Supplementary Materials

Detection of Metabolic Changes Induced via Drug Treatments in Live Cancer Cells and Tissue Using Raman Imaging Microscopy

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Table S1. Metabolites and pathway altered for HT1080 cells treated with FK866 from LC/MS.

Compound ID	FC	log2(FC)	raw.pval	FDR.pval	pathway
Isovaleric acid amine	0.70	-0.51	0.0010	0.290	Lysine metabolism
Diacylglycerol -DG 56-9	0.79	-0.33	0.0017	0.290	Glycerolipid metabolism
N-acetyldopamine	0.55	-0.87	0.0022	0.290	Tyrosine metabolism
Diacylglycerol -DG 66-1	0.77	-0.38	0.0051	0.290	Glycerolipid metabolism
Pyroglutamic acid	0.64	-0.65	0.0052	0.290	Glutathione metabolism
Pyrrolidonecarboxylic acid	0.64	-0.65	0.0052	0.290	D-Glutamine and D-glutamate metabolism
Diacylglycerol -DG 64-1	0.89	-0.17	0.0071	0.290	Glycerolipid metabolism
Isovalerylglutamic acid	0.70	-0.52	0.0077	0.290	Isovaleryl-CoA Dehydrogenase
Glyceraldehyde	0.68	-0.56	0.0089	0.290	Glycerolipid metabolism
Diacylglycerol -DG 61-1	0.93	-0.10	0.0090	0.290	Glycerolipid metabolism
1-O-eicosanoyl-Cer d18-1,16-0	0.85	-0.23	0.0094	0.290	Sphingolipid
PC 22-4,21-0	0.84	-0.24	0.0101	0.290	Glycerophospholipid metabolism
Cholesteryl ester - CE 31-0	0.83	-0.27	0.0103	0.290	Sterol Lipid metabolism
Phosphoglycolic acid	0.66	-0.61	0.0104	0.290	Glyoxylate and dicarboxylate metabolism
Cer d45-1	0.82	-0.28	0.0104	0.290	Sphingolipid
Diacylglycerol 60-0	0.87	-0.21	0.0117	0.290	Glycerolipid metabolism
Diacylglycerol -DG P-44-4	0.80	-0.32	0.0119	0.290	Glycerolipid metabolism
Cer d51-1	0.84	-0.25	0.0125	0.290	Sphingolipid
1-O-tricosanoyl-Cer d18-1,18-0	0.85	-0.23	0.0125	0.290	Sphingolipid
Methyldeoxycytidine	0.74	-0.43	0.0132	0.290	DNA methyltransferase
Diacylglycerol -DG 64-0	0.82	-0.29	0.0147	0.290	Glycerolipid metabolism
GluCer d39 -0	0.90	-0.16	0.0152	0.290	Sphingolipid
DeoxyCer m18-0,20-0	0.86	-0.22	0.0160	0.290	Sphingolipid
Phyto-Cer t48-1	0.86	-0.22	0.0179	0.290	Sphingolipid
O-tricosanoyl-N-hexadecanoyl-sphing-4-enine	0.90	-0.15	0.0181	0.290	Sphingolipid
PE 40-2	0.79	-0.34	0.0181	0.290	Glycerophospholipid metabolism
Diacylglycerol -DG P-49-0	0.88	-0.19	0.0187	0.290	Glycerolipid metabolism
Deoxy-Cer m18-0,26-0	0.83	-0.27	0.0200	0.290	Sphingolipid
PA 49-4	0.88	-0.19	0.0205	0.290	Glycerophospholipid metabolism
Diacylglycerol P-51 -0	0.83	-0.27	0.0226	0.290	Glycerolipid metabolism
Diacylglycerol -DG P-43-0	0.82	-0.29	0.0234	0.290	Glycerolipid metabolism

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Diacylglycerol -DG P-39-0	0.80	-0.32	0.0242	0.290	Glycerolipid metabolism
Phyto-Cer t53-1	0.90	-0.15	0.0243	0.290	Sphingolipid
Diacylglycerol -DG 46-5	0.80	-0.31	0.0249	0.290	Glycerolipid metabolism
PS 43-2	0.78	-0.35	0.0253	0.290	Aminoacyl-tRNA biosynthesis
Diacylglycerol -DG P-50-0	0.85	-0.23	0.0258	0.290	Glycerolipid metabolism
Cer d50-2	0.84	-0.26	0.0284	0.290	Sphingolipid
L-histidine	0.78	-0.35	0.0299	0.290	Aminoacyl-tRNA biosynthesis
N-succinyl-2-amino-6-ketopimelate	0.77	-0.37	0.0300	0.290	Lysine metabolism
PA 52-4	0.82	-0.28	0.0302	0.290	Glycerophospholipid metabolism
Dopamine	0.72	-0.47	0.0302	0.290	Tyrosine metabolism
Triacylglycerol - TG 21-0,21-0,21-0	0.85	-0.23	0.0303	0.290	Glycerolipid metabolism
PhytoLacCer t50 -0	0.81	-0.31	0.0308	0.290	Sphingolipid
Diaceylglycerol P-36 -3	0.79	-0.33	0.0308	0.290	Glycerolipid metabolism
Diacylglycerol -DG P-48-0	0.89	-0.17	0.0316	0.290	Glycerolipid metabolism
PE 49-4	0.85	-0.23	0.0325	0.290	Glycerophospholipid metabolism
PI P-36-4	0.70	-0.51	0.0337	0.290	Glycerophospholipid metabolism
N2,n2-dimethylguanosine	0.76	-0.40	0.0342	0.290	Amino-acyl tRNA Degradation
S-Succinyldihydrolipoamide	0.68	-0.57	0.0344	0.290	Citrate cycle (TCA cycle)
Diacylglycerol -DG P-48-4	0.78	-0.35	0.0346	0.290	Glycerolipid metabolism
PC 40-3	0.87	-0.20	0.0381	0.313	Glycerophospholipid metabolism
PA 43-2	0.78	-0.36	0.0395	0.319	Glycerophospholipid metabolism
Triacylglycerol - TG 15-0,18-1,14-1	0.93	-0.10	0.0418	0.323	Glycerolipid metabolism
Diacylglycerol -DG 67-0	0.81	-0.30	0.0425	0.323	Glycerolipid metabolism
PA O-41-0	0.80	-0.32	0.0436	0.323	Glycerophospholipid metabolism
Glutaminyl-arginine	0.58	-0.78	0.0449	0.323	Amino acid degradation or cell-signaling
Acetylcysteine	0.77	-0.38	0.0456	0.323	Glutathione metabolism
Dopamine quinone	0.64	-0.64	0.0457	0.323	Tyrosine metabolism
Epinephrine sulfate	0.87	-0.21	0.0461	0.323	Tyrosine metabolism
PC 39-6	0.91	-0.14	0.0463	0.323	Glycerophospholipid metabolism
Diacylglycerol -DG 57-0	0.85	-0.24	0.0468	0.323	Glycerolipid metabolism
Glutamylcysteine	1.23	0.30	0.0472	0.323	Glutathione metabolism
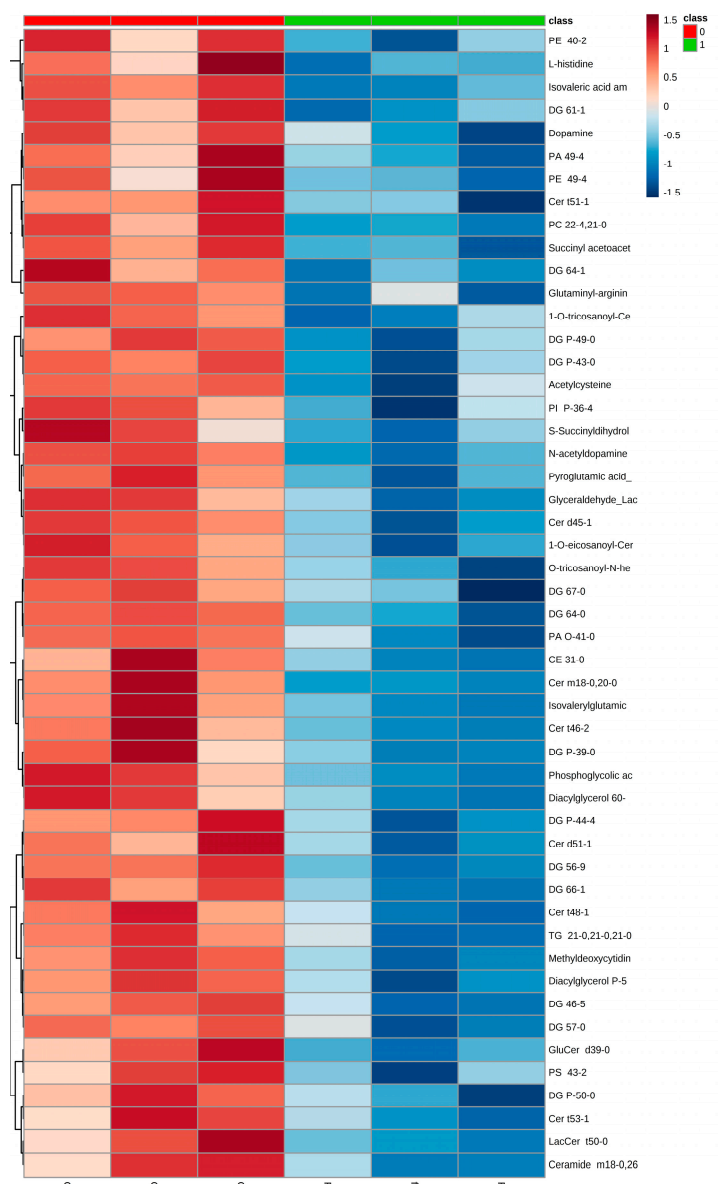
Figure S1. Heatmap of metabolite levels resulted as a function of FK866 treatment obtained via LC/MS. The following abbreviations were used: CE, Cholesteryl Ester, FA, Fatty Acid; PE, Phosphatidylethanolamine; PC, Phosphatidylcholine; PS, Phosphatidylserine; PA, Phosphatyidic Acid; PI, Phosphoinositol; PIP, Phosphoinositol monophosphates; PIP2, Phosphoinositol bisphosphates; DG, Diglyceride, TG, Triglyceride; MG, Monoglyceride; SM, Sphingomyelin; Cer, Ceramide; GluCer, Glucosylceramide; LacCer, Lactosylceramide; CAR, Carnitine; NAT, N-acyltaurine.
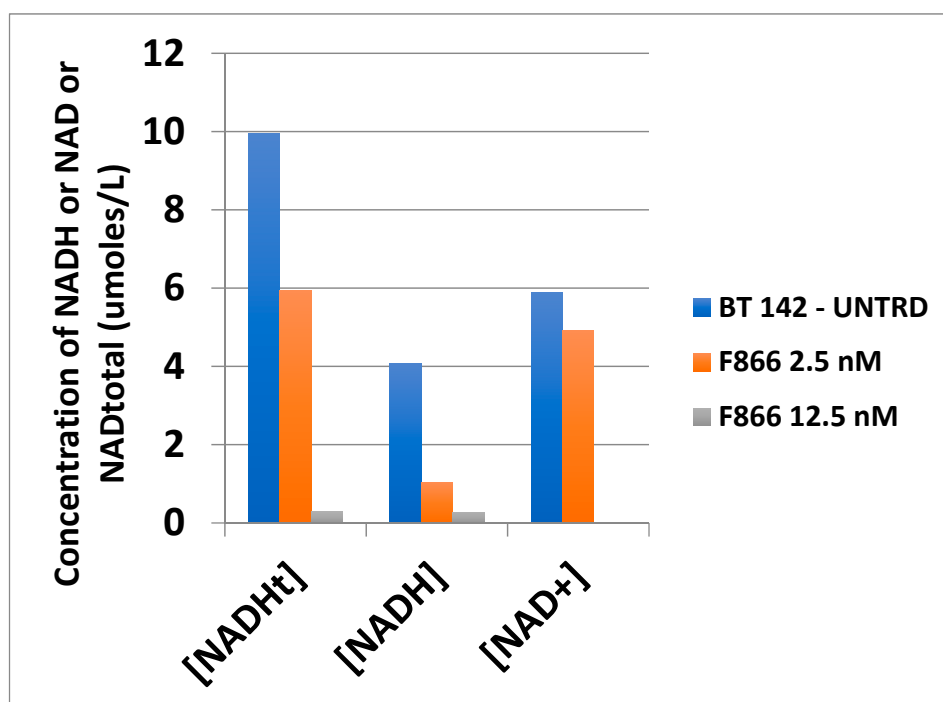
Figure S2. FK866 decreases the concentration of all NADH drastically in cells obtained via LC/MS. Total NADHt as well as the reduced and oxidized forms of NAD are decreased significantly in the cell after the treatment with FK866 (orange and grey bars). Levels of NADH in the untreated BT142 cell are shown in blue, low dose FK866 is shown in orange while high dose FK866 is shown in grey.