Table SI. Comparison of metabolite changes (Δ) between baseline (fraction 0) and end of radiotherapy (fraction 38) between AE(+) and AE(-) groups, with and without exclusion of the UDCA-treated patient (patient 7).

	AE(+) (n=7) versus AE(-) (n=4)			**AE(+) (n=6) versus AE(-) (n=4) (excluding the UDCA-treated patient)**		
Metabolite	**AE(+) Δ [median (range); μM]**	**AE(-) Δ [median (range); μM]**	**P-value**	**AE(+) Δ [median (range); μM]**	**AE(-) Δ [median (range); μM]**	**P-value**
CE (20:4)	0.001 (-0.030 to 0.073)	-0.0230 (-0.0610 to 0.0250)	0.2303	0.0075 (-0.0300 to 0.0730)	-0.0230 (-0.0610 to 0.0250)	0.2571
TDCA	0.001 (-0.030 to 0.073)	-0.0055 (-0.006 to -0.0010)	0.5714	0.0030 (-0.0080 to 0.0110)	-0.0055 (-0.0060 to -0.0010)	0.3697
TG (18:0_32:2)	0.001 (-0.007 to 0.004)	-0.0025 (-0.0180 to 0.0130)	0.8285	0.0010 (-0.0070 to 0.0040)	-0.0025 (-0.0180 to 0.0130)	0.7545
TG (18:3_34:1)	0.0001 (-0.008 to 0.007)	0.0035 (0.000 to 0.0160)	0.3809	0.0010 (-0.0020 to 0.0070)	0.0035 (0.0000 to 0.0160)	0.2485
PC aa C42:2	-0.001 (-0.021 to 0.010)	0.0105 (0.0040 to 0.0130)	0.0666	-0.0015 (-0.0210 to 0.0100)	0.0105 (0.0040 to 0.0130)	0.0667
TG (16:0_38:1)	-0.015 (-0.0300 to 0.0100)	0.0185 (0.0100 to 0.0250)	0.0190	-0.0055 (-0.0300 to 0.0100)	0.0185 (0.0100 to 0.0250)	0.0121
PC ae C42:1	-0.004 (-0.016 to 0.007)	-0.012 (-0.104 to 0.037)	0.4476	-0.0040 (-0.0160 to 0.0070)	0.0025 (-0.0130 to 0.0040)	0.4363
FA (20:2)	-0.012 (-0.104 to 0.037)	0.019 (-0.010 to 0.096)	0.1142	-0.0180 (-0.0100 to 0.0960)	0.0190 (-0.0100 to 0.0960)	0.1636
DG (18:1_18:1)	-0.013 (-0.027 to 0.009)	0.0245 (-0.017 to 0.038)	0.0066	-0.0185 (-0.0270 to 0.0090)	0.0245 (-0.0170 to 0.0380)	0.0727

Changes in metabolite levels (Δ) were calculated for each patient as the difference between metabolite levels at the end of radiotherapy (fraction 38) and baseline (fraction 0). These Δ values were compared between the AE(+) and AE(-) groups using the Mann-Whitney U test. Only nominal P-values are shown. Sensitivity analysis was performed by excluding the UDCA-treated patient (patient no. 7). AE, adverse event; DG, diglyceride; FA, fatty acid; PC, phosphatidylcholine; TDCA, taurodeoxycholic acid; TG, triglyceride; UDCA, ursodeoxycholic acid.

Table SII. Correlation-based sensitivity analysis of patient-level Spearman's rank correlation coefficients (ρ) with and without exclusion of the UDCA-treated patient (patient 7).

	AE(+) (n=7) versus AE(-) (n=4)		**AE(+) (n=6) versus AE(-) (n=4) (excluding the UDCA-treated patient)**	
Metabolite	**P-value**	**Q-value**	**P-value**	**Q-value**
CE (20:4)	0.07	0.81	0.07	0.79
TDCA	0.01	0.49	0.01	0.64
TG (18:0_32:2)	0.02	0.65	0.02	0.74
TG (18:3_34:1)	0.01	0.49	0.01	0.64
PC aa C42:2	0.01	0.49	0.01	0.64
TG (16:0_38:1)	0.01	0.49	0.01	0.64
PC ae C42:1	0.01	0.51	0.02	0.64
FA (20:2)	0.05	0.81	0.04	0.80
DG (18:1_18:1)	0.23	0.93	0.26	0.95

Correlation-based comparisons were performed using patient-level Spearman's rank correlation coefficients (ρ). Group differences in ρ were assessed using the Mann-Whitney U test. P-values were adjusted for multiple testing using the Benjamini-Hochberg false discovery rate procedure. Sensitivity analysis was performed by excluding the UDCA-treated patient (patient no. 7). AE, adverse event; DG, diglyceride; FA, fatty acid; PC, phosphatidylcholine; TDCA, taurodeoxycholic acid; TG, triglyceride; UDCA, ursodeoxycholic acid.

Table SIII. Enzymes and genes associated with the phosphatidylcholine-fatty acid interaction network identified by OmicsNet analysis.

A. Triglyceride-associated enzymes and genes

Gene/enzyme	Name	KEGG KO
LIPF	Gastric triacylglycerol lipase	K14452
PNLIPRP1	Pancreatic lipase-related protein 1	K14074
PNLIPRP2	Pancreatic lipase-related protein 2	K14075
PNLIPRP3	Pancreatic lipase-related protein 3	K14076
PNLIP	Pancreatic triacylglycerol lipase	K14073
AADAC	Arylacetamide deacetylase	K13616
PNPLA2	Patatin-like phospholipase domain-containing protein 2	K16816
PNPLA3	Patatin-like phospholipase domain-containing protein 3	K13534
DGAT1	Diacylglycerol O-acyltransferase 1	K11155
DGAT2	Diacylglycerol O-acyltransferase 2	K11156
LIPE	Hormone-sensitive lipase	K07188
LPL	Lipoprotein lipase	K01059
LIPG	Endothelial lipase	K22284
LIPC	Hepatic triacylglycerol lipase	K22283
MOGAT3	2-acylglycerol O-acyltransferase 3	K14456

B. Cholesterol ester-associated enzymes and genes

Gene/enzyme	Name	KEGG ID
SOAT1	Sterol O-acyltransferase 1	K00637
SOAT2	Sterol O-acyltransferase 2	K00637

LIPA	Lysosomal acid lipase/cholesteryl ester hydrolase	K01052

C. Triacylglycerol-cholesteryl ester interaction enzymes and genes

Gene/enzyme	**Name**	**KEGG ID**
CEL	Bile salt-activated lipase	K12298

CE, cholesteryl ester; KEGG, Kyoto Encyclopedia of Genes and Genomes; KO, KEGG Orthology.

Table SIV. Enzymes and genes associated with the fatty acid-diglyceride/triglyceride interaction network identified by OmicsNet analysis.

Gene/enzyme	**Name**	**KEGG KO**
PLA2G2E	Phospholipase A2 group IIE	K01047
PLA2G16	HRAS-like suppressor 3	K16817
PLB1	Phospholipase B1	K14621
PLA2G4B	Cytosolic phospholipase A2 β	K16342
PLA2G4D	Cytosolic phospholipase A3 δ	K16342
PLA2G2F	Phospholipase A2 group IIF	K01047
PLA2G6	85/88 kDa calcium-independent phospholipase A2	K16343
PLA2G3	Phospholipase A2 group3	K01047
CLC	Eosinophil lysophospholipase	K13334
PNPLA7	Patatin-like phospholipase domain-containing protein 7	K14676
PLA2G12A	Phospholipase A2 group XIIA	K01047
PLAAT2	Phospholipase A and acyltransferase 2	K16817
LYPLA1	Acyl-protein thioesterase 1	K06128
PLA2G4A	Cytosolic phospholipase A2	K16342
LYPLA2	Acyl-protein thioesterase 2	K06130
PLA2G10	Phospholipase A2 group 10	K01047
ASPG	60 kDa lysophospholipase	K13278
PLA2G4C	Cytosolic phospholipase A2 γ	K16342
PLA2G4F	Cytosolic phospholipase A2 ζ	K16342
PLA2G2C	Phospholipase A2 putative inactive group IIC	K01047
PLA2G15	Phospholipase A2 group XV	K06129
PNPLA6	Neuropathy target esterase	K14676

PLA2G2A	Phospholipase A2	K01047
(JMJD7-)PLA2G4B	Cytosolic phospholipase A2 β	K16342
PLA2G2D	Phospholipase A2 group IID	K01047
PLA2G1B	Phospholipase A2	K01047
PLA2G5	Phospholipase A2 group V	K01047
PLA2G12B	Phospholipase A2-like protein group XIIB	K01047

Multiple genes may share the same KEGG KO identifier because KO represents a functional orthology group. FA, fatty acid; KEGG, Kyoto Encyclopedia of Genes and Genomes; KO, KEGG Orthology; PC, phosphatidylcholine.

Table SV. Enzymes associated with the hypothesized triglyceride-fatty acid lipolysis pathway identified in the network analysis.

Gene/enzyme	**Name**	**KEGG KO**
LIPH	Lipase member H	K19404
PNPLA2	Patatin-like phospholipase domain-containing protein 2	K16816
PNLIPRP3	Pancreatic lipase-related protein 3	K14076
LIPG	Endothelial lipase	K22284
AADAC	Arylacetamide deacetylase	K13616
CEL	Bile salt-activated lipase	K12298
LIPC	Hepatic triacylglyserol lipase	K22283
PNLIPRP2	Pancreatic lipase-related protein 2	K14075
PNPLA3	Patatin-like phospholipase domain-containing protein 3	K13534
PNLIP	Pancreatic triacylglycerol lipase	K14073
PNLIPRP1	Inactive pancreatic lipase-related protein 1	K14074

KEGG, Kyoto Encyclopedia of Genes and Genomes; KO, KEGG Orthology.