiers are ranked according to that error measurement. $\Delta \varepsilon_{\text{bolstered}}$ denotes the decrease in error for each feature set relative to its highest ranked subset of features.

1 feature	2 feature	3 feature	$\varepsilon_{\text{bolstered}}$	$\Delta \varepsilon_{\text{bolstered}}$
Bdkrb2			0.1004	
Ca3			0.1618	
Pik3r1			0.1625	
Grem1			0.1686	
Pai2a			0.1736	
Raf1			0.1774	
Tnfrsf1a			0.1919	
Arg2			0.1963	
IL2RB			0.2043	
Plat			0.219	
Bdkrb2	Ceacam3		0.0453	0.0551
elk	Bdkrb2		0.0496	0.0508
Bdkrb2	Il2rb		0.0564	0.044
Bdkrb2	Sell		0.0628	0.0376
Plat	Ca3		0.0642	0.0976
Bdkrb2	hoxa1		0.0648	0.0356
Bdkrb2	Bmp4		0.0672	0.0332
Bdkrb2	Rbbp9		0.0693	0.0311
Bdkrb2	Gja1		0.0727	0.0277
Mapk7	Bdkrb2		0.0735	0.0269
elk	Bdkrb2	Rbbp9	0.0233	0.0263
Bdkrb2	Il2rb	Rbbp9	0.0238	0.0326
Bdkrb2	Ceacam3	Serpinh2	0.0312	0.0141
Bdkrb2	Col2a1	Rbbp9	0.0321	0.0372
Itgb7	Bdkrb2	Ceacam3	0.0321	0.0132
Bdkrb2	Ceacam3	Shh	0.0325	0.0128
Bdkrb2	Ceacam3	Tgfb1	0.0335	0.0118
Bdkrb2	Ceacam3	Pkcb	0.0342	0.0111
elk	Bdkrb2	Shh	0.0351	0.0145
Bdkrb2	hoxa1	Rbbp9	0.0372	0.0321

Supplementary Table 8. Classification of fish versus corn oil colonic expression values at the progression stage (10 wk). The top 10 single, pair-wise, and triplet-wise gene LDA classifiers are shown. $\varepsilon_{bolstered}$ denotes bolstered resubstitution error for the respective classifier; the classifiers are ranked according to that error measurement. $\Delta \varepsilon_{bolstered}$ denotes the decrease in error for each feature set relative to its highest ranked subset of features.

1 feature	2 feature	3 feature	$\varepsilon_{bolstered}$	$\Delta \varepsilon_{bolstered}$
Hoxa1			0.0463	
Bmp4			0.0547	
Grem1			0.0666	
Serpinh2			0.1071	
Tgfb1			0.1137	
Ca3			0.1362	
Tgfbr3			0.1459	
elk			0.1478	
Apt1lg1			0.152	
Pkcb			0.1527	
Hoxa1	Grem1		0.0192	0.0271
Bmp4	Pla2g2c		0.0203	0.0344
Bdkrb2	Bmp4		0.0225	0.0322
Bdkrb2	Grem1		0.0247	0.0419
Bmp4	Hoxa1		0.0288	0.0175
Gpx4	Hoxa1		0.0326	0.0137
Fgfr2	Hoxa1		0.0332	0.0131
Pla2g2c	Grem1		0.0347	0.0319
Foxa1	Bmp4	Pla2g2c	0.0085	0.0118
Cacnb4	Bdkrb2	Bmp4	0.0119	0.0106
Bmp4	Pla2g2c	LTBP1	0.0152	0.0051
Esr	BMP4	Pla2g2c	0.0158	0.0045
Gpx4	Bdkrb2	Bmp4	0.0161	0.0064
Bdkrb2	Ucp	Bmp4	0.0174	0.0051
Bdkrb2	Bmp4	Sycp3	0.0174	0.0051
Gpx4	Hoxa1	Tgfb1	0.0185	0.0141

Supplementary Table 9. Classification of olive versus corn oil colonic expression values at the progression stage (10 wk). The top 10 single, pair-wise, and triplet-wise gene LDA classifiers are shown. $\varepsilon_{\text{bolstered}}$ denotes bolstered resubstitution error for the respective classifier; the classifiers are ranked according to that error measurement. $\Delta\varepsilon_{\text{bolstered}}$ denotes the decrease in error for each feature set relative to its highest ranked subset of features.

1 feature	2 feature	3 feature	$\varepsilon_{\text{bolstered}}$	$\Delta\varepsilon_{\text{bolstered}}$
Bmp4			0.0515	
Serpinh2			0.0738	
Pkcb			0.1128	
Sparc			0.1212	
Rac1			0.134	
elk			0.1429	
Cchla2			0.1739	
Gja1			0.1797	
Tgfb1			0.1841	
Pdir			0.1885	
Bmp4	Col2a1		0.0245	0.027
Pkcb	Bmp4		0.0249	0.0266
NGFR	Bmp4		0.0254	0.0261
elk	Bmp4		0.0283	0.0232
Bmp4	Pla2g2c		0.0288	0.0227
Pkcb	Serpinh2		0.0312	0.0426
Bmp4	Serpinh2		0.0327	0.0188
Bmp4	Cchla2		0.0372	0.0143
Esr	Bmp4		0.0389	0.0126
Egf	Serpinh2		0.0389	0.0126
elk	Bmp4	Ptger1	0.0141	0.0142
Sparc	Egf	Serpinh2	0.0164	0.0225
Bmp4	Col2a1	Nes	0.0169	0.0076
Pkcb	Bmp4	Serpinh2	0.0172	0.0077
Pkcb	Bmp4	Shh	0.0213	0.0036
Bmp4	Cchla2	Serpinh2	0.0238	0.0089
Ngfr	Bmp4	Hpta	0.027	
Gpx4	Bmp4	Serpinh2	0.0279	0.0048